

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72  
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71  
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein; 6.70  
 445363; NM\_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70  
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63  
 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59  
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57  
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57  
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55  
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete; 6.55  
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55  
 422785; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51  
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49  
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A; 6.44  
 427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42  
 430280; AA381258; Hs.237868; interleukin 7 receptor; interleukin 7 receptor; 6.42  
 432938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42  
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40  
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3\_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3\_HUMAN TUBBY; 6.40  
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39  
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39  
 441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38  
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34  
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34  
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypept; 6.31  
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright; 6.31  
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mis5, S. pombe) 6; minichromosome maintenance deficient (mi; 6.31  
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30  
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30  
 415829; AW450198; Hs.163742; ESTs; ESTs; 6.28  
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26  
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25  
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25  
 428918; AL036967; Hs.2324; protamine 2; protamine 2; 6.24  
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19  
 424415; NM\_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19  
 407245; X90568; Hs.172004; titin; titin; 6.18  
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18  
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16  
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13  
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12  
 430521; NM\_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10  
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10  
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino; 6.09  
 402260; ; NM\_001436; Homo sapiens fibrillarin (FBL), mRNA, transcript (FBL), mRNA; NM\_001436; Homo sapiens fibrillarin (FBL); 6.09  
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05  
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IF-6-16); interferon, alpha-inducible protein (clo; 6.04  
 402678; ; Target Exon; Target Exon; 6.03  
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01  
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01  
 420596; NM\_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01  
 420676; AI434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00  
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99  
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98  
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98  
 413313; NM\_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95  
 417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94  
 449569; AI656634; Hs.195389; ESTs; ESTs; 5.92  
 436576; AI458213; Hs.77542; ESTs; ESTs; 5.90  
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89  
 420005; AW271106; Hs.133294; ESTs; ESTs; 5.89  
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88  
 403171; ; C2001472; gij5809678[gijAAB41848.2] (U64675) sperm membrane protein BS-63 [Homo sapiens]; C2001472; gij5809678[gijAAB41848.2] (U64; 5.87  
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87  
 406137; ; NM\_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA, VERSION NM\_000178.1 GI; NM\_000179; Homo sapiens mutS (E. coli) h; 5.85  
 423787; AJ295745; Hs.236204; nuclear pore complex protein; nuclear pore complex protein; 5.85  
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84  
 452796; AB011100; Hs.30666; KIAA0528 gene product; KIAA0528 gene product; 5.84  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80  
 447359; NM\_012093; Hs.18268; adenylate kinase 5; adenylate kinase 5; 5.79  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78  
 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1\_HUMAN ALU S; 5.75  
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5\_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5\_HUMAN LEUKE; 5.74  
 436251; BE515055; Hs.296585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73  
 421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71  
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69  
 425159; NM\_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspart; 5.69  
 401704; ; NM\_021195; Homo sapiens claudin 6 (CLDN6), mRNA, VERSION NM\_020982.1 GI; NM\_021195; Homo sapiens claudin 6 (CLDN6); 5.66  
 425358; AL079658; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin assoc; 5.65  
 402677; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.64  
 409264; NM\_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63  
 432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63  
 409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63  
 430252; AI638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61  
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61  
 452816; AA131789; Hs.61509; ESTs; ESTs; 5.60  
 402679; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.59  
 414291; AI289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58  
 453028; AB006532; Hs.31442; RecQ protein-like 4; RecQ protein-like 4; 5.58  
 453905; NM\_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56  
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-assoc; 5.55  
 419660; BE280337; Hs.194653; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino ; 5.55  
 446979; AI654443; Hs.197683; ESTs; ESTs; 5.54  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kin; 5.53  
 418962; AA714835; Hs.271863; ESTs; ESTs; 5.53  
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 5.52  
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); integrin, alpha L (antigen CD11A (p180); 5.52  
 449322; AI638616; Hs.196566; ESTs; ESTs; 5.51  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51  
 415141; AA189099; Hs.26817; ESTs, Weakly similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7\_HUMAN ALU S; 5.48  
 454048; H05626; Hs.6921; ESTs; ESTs; 5.46  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45  
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 fis, clone HE; 5.44  
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44  
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisi; 5.44  
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class ; 5.44  
 427668; AA289760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43  
 449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22802 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 5.41  
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40  
 450746; D82673; Hs.278589; general transcription factor II, i; general transcription factor II, i; 5.40  
 425966; NM\_001761; Hs.1973; cyclin F; cyclin F; 5.39  
 418134; AA397769; Hs.86617; ESTs; ESTs; 5.38  
 432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37  
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, m; 5.36  
 428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.; 5.35  
 406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 5.34  
 415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII); 5.33  
 448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor; 5.32  
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 5.32  
 429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32  
 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A; 5.30  
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30  
 422997; BE018212; Hs.122808; DNA replication factor; DNA replication factor; 5.29  
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosop; 5.28  
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26  
 416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer anti; 5.21  
 450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20  
 409670; AJ368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20  
 429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19  
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 doma; 5.19  
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 5.16  
 437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-asso; 5.15  
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15  
 436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor t; 5.14  
 426752; X69490; Hs.172004; titin; titin; 5.13  
 415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2; 5.13  
 400263; ; Hs.75309; Eos Control; Eos Control; 5.13  
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin alpha; 5.12  
 427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10  
 407347; AA829847; ; gb:od40d07.s1 NCL\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gb:od40d07.s1 NCL\_CGAP\_GCB1 Homo sapiens; 5.10  
 458933; AI638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10  
 450431; AW136797; Hs.266041; ESTs; ESTs; 5.09  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08  
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-recept; 5.08  
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05



- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03  
 417856; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03  
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02  
 433592; NM\_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog) ; 5.02  
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha 2 (RAG cohort 1, importin alpha 1); 5.00  
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00  
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99  
 402145; ; Target Exon; Target Exon; 4.99  
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99  
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, cont; 4.98  
 419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97  
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97  
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96  
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96  
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94  
 426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91  
 440129; AA865818; Hs.369523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-like; 4.91  
 453922; AF053306; Hs.35708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1 ; 4.90  
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88  
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88  
 437162; AW005505; Hs.5454; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87  
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG51) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIG; 4.87  
 421350; AF030168; Hs.278188; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 4.87  
 409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86  
 424304; NM\_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86  
 437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase tra; 4.84  
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83  
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82  
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82  
 424081; NM\_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81  
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81  
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor ( ; 4.81  
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80  
 409101; NM\_004297; Hs.50512; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79  
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79  
 447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79  
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78  
 448950; AF286887; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78  
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C; 4.78  
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76  
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 4.76  
 421905; AI660247; Hs.32699; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H; 4.75  
 413880; AI660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74  
 418355; L42563; Hs.1165; ATPase, H<sup>+</sup> transporting, nongastric, alpha polypeptide; ATPase, H<sup>+</sup> transporting, nongastric, alp; 4.74  
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74  
 428024; Z29057; Hs.2238; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74  
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72  
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72  
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70  
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (barnam); chondroitin sulfate proteoglycan 6 (barnam); 4.70  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69  
 449475; AI348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69  
 420062; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69  
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIIB (25-hy; 4.69  
 436856; AI469355; Hs.127310; ESTs; ESTs; 4.68  
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds. ; gb:Human transketolase-like protein gene; 4.67  
 411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67  
 426726; AA488915; Hs.171955; trophinin associated protein (tastin); trophinin associated protein (tastin); 4.67  
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67  
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66  
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65  
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, ; 4.65  
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64  
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64  
 415724; NM\_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63  
 435045; BE297155; Hs.143898; ESTs; ESTs; 4.62  
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62  
 414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62  
 436685; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62  
 449515; AI653378; Hs.302012; ESTs; ESTs; 4.61  
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61  
 420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61  
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61  
 413441; AI929374; Hs.75367; Src-like-adaptor; Src-like-adaptor; 4.60  
 456847; AI360456; Hs.86088; ESTs; ESTs; 4.58  
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57  
 426935; NM\_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57  
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56  
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L ORF; 4.55

- 443068; A1188710; Hs.374480; ESTs; ESTs; 4.55  
 441607; NM\_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54  
 453227; AW135862; Hs.243991; ESTs; ESTs; 4.52  
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51  
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascin homolog like); singed (Drosophila)-like (sea urchin fas); 4.51  
 453613; F06838; Hs.374476; ESTs; ESTs; 4.50  
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H); 4.50  
 412507; L36645; Hs.73964; EphA4; EphA4; 4.50  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49  
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo); 4.49  
 406547; ; Target Exon; Target Exon; 4.49  
 443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48  
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47  
 448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47  
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46  
 446236; NM\_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46  
 429150; AF120103; Hs.197368; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46  
 420340; NM\_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 complex); CD32 antigen, zeta polypeptide (TIT3 com); 4.46  
 413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt); 4.44  
 421819; NM\_013403; Hs.108665; zinedin; zinedin; 4.44  
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44  
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, Dr; 4.43  
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; ESTs, Highly similar to A35661 DNA excis; 4.43  
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42  
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42  
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42  
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic); 4.42  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40  
 424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39  
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37  
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35  
 400440; X83957; Hs.83870; nebulin; nebulin; 4.35  
 437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34  
 430478; NM\_014349; Hs.241535; apolipoprotein L, 3; apolipoprotein L, 3; 4.34  
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33  
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33  
 415995; NM\_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33  
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30  
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfam; 4.29  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29  
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled recepto; 4.28  
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28  
 426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28  
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component; 4.27  
 437908; A1082424; Hs.351043; ESTs; ESTs; 4.27  
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27  
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26  
 439334; A1148976; Hs.112062; ESTs; ESTs; 4.26  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25  
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24  
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24  
 447528; A1612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22  
 449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22  
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22  
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22  
 425356; BE244879; Hs.155939; inositol polyphosphate 5-phosphatase, 145kD; inositol polyphosphate 5-phosphatase, 14; 4.22  
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21  
 444535; AF011466; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21  
 417088; M54915; Hs.81170; pim-1 oncogene; pim-1 oncogene; 4.20  
 421707; NM\_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20  
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20  
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18  
 418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18  
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17  
 413686; A1469213; Hs.71404; ESTs; ESTs; 4.17  
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus; 4.16  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16  
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15  
 409421; AA199883; Hs.67624; ESTs; ESTs; 4.15  
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14  
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14  
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to M; 4.13  
 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbonate; 4.13  
 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitochond; 4.13  
 420253; A1656055; Hs.56200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 9; 4.12  
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12  
 400205; Hs.81848; NM\_005265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM\_005265; Homo sapiens RAD21 (S. pombe); 4.12  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11  
 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10  
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31611 hypothetical; 4.10  
 432512; NM\_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to ; 4.10  
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09  
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription factor; 4.09  
 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09  
 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G pr; 4.09  
 425003; AF119046; Hs.154149; apurinic/aprimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/aprimidinic endonuclease(APEX); 4.08  
 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08  
 423841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-receptor; 4.08  
 452069; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08  
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker; 4.07  
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic; 4.07  
 424517; AJ539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12169 fis, clone MA; 4.07  
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe co; 4.06  
 446791; AJ632278; Hs.195922; ESTs; ESTs; 4.06  
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), cata; 4.06  
 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta; 4.06  
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory su; 4.06  
 425923; NM\_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, de; 4.05  
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04  
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrat; 4.04  
 439176; AJ446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 pr; 4.04  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule; 4.04  
 410068; A1633888; Hs.58435; FYN-binding protein (FYN-120/130); FYN-binding protein (FYN-120/130); 4.03  
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03  
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03  
 451050; AW937420; Hs.351869; ESTs; ESTs; 4.02  
 449667; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02  
 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01  
 437527; AJ241019; Hs.145644; ESTs; ESTs; 4.01  
 425118; AU076511; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase; 4.00  
 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF1210; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00  
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor; 4.00  
 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99  
 433577; AW007080; Hs.284192; ESTs; ESTs; 3.99  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrolase; 3.99  
 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99  
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98  
 402398; ; C19000263.gi|3108023|gb|AAC15755.1| (AC004659) BC62940.2 [Homo sapiens] |j65335; C19000263.gi|3108023|gb|AAC15755.1| (AC0; 3.97  
 408414; AJ114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.97  
 415012; NM\_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97  
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kin; 3.95  
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial ; 3.95  
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine pr; 3.95  
 430770; AA765694; Hs.123296; ESTs; ESTs; 3.94  
 442994; AJ026718; Hs.16954; ESTs; ESTs; 3.94  
 420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor, NK-p46); lymphocyte antigen 94 (mouse) homolog (a; 3.94  
 438456; AA913381; Hs.279763; ESTs; ESTs; 3.94  
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A); 3.93  
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93  
 424829; NM\_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR super; 3.93  
 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93  
 425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93  
 421910; NM\_014568; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associat; 3.92  
 413761; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenase; 3.92  
 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92  
 400262; ; Hs.75309; Eos Control; Eos Control; 3.90  
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90  
 435206; AJ432364; Hs.160594; ESTs; ESTs; 3.90  
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90  
 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90  
 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89  
 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89  
 407013; U36537; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89  
 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88  
 400261; ; Hs.1802; Eos Control; Eos Control; 3.88  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88  
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glut; 3.87  
 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87  
 417767; BE242241; Hs.82542; acylglycerol hydrolase (neutrophil); acylglycerol hydrolase (neutrophil); 3.87  
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor; 3.87

- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86  
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86  
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86  
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86  
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86  
 5 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85  
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85  
 418978; T85295; Hs.268606; ESTs; ESTs; 3.84  
 10 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84  
 442980; AAB57025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84  
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84  
 434589; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83  
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83  
 15 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83  
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82  
 449433; A1672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82  
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81  
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80  
 20 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80  
 422753; A1928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79  
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79  
 428023; AL039843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79  
 25 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79  
 439668; A1091277; Hs.302634; frizzled (Drosophila) homolog 6; frizzled (Drosophila) homolog 6; 3.79  
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78  
 425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78  
 30 423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78  
 429687; A1675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77  
 414177; A1351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77  
 35 445817; NM\_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77  
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76  
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repai; 3.76  
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76  
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76  
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor, alpha polypeptide); Integrin, alpha 5 (fibronectin receptor; 3.75  
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75  
 40 405484; ; C3002124\*<sup>g</sup>g[12737280]ref[XP\_006682.2] keratin 18 [Homo sapiens][16633; C3002124\*<sup>g</sup>g[12737280]ref[XP\_006682.2] k; 3.75  
 450998; BE387149; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75  
 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75  
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74  
 418884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 45 to ALU8\_HUMAN ALU S; 3.74  
 453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell; 3.74  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74  
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74  
 50 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74  
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activ; 3.73  
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypotheti; 3.73  
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73  
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73  
 55 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpo; 3.71  
 423523; AW299828; Hs.193580; ESTs; ESTs; 3.71  
 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71  
 446336; R53848; Hs.44976; ESTs; ESTs; 3.70  
 60 422083; NM\_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70  
 416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70  
 442200; AW590572; Hs.235768; ESTs; ESTs; 3.70  
 414280; BE410769; Hs.75873; zyxin; zyxin; 3.69  
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69  
 65 415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69  
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69  
 446522; NM\_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69  
 422785; A1824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68  
 401083; ; NM\_016582\*<sup>g</sup>g[12737280]ref[XP\_006682.2] keratin 18 [Homo sapiens][16633; C3002124\*<sup>g</sup>g[12737280]ref[XP\_006682.2] k; 3.75  
 413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68  
 70 452690; A1536070; Hs.15085; ESTs; ESTs; 3.68  
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2\_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 to ALU2\_HUMAN ALU S; 3.68  
 415010; NM\_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68  
 428579; NM\_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68  
 75 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66  
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG Islands. Contains the NIFS gene for  
 cysteine desulfurase, two genes for novel proteins and the gene for thar; Human DNA sequence from clone RP11-353C1; 3.66  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65  
 414226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;  
 80 3.65  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65  
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C; 3.65  
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN20), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

- 451558; NM\_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65  
 450295; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyros; 3.64  
 437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA657999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64  
 414029; BE297731; Hs.175709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep; 3.64  
 444388; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64  
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63  
 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63  
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63  
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc; 3.62  
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62  
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62  
 411165; NM\_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62  
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62  
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61  
 438795; AA825792; Hs.377119; gb:od84b11.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCI\_CGAP\_Ov2 Homo sapiens ; 3.61  
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61  
 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60  
 423217; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60  
 444985; AI677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60  
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM\_023929); zinc finger protein RINZF (NM\_023929); 3.59  
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59  
 415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel  
 glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59  
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57  
 458715; AK000973; Hs.1705; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57  
 423576; NM\_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57  
 440270; NM\_015966; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57  
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57  
 404976; ; NM\_014323; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM\_014323; Homo sapiens zinc finger prot; 3.57  
 449656; AA002008; Hs.188633; ESTs; ESTs; 3.56  
 413795; AL040178; Hs.142003; ESTs; ESTs; 3.56  
 406859; AI581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56  
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56  
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; 3.56  
 424263; MT77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)  
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high affi; 3.55  
 443456; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; inducible Ik; 3.55  
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55  
 450931; N25158; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55  
 425836; AW955696; Hs.90960; ESTs; ESTs; 3.54  
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54  
 440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54  
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53  
 421652; NM\_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53  
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); transformer-2 alpha (htra-2 alpha); 3.53  
 424870; T15545; Hs.244624; ESTs; ESTs; 3.52  
 442794; AJ744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51  
 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.1 - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51  
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51  
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51  
 421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50  
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50  
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50  
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50  
 429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49  
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211\_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211\_HUMAN ZINC; 3.47  
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44  
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07  
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77  
 430439; AL133561; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76  
 435897; AF269223; Hs.128322; t-complex 11 (a murine tcp homolog); t-complex 11 (a murine tcp homolog); 2.53  
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46  
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35  
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33  
 426527; AF012359; Hs.195685; ESTs; ESTs; 2.12  
 438983; AF085884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precursor; 2.07  
 425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99  
 433724; AI827749; Hs.144924; serine/threonine protein kinase SSKT; serine/threonine protein kinase SSKT; 1.68  
 420710; NM\_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
------	------------	-----------

417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
432407	MH1429_12	BG036675 BF772005 BF771866 BG960385 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
5		AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279
		BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 B1861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
		AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 A1075321 L13823 AA216700 BF771864 AW861859
		BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
		AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
434414	35978_1	AF134164 BF809407 AA218567 BF842863 A1267168 BF876178 BG999253 AW861851 AW858362 A1817548 BF771300 AA113928 AA223422
10		AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
		AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 A1694265 AA045564 BG950256 A1829309 BG987850 BE093175
		BF854337
427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
427521	513212_1	AW973352 BF229299 AW016853 BF059130 A1651829 BE551767 AA558414 A1339359 BF059601 A1961162 A1341422 A1206248 A1206165
15		AA548736 AA768578 A1539081 AW025957 AA736837 N79575 AW594357 AA480892
407347	810943_1	T23514 A1655785
430439	6750_2	AL133561 AL117481 AL122069 AW439292 A1968826 ALO41090

TABLE 57C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
25	Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768, 139702-139893, 140475-14059
402260	3399665	Minus	113765-113910, 115653-115765, 116808-11694
402678	8113438	Plus	37395-37514, 37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3097841	Plus	24712-25374
35	402677	Plus	22135-22309, 23063-23238
	402679	Plus	132079-132216
	402145	Plus	113086-114800
	406547	Minus	172780-174358
40	402398	Minus	24019-24973
	405484	Plus	199214-199579, 199572-199920, 200262-20049
	401083	Plus	33192-33360
	404976	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

55	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
	Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
60	UniGene Title:	UniGene gene title
	R1	90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Prod.Domains; R1

65	430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; 35.25
	422282; AF019225; Hs.114309; apolipoprotein L; MoLA_ExcB; TM=Y; SS=M; 33.25
	414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phospho; TM=M; SS=Y; 31.68
	415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3; aldo_ket_red; TM=M; 31.04
	417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none, none; 28.50
70	439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 27.43
	417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 25.98
	413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT; none; 25.38
	418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT; none; 25.28
	425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB_DNA_topoisolv_HATPase_c; SS=M; 23.58
75	421733; AL119571; Hs.1420; fibroblast growth factor receptor 3 (ach; ig, pkinase; TM=Y; SS=M; 21.24
	424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1; TM=Y; SS=M; 20.45
	447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 19.78
	408243; Y00787; Hs.624; interleukin 8; HLH_PAS; IL8; TM=M; 18.90
	427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; 18.75
80	410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; SS=M; 18.63
	444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothet; Collagen; TM=M; SS=M; 18.60
	452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig_Rhbd_glycop; TM=Y; SS=M; 18.55
	415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4; LM; TM=M; 18.25



- 413132; NM\_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic); PKI;SS=M; 17.73  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig;TM=Y;SS=M; 17.68  
 450746; D82673; Hs.278589; general transcription factor II, i; none;SH3,PX; 17.12  
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase;PLAT;TM=M; 16.88  
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone\_rec,zf-C4;TM=M; 16.78  
 439941; AI392640; Hs.18272; amino acid transporter system A1; Aa\_trans;TM=Y; 16.75  
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 16.56  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys.ig.FAD\_Synth,ldh,ldh\_C,kinase;SS=M; 16.43  
 414883; AA926960; CDC28 protein kinase 1; CKS; 16.20  
 438091; AW373062; nuclear receptor subfamily 1, group I, m; hormone\_rec,zf-C4,none; 15.80  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH\_Ib,Lipase\_GDSL;TM=M; 15.70  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,kinase;TM=M; 15.63  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 15.45  
 434293; NM\_004445; Hs.3796; EphB6; EPH\_Ibd,fn3,kinase,SAM;TM=Y;SS=M; 15.43  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF,lectin\_c,sushi;TM=M;SS=M; 15.28  
 443991; NM\_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK\_channel,ion\_trans;TM=Y;SS=M; 15.10  
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 14.90  
 432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib); CBM\_21;TM=M; 14.80  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; kinase;TM=M; 14.73  
 429345; R11141; Hs.199695; hypothetical protein; K\_tetra,SAM; 14.58  
 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig,Isodh,Ribosomal\_L6,F-box;TM=Y;SS=M; 14.55  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; PAAD\_DAPIN,HIN;TM=M; 14.53  
 446008; NM\_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35  
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 14.18  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 14.13  
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y\_phosphatase,Band\_41,PDZ;SS=M; 13.90  
 426657; NM\_015865; Hs.171731; solute carrier family 14 (urea transport; UT;TM=Y; 13.83  
 428157; AJ738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80  
 400843; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 13.78  
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC\_tran,CoaE;TM=M; 13.38  
 432314; AA533447; Hs.312989; ESTs; Xlink,none; 13.25  
 413109; AW389845; Hs.110855; ESTs; PHO4,none; 13.15  
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,kinase;TM=M; 13.13  
 426490; NM\_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M; 12.93  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,kinase,Recep\_L\_domain,Furin-like,kinase,Recep\_L\_domain,Peptidase\_M24; 12.43  
 440249; AJ246590; Hs.249175; ESTs; TatD\_DNase,kinase,death,none; 12.38  
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38  
 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 12.03  
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR\_c6,granulin,CUB,Keratin\_B2,TIL;TM=M;SS=M; 11.93  
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 f1s, clone NT; Aa\_trans,none; 11.88  
 408000; L11690; Hs.198689; bulous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh\_C,CH,AlP3;TM=M; 11.88  
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; rrm,hormone\_rec,zf-C4,sugar\_tr; 11.85  
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb\_DNA-binding,THF\_DHG\_CYH,THF\_DHG\_CYH\_C,CAP\_GLY,AAA,LON,Peptidase\_C9,bZIP,M,xan\_ur\_permease,HCO3\_cotransp;TM=M; 11.69  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus); 7tm\_1,7tm\_2;TM=Y;SS=M; 11.50  
 426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp58612022 (f; none;TM=Y;SS=M; 11.48  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C,IMPDH\_N,CBS,integrin\_B,Ricin\_B\_lectin; 11.38  
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23  
 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18  
 409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02  
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate\_kin;TM=M; 10.78  
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofillin\_ADF;SS=M; 10.63  
 427654; AA410183; Hs.137475; ESTs; ion\_trans,vwc,IGFBP,isp\_1; 10.58  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 10.53  
 447355; BE383676; Hs.334; Rho guanine nucleotide exchange factor ( ; SH3,PH,RhoGEF;TM=M; 10.53  
 449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone K; none,none; 10.52  
 436856; AI469355; Hs.127310; ESTs; kinase,rrm;TM=M; 10.48  
 451035; AU076785; Hs.430; plasmin 1 (I isoform); efhand,CH,Adaptin\_N;SS=M; 10.38  
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; integrin\_B,EGF,PSI;TM=Y;SS=M; 10.35  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin\_A,FG-GAP;TM=Y;SS=M; 10.34  
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD\_DAPIN,NA;NA; 10.25  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5;TM=Y;SS=M; 10.18  
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365012.1 [H.s.a; GPS,7tm\_2;TM=Y; 10.13  
 400752; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 10.08  
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M; 10.05  
 426728; NM\_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,ig,kinase,PH,spectrin,RhoGEF;TM=M; 10.05  
 400496; ; ENSP00000224716; GTP-binding protein SAR; none;TM=Y; 10.01  
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate\_kin;TM=M; 10.00  
 404568; ; NM\_022071; Homo sapiens hypothetical pro; SH2;TM=M; 10.00  
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 9.93  
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,art,ras,7tm\_1;TM=M; 9.90  
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 9.90  
 424954; NM\_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M; 9.88  
 452269; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; kinase;TM=M; 9.85  
 439223; AW238299; Hs.250518; UL16 binding protein 2; ldl\_recept\_a,PKD,MHC\_1;TM=M;SS=Y; 9.83  
 429238; NM\_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y\_phosphatase;TM=Y;SS=M; 9.80  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y\_phosphatase;TM=M; 9.73  
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y\_phosphatase,DSPc;TM=M; 9.72  
 403912; ; C5000394; g[i12737280]rel[XP\_006682.2] k; none;TM=M; 9.70  
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 9.70

- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase;TM=M; 9.68  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinasin,fn3,Y\_phosphatase;TM=M; 9.63  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M; 9.63  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3\_P14\_kinase,FAT,FATC;TM=M; 9.55  
 430259; BE550182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 9.50  
 428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none;TM=M; 9.50  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M; 9.50  
 448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST\_C,Ets,SAM\_PNT,ABC2\_membrane,myosin\_head,IQ,Myosin\_N,bZIP,zf-  
 C2H2,PHD,BTB,TFIS,AT\_hook,SAM;TM=M; 9.50  
 414911; NM\_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40,homeobox,LM;TM=M; 9.48  
 451295; AJ557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase,DAG\_PE-bind,pkinase\_C,OPR;none; 9.45  
 402328; ; Target Exon; pkinase;TM=M; 9.44  
 443710; AJ928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha;none; 9.42  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 9.42  
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS\_kinase,ATP-sulfurylase,PRK,Thymidylate\_kin;SS=M; 9.40  
 418827; BE327311; Hs.47166; HT021; none;TM=M; 9.40  
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1\_HUMAN CALCI; pkinase;none; 9.35  
 433376; AJ249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE\_p10,ICE\_p20;SS=M; 9.28  
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR\_c6;TM=Y;SS=M; 9.25  
 430024; AJ808780; Hs.227730; integrin, alpha 6; integrin\_A\_FG-GAP;TM=Y;SS=M; 9.23  
 452696; AJ826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate\_kin,PDZ,SH3; 9.13  
 434263; N34895; Hs.44648; ESTs; ig;none; 9.13  
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal\_S14,ank,pkinase,death;none; 9.10  
 429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase,metallothio;TM=M;SS=M; 9.08  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,laminin\_Nterm,integrin\_B;SS=M; 9.08  
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22,Claudin;none; 9.07  
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE; 8.98  
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M; 8.93  
 438000; AJ825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M; 8.90  
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.90  
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.88  
 437056; AJ147061; ; gbokK33a11.s1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S; none,spectrin,SH3,PH,CH; 8.78  
 445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGap;TM=M; 8.78  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 8.70  
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.68  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 8.65  
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept\_Y\_phosphatase;SS=M; 8.65  
 430397; AJ924533; Hs.105607; bicarbonate transporter related protein; HCO3\_cotransp;TM=Y; 8.64  
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M; 8.60  
 442994; AJ026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal\_S14; 8.60  
 429109; ALD08637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M; 8.60  
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8\_HUMAN ALU S; none,7tm\_1; 8.55  
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG\_PE-bind,RBD; 8.43  
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none;none; 8.40  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 8.39  
 448209; AW160489; Hs.20709; tetraspan 5; transmembrane4;TM=Y;SS=M; 8.33  
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 8.33  
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase\_2;TM=M; 8.31  
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm\_1;TM=Y;SS=M; 8.30  
 445633; AJ453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK;none; 8.28  
 446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA,SKI;TM=M; 8.23  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none;none; 8.20  
 427274; NM\_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 8.18  
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none;none; 8.15  
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 8.15  
 417386; AL037228; Hs.82043; D123 gene product; NUDIX,secY,E1\_dehydrog,transket\_pyr;TM=Y;SS=M; 8.13  
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 8.10  
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 8.09  
 425424; NM\_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M; 8.08  
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin\_A;none; 8.05  
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo\_seg;TM=M;SS=M; 8.03  
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 8.03  
 404891; ; Target Exon; none;none; 7.95  
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none;none; 7.93  
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 7.93  
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 7.91  
 438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase,ABC1;none; 7.90  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13592 fis, clone PL; HLH,death,TNFR\_c6,Acyl-CoA\_hydro; 7.90  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan\_ur\_pemase,RA; 7.88  
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like,pkinase,Recep\_L\_domain,YLP;TM=Y;SS=M; 7.86  
 405036; ; NM\_021628; Homo sapiens arachidonate lip; lipoxygenase,complex1\_49kd,PLAT;TM=M; 7.83  
 418529; AW005695; Hs.250897; TRK-fused gene; Band\_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 7.83  
 431912; AJ660552; Hs.76549; ESTs, Weakly similar to A56154 Abi subst; none,Acyl-CoA\_dh,Acyl-CoA\_dh\_M,Acyl-CoA\_dh\_N; 7.80  
 432981; NM\_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS,Aa\_trans;TM=M; 7.78  
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo; Sec7,PH,ANF\_receptor,lig\_chan,WD40,IRK; 7.78  
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH,DAG\_PE-bind,PH,Involucrin,M;TM=M; 7.78  
 431183; NM\_005855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER\_Lumen\_recept;TM=M;SS=M; 7.78  
 400845; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 7.73  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran,M,SMC\_N,SMC\_C,DUF164;none; 7.73  
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ\_con,Y\_phosphatase,SH2; 7.70  
 403212; ; NM\_019595; Homo sapiens Intersectin 2 (IT; SH3,ethand,C2,PH,RhoGEF;TM=M; 7.70  
 441190; H09073; Hs.25046; ESTs; E1-E2\_ATPase,C,Calcium\_ATPase\_N,Hydrolase;none; 7.68

- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm\_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,ve,zf-B\_box;TM=Y;SS=M; 7.68
- 428840; M15990; Hs.194140; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,kinase;SS=M; 7.65
- 447898; AW969638; Hs.112318; 6.2 kd protein; none;none; 7.65
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN,HIN;SS=M; 7.63
- 5 401927; ; C17000914; gi8394367[ref]NP\_058549.1; s; none;; 7.60
- 407347; AA829847; ; gb:cd40407.s1 NCI\_CGAP\_GCB1 Homo sapiens; RhoGAP,SH2,kinase,POLO\_box,none; 7.58
- 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3,none; 7.57
- 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin\_A,PHO4,kinase,ubiquitin; 7.55
- 10 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase; ty; none;none; 7.55
- 421489; A1922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
- 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
- 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylatekinase,SRP54;TM=M; 7.50
- 430570; A1417881; Hs.292464; ESTs; 7tm\_2,Fz,Frizzled,none; 7.50
- 15 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
- 420676; A1434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG\_PE-bind,none; 7.48
- 444252; R21135; Hs.54985; ESTs; none;none; 7.47
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3,PI4\_kinase;TM=M; 7.47
- 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
- 20 418546; AA224827; ; gb:nc32g04.s1 NCI\_CGAP\_Pr2 Homo sapiens ; vwa,Integrin\_A,FG-GAP,none; 7.45
- 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43
- 452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypothet; none,kinase; 7.40
- 432407; AA221036; ; gb:z03f12.r1 Stratagene NT2 neuronal pr; DEAD,helicase\_C,rrm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp\_1,Ribosomal\_S21,rvp;TM=M; 7.40
- 25 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,kinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 7.40
- 421429; NM\_014922; Hs.104305; death effector filament-forming Ced-4-l; LRR,PAAD\_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
- 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone\_rec,zf-C4;SS=M; 7.38
- 430016; NM\_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
- 422813; AV656571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
- 30 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 ( ; none,spectrin,SH3,PH,CH; 7.25
- 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,kinase;TM=M; 7.24
- 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
- 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 7.19
- 407591; NM\_000910; Hs.37125; neuropeptide Y receptor Y2; 7tm\_1;TM=Y; 7.18
- 35 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
- 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
- 403344; ; NM\_000341; Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
- 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage\_CLC;TM=Y; 7.14
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar Jr;TM=Y;SS=M; 7.14
- 40 404875; ; NM\_022819; Homo sapiens phospholipase A2; phoslip;SS=M; 7.11
- 433618; AA602539; Hs.345494; ESTs; G-alpha\_A\_deaminase; 7.10
- 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate\_transp,STAS,HMG\_box; 7.08
- 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPSS;TM=M;SS=M; 7.05
- 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05
- 45 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm\_2,HRM,CSD;TM=Y;SS=M; 7.03
- 400211; ; NM\_003899; Homo sapiens PAK-interacting ; SH3,PH,RhoGEF,Terpene\_synth;TM=M; 7.03
- 438150; AA037534; Hs.342874; transforming growth factor, beta receptor; zona\_pellucida,none; 6.93
- 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M; 6.93
- 405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys\_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
- 50 415392; Z44067; Hs.10957; ESTs; PIP5K,none; 6.89
- 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo\_seg,none; 6.88
- 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic ; C2,PLA2\_B;TM=M; 6.85
- 427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2\_N,helicase\_C,Armadillo\_seg,HEAT;TM=M; 6.83
- 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20,DED;TM=M; 6.80
- 400158; ; ENSP00000244302; cDNA FLJ11591 fis, clone; Sm;SS=M; 6.78
- 55 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT\_bind,STAT\_prot,ion\_trans,PAC,PAS,none; 6.78
- 400844; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,IdL\_recept\_a,IdL\_recept\_b,granulin,BNR;TM=Y;SS=M; 6.73
- 457238; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase;; 6.73
- 404440; ; NM\_021048; Homo sapiens melanoma antigen; MAGE;TM=M; 6.73
- 60 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kin; Els,SAM\_PNT;TM=M; 6.70
- 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase;TM=M; 6.70
- 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
- 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate\_kin;SS=M; 6.64
- 408638; AW451353; Hs.173328; ESTs; B56,none; 6.63
- 65 408058; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
- 401057; BE563198; ; eukaryotic translation elongation factor; ion\_trans,IQ;TM=Y; 6.60
- 446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none;none; 6.60
- 400528; ; NM\_020975; Homo sapiens ret proto-oncoge; cadherin,kinase;TM=Y;SS=M; 6.58
- 418562; R60669; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
- 55 453826; AL138129; ; gb:DKFZp547F152\_r1 547 (synonym: htrf1); PK,PK\_C,none; 6.55
- 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C135 (fr,ABC\_tran,GTP\_EFTU,ABC\_membrane,none; 6.54
- 415088; AJ077288; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 6.50
- 453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5\_F8\_type\_C,kinase,Els,F5\_F8\_type\_C,kinase,Els; 6.47
- 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46
- 75 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46
- 441712; AW391927; Hs.7946; KIAA1288 protein; AIP3;TM=M; 6.44
- 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7tm\_1; 6.43
- 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY\_C;TM=M; 6.43
- 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
- 80 438941; AF075047; Hs.31864; ESTs; Ca\_channel\_B,SH3,arf,none; 6.40
- 441456; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB,none; 6.33
- 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothet; lipoxigenase,PLAT,none; 6.33
- 433255; AJ274270; Hs.96840; KIAA1527 protein; MHCK\_EF2\_kinase;TM=M;SS=M; 6.33
- 427801; AW979155; Hs.298275; amino acid transporter 2; Aa\_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin, BAG, Tropomyosin;; 6.30  
 438464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none, none; 6.30  
 453977; AA886006; Hs.250427; ESTs; pkinase, P2X\_receptor, E1-E2, ATPase, Hydrolase; 6.30  
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras, arf, PP2C; TM=M; 6.30  
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180KD); DNA\_gyraseB, DNA\_topoisolv, HATPase\_c, DNA\_gyraseB, DNA\_topoisolv, HATPase\_c; 6.29  
 404342; ; C7002192; gij7299207[gib]AAF54404.1; (AE0; none; TM=M; 6.27  
 409274; NM\_003930; Hs.52644; SKAP55 homologue; SH3, PH; SS=M; 6.25  
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1, PLM, MAT8; TM=Y; SS=M; 6.23  
 405429; ; Target Exon; Y\_phosphatase, none; 6.23  
 404975; AL042279; uncharacterized hypothalamus protein HT0; kringle; TM=Y; SS=M; 6.20  
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin, EGF, ig, Neuregulin, EGF, ig; 6.18  
 446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD, helicase, C, rm, Ndr, Cys\_kno1, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, lrp\_1, Ribosomal\_S21, rvp; TM=M; 6.18  
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3, z-C3HC4; TM=M; 6.15  
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none; TM=Y; 6.15  
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none, none; 6.14  
 447727; AI421079; tumor necrosis factor receptor superfamily; none, synaplobravin; 6.13  
 401536; ; NM\_002530; Homo sapiens neurotrophic tyr; ig, pkinase, LRR, LRRNT, LRRCT; TM=M; SS=M; 6.11  
 444317; AI140566; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H]; PAN, kringle, trypsin, PI-PLC-X, C2, SH2, PH, SH3, PI-PLC-Y, PAN; 6.10  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR, LY6, ET, PLA2\_inh; SS=M; 6.08  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; 6.08  
 450107; AI873287; Hs.257812; ESTs; ICE\_p20, DED; TM=M; 6.05  
 418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypotheti; z-C2H2, BTB, K\_tetra, Synlaxin, none; 6.05  
 408983; NM\_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC\_tran, ABC\_membrane, PRK, Bac\_export\_3; TM=Y; 6.05  
 439738; BE245502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, integrin\_B; TM=Y; 6.03  
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none, none; 6.03  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese, none; 6.03  
 446650; AB016625; Hs.15813; solute carrier family 22 (organic cation; sugar\_tr; TM=Y; SS=M; 6.03  
 405102; ; C15001220; gij4469558[gib]AAD21311.1; (AF; DAG\_PE-bind, PH, RhoGEF, DC1; SS=M; 6.03  
 400121; ; Eos Control; SH3, PH, RhoGEF, Terpene\_synth; TM=M; 6.03  
 415327; H22769; ; gbyrm54c02.r1 Soares infant brain 1N1B H; SH3, PDZ, Guanylate\_kin; SS=M; 6.03  
 404148; ; NM\_002944; Homo sapiens v-ros avian UR2 ; fn3, pkinase, DUF139; TM=Y; SS=M; 6.03  
 405531; ; Target Exon; PDZ, CARD, Guanylate\_kin; TM=M; 6.00  
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B) ; NDK, none; 6.00  
 427270; H47921; Hs.174139; chloride channel 3; voltage\_CLC, CBS, none; 5.99  
 423774; L39064; Hs.1702; interleukin 9 receptor; none; TM=M; SS=M; 5.98  
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked ; pkinase, TBC; 5.98  
 411040; AF007393; Hs.177574; protein-kinase, interferon-inducible dou; HLH; TM=M; 5.95  
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer, 7tm\_1, none; 5.88  
 453902; BE502341; Hs.3402; ESTs; none, none; 5.88  
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa\_trans; TM=Y; 5.86  
 436154; AA764950; Hs.119898; ESTs; ethanol, DAG\_PE-bind, DAGKa, PHD, DAGKc, PSI, none; 5.85  
 455358; AW902641; ; gb:OV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase, Somatomedin\_B, Phosphodiester, none; 5.83  
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxytelol\_BP, pkinase; TM=M; 5.82  
 452547; AA335295; Hs.74120; adipose specific 2; LEA; TM=M; 5.82  
 415204; T27434; ; gb:hbc2294 Human pancreatic islet Homo s; Na\_Ca\_Ex, Calx-beta, none; 5.80  
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar\_tr; TM=Y; 5.78  
 456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene ; dsrm, FKBP; 5.78  
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle; E1-E2, ATPase, Cation\_ATPase\_C, Cation\_ATPase\_N, Hydrolase; TM=Y; 5.77  
 436246; AW400963; Hs.119991; ESTs; none, DNA\_gyraseB, DNA\_topoisolv, HATPase\_c; 5.75  
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC\_tran, PRK; TM=Y; SS=M; 5.75  
 425854; AA749190; ; ESTs; RhoGAP, SH2, pkinase, POLO\_box, none; 5.74  
 424160; T74062; ; gbyrc1f01.r1 Soares infant brain 1N1B H; ROK, none; 5.70  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN, MKT; TM=M; SS=Y; 5.69  
 437613; R19892; Hs.10267; MIL1 protein; none, none; 5.68  
 410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4 ; TBC; SS=M; 5.68  
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase, PBD; TM=M; 5.66  
 426500; NM\_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; 5.63  
 406930; U04691; ; gb:Human olfactory receptor (OR17-219) g; none; TM=Y; SS=M; 5.60  
 401044; ; Target Exon; none, ICE\_p20, ICE\_p10, CARD, Peptidase\_M1; 5.56  
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase, ICE\_p10, ICE\_p20; TM=M; SS=M; 5.55  
 421970; AF227155; Hs.110103; RNA polymerase I transcription factor RR; aa\_permeases, pyridoxal\_deC, bromodomain, PHD, MBD, AT\_hook, DOT, PI3\_P14\_kinase, FAT, FATC, BolA, RUN; TM=M; 5.53  
 426248; T18988; Hs.293668; ESTs; pkinase, none; 5.50  
 418426; NM\_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase, death; TM=M; 5.43  
 417086; AA194446; ; ESTs, Weakly similar to S55024 nebulin ; ank, death, ZUS, EGF, kringle, trypsin, Nebulin, LIM; SS=M; 5.43  
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupl; 7tm\_1, SH2; TM=Y; SS=M; 5.40  
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF; SS=M; 5.40  
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, com; pkinase, TBC, Rhodanese; TM=M; 5.38  
 419355; AA428520; Hs.90061; progesterone binding protein; hema\_1; TM=Y; SS=M; 5.35  
 411188; BE161168; ; gb:PMO-HT0425-170100-002-a10 HT0425 Homo; adenylylase, none; 5.35  
 422461; NM\_003417; Hs.117077; zinc finger protein 264; z-C2H2, KRAB, TFIIS; TM=M; 5.28  
 426348; BE466586; Hs.17433; hypothetical protein FLJ20967; none, none; 5.25  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPc, Y\_phosphatase, Ribosomal\_S3\_N; TM=M; 5.23  
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin, Exo\_endo\_phos, IQ; TM=M; 5.22  
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER\_lumen\_recept, Ribosomal\_L11, Ribosomal\_L11\_N; TM=Y; SS=M; 5.21  
 434368; AW519020; Hs.73893; dopamine receptor D2; pkinase, SH3, none; 5.15  
 405586; ; NM\_000299; Homo sapiens plakophilin 1 (ec; Armadillo\_seg; TM=M; 5.13  
 408176; AK001553; Hs.43436; adenylylase kinase 3 alpha like; adenylylase, none; 5.12  
 407443; AF227138; ; gb:Homo sapiens candidate taste receptor; none; TM=Y; SS=M; 5.11  
 416817; AA398045; Hs.104679; ESTs; Furin-like, pkinase, Recep\_L\_domain, fn3, none; 5.10  
 401886; ; NM\_021783; Homo sapiens XEDAR (XEDAR); mR; TNFR\_c6; TM=M; SS=M; 5.08  
 410314; AW860708; Hs.18851; hypothetical protein FLJ10875; myb\_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 5.08

- 401579; AL031447; ; Homo sapiens, clone IMAGE:4053044, mRNA; Neur\_chan\_LBD, Neur\_chan\_memb, none; 5.05  
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-; PABP, rrm, kinase, 14-3-3; 5.05  
 417529; AA203634; ; gb:zx58b09.r1 Soares\_fetal\_liver\_spleen.; kinase, UBA, KA1, none; 5.03  
 417527; AA203524; ; gb:zx56e10.r1 Soares\_fetal\_liver\_spleen.; SH3; SS=M; 4.98  
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB; TM=M; 4.96  
 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid\_phosphat, none; 4.93  
 404298; ; C6001238; gjl121715|sp|P26697|GTA3\_CHICK; none; GST\_C, GST\_N, kinase; 4.85  
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; none; TM=M; 4.82  
 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC, tran, ABC, membrane; TM=Y; 4.73  
 422356; TB3882; Hs.97927; ESTs; kinase, none; 4.64  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; kinase; TM=M; 4.48  
 426925; NM\_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 f1s, clone H; Esterase, enolase, Peptidase\_S9; TM=M; 4.45  
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm\_1; TM=Y; SS=M; 4.40  
 400749; ; NM\_003105; Homo sapiens sortilin-related; EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 4.38  
 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4; TM=Y; SS=M; 4.33  
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; k1\_recept\_a, PKD, MHC\_I; TM=M; SS=Y; 4.31  
 400751; ; NM\_003105; Homo sapiens sortilin-related; EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 4.18  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; kinase; SS=M; 3.90  
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none, none; 3.88  
 458760; AA98631; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3, cotransp, SH3, RhoGAP, xan, ur, permease, FCH; SS=M; 3.85  
 441218; BE327561; Hs.202345; ESTs; none; WD40, E1-E2, ATPase, Cation, ATPase\_C, Cation, ATPase\_N, Hydrolase; 3.78  
 419073; AW972170; Hs.183918; Homo sapiens cDNA FLJ12797 f1s, clone NT; death, ZUS; SS=M; 3.76  
 451385; AA017656; ; gb:ze39h01.r1 Soares retina N2b4HR Homo; Atrophin-1, enolase, Atrophin-1, Y\_phosphatase, SH2, fibrinogen\_C, TIM; 3.60  
 412604; AW978324; Hs.1904; protein kinase C, iota; kinase, DAG, PE-bind, kinase\_C, OPR; TM=M; 3.30  
 409582; R27430; Hs.271565; ESTs; none; Neur\_chan\_LBD, Neur\_chan\_memb; 3.28  
 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1\_LC3; SS=M; 3.23  
 436740; AW975133; ; gb:EST387239 MAGGE resequences, MAGN Homo; none, EPH, lbd, fn3, kinase, SAM; 3.20  
 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked; none, IRK; 3.20  
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 f; none; NA; NA; 3.13  
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit; none, none; 3.10  
 400846; ; ; sortilin-related receptor, L(DLR class); EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 3.09  
 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 f; none, Na, H\_Exchange; 3.03  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar, tr; TM=Y; SS=M; 3.02  
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK; none; 2.98  
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member, death, TNFR\_c6; TM=Y; SS=M; 2.93  
 401279; ; C13000351; gjl2494033|sp|Q64398|KGDG\_MES; none, none; 2.88  
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema, kinase, TIG, PSI, none; 2.83  
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK; TM=Y; 2.80  
 453519; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; kinase; TM=M; 2.75  
 441699; AW511126; Hs.127572; ESTs; none, Aa, trans; 2.73  
 458781; A444821; Hs.63085; ESTs, Weakly similar to MPP3\_HUMAN MAGUK; SH3, PDZ, Guanylate\_kin, L27; TM=M; 2.73  
 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4; TM=Y; SS=M; 2.70  
 453487; R31770; Hs.56562; ESTs; 7tm\_1, none; 2.68  
 421279; AW654878; Hs.106645; ESTs; kinase, none; 2.68  
 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none, none; 2.65  
 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc; TM=M; 2.63  
 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF; TM=Y; 2.62  
 425212; AW962253; Hs.171618; ESTs; kinase, none; 2.60  
 427344; NM\_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur\_chan\_LBD, Neur\_chan\_memb; TM=Y; SS=M; 2.58  
 423629; AW021713; Hs.18612; Homo sapiens cDNA: FLJ21909 f1s, clone H; voltage, CLC, CBS, none; 2.55  
 456737; BE247203; Hs.124831; CGI-57 protein; abhydrolase\_2; TM=M; SS=M; 2.53  
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm\_1; TM=Y; SS=M; 2.53  
 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 f1s, clone Y7; none, none; 2.50  
 446324; A1571356; Hs.34174; ESTs, Moderately similar to ALU8\_HUMAN A; ICE\_p20, CARD, ICE\_p10, none; 2.50  
 402256; ; Target Exon; kinase, UBA, none; 2.43  
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 f1s, clone HE; GDI, 7tm\_1, none; 2.40  
 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothet; none, spectrin, SH3, PH, CH, 2.40  
 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP\_binding, ion, trans; TM=Y; 2.35  
 419630; W57756; ; gb:zd20g10.r1 Soares\_fetal\_heart\_NbHH19W; z-C3HC4, none; 2.35  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm\_1; TM=Y; SS=M; 2.35  
 400704; ; Target Exon; lig\_chan, SBP\_bac\_3, ANF\_receptor; TM=Y; SS=M; 2.33  
 400149; ; Eos Control; acid\_phosphat; TM=Y; SS=M; 2.30  
 459327; AW149706; Hs.7859; gb:xf41d02.x1 NCL\_CGAP\_Bm50 Homo sapien; PHD, PWWP, SET, kinase, ig; 2.30  
 452220; BE158006; Hs.212296; ESTs; Integrin\_A, FGF-GAP, none; 2.25  
 416690; H84078; Hs.108551; ESTs; kinase, none; 2.23  
 408354; A1382803; Hs.159235; ESTs; none, none; 2.23  
 452203; X57522; transporter 1, ATP-binding cassette, sub; ABC, tran, ABC, membrane, SRP54, Thymidylate\_kin; TM=Y; SS=M; 2.21  
 405093; ; C12001101; gjl7522643|pir|T32733 AMPA g; none, none; 2.20  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; 2.20  
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 2.18  
 417185; NM\_002484; Hs.81459; nucleotide binding protein 1 (E.coli Min; ParA, fer4\_NiH, ArsA, ATPase; TM=M; 2.18  
 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 2.18  
 413627; BE182082; Hs.246973; ESTs; Armadillo\_seg, IBB; TM=M; 2.18  
 407415; AF073328; ; gb:Homo sapiens tetracycline transporter-; none, none; 2.15  
 450592; A1701555; Hs.202562; ESTs; kinase, none; 2.15  
 428767; A421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1; none, kinase, ig; 2.15  
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 2.15  
 419122; A401360; Hs.44410; ESTs; ABC, tran, ABC, membrane, none; 2.10  
 446420; AW015693; Hs.135614; ESTs; ion, trans, none; 2.05  
 420076; AA827860; Hs.293717; ESTs; DUF59, kinase; 2.05  
 409416; AW388359; Hs.10667; ESTs; transmembrane4; TM=Y; SS=M; 2.03  
 428766; AA477989; Hs.98800; ESTs; TPR, 7tm\_1; 2.03  
 427001; NM\_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; kinase; TM=M; 2.03

453709; AL119133; ; protein kinase C substrate B0K-H; none,histone; 2.03  
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00  
 456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88  
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7Im\_1; 1.65  
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00  
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 58B

Pkey: Unique Eos probeset Identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828995 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI368880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348244 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
438091	22448_1	AK054860 AV652198 AV652198 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646384 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D56017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T55222 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AW192769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AI136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08083 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858935 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262300 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL50751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 AI872628 AI927217 AI453453 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478055 BE790435 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA448005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AI136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08083 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858935 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262300 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL50751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 AI872628 AI927217 AI453453 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478055 BE790435 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA448005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AI136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08083 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858935 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262300 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL50751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 AI872628 AI927217 AI453453 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478055 BE790435 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895



			AW651691 BMD48974 BMD43805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528531 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316958 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
5	437056 422940 409745	428504_3 58443_1 MH1944_5	AW976398 AI147061 AA765223 AA743380 AI803927 BC012771 BG397153 BF366196 AA337277 AA319285 AW843252 BI030997 AA921874 AW188822 BI027862 AJ347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI002986 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
10	407347 418546 432407	810943_1 242836_1 MH1429_12	T23514 AI655785 T59708 AA224827 T59843 BE156903 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AW071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
15	423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128665 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE263232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA902454 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA771194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988885 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
20	400211	3532_1	BC000486 BC001930 UI5008 NM_004597 BG326561 AV761269 BF212132 BG113313 BI838038 BG944198 BG255198 BG164334 BM013507 AV682717 BF028761 BG755489 BG030141 BG105499 BE440103 BF727449 BM454228 BG912181 BM015197 BG359595 AI126579 AW248204 BI857394 BI857319 BG944205 BG323958 BI092930 AV756576 AA280958 BF033078 BE539360 AW247174 BG107836 BE796975 BG170920 AI148142 AI092009 AI336349 AV713409 BF685591 BE516029 AV713166 BE909458 BE743868 BM018218 AJ40153 BI370014 BE72567 BE206806 AI159916 AI184271 BE208585 BI862286 C18760 BG219364 AI122677 BE207297 BF754798 AA314384 BE873951 BG207294 AI148198 AI336189 AI141094 AI308985 BF220098 AI143289 BE856397 AA644001 BE675402 AJ346708 AI052809 AI140082 BF081542 AI342428 AI479625 AA278456 AI750163 BE707501 BG944510 AA314616 AA315774 BF360721 BF738404 AA814194 AA477195 AA932107 F36858 AA363159 BE865458 AA354147 AW904224 AI055855 AA380365 F28474 D59140 AA341946 AA993339 AA323350 F24344 AA374436 BG942061 AA636015 AA852919 T31486 BF36334 BG943190 T30319 BG943153 BG941836 T32659 T31160 AA311749 BE710086 BE709911 W23826 BG941639 BF769034 AA026407 AA229555 AV756340 AV714380 AL138129 BG003205 AL138179 BI021773 BE064231 ALM20734 BI666852 BF870571 BF945361 BF945354 AI770086 BI861138 AI241079 AL043200 BG683612 AW946255
25	453826 447727 400121	355136_1 10123_14 3532_1	N503899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE263232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 BI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA902454 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA771194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988885 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
30	415327	9792_2	BM048470 BG983877 N92089 Z43545 F05783 R35182 H27269 H71928 H63921 R94394 AW195830 AA630220 F02030 R60760 R08204 H71929 BE464731 R62568 H63520 H77840 AL515501 F01971 T71768 N55275 AA883505 AW606824 AA704682 N74193 W57593 AW753776 H60439 AI076352 R31485 BE160931 AW130730 BE160869 AW580256 AW902073 BE702158 AW382079 N76884 BF431013 H38156 AV648937 H80573 AW902569 AW902557 AW902654 AW902641 AW902650 AW902741 AW902644 Z25288 R55077 F00323 D82802 T27434 BF184345 AA364846 BI494468 AA775693 BF195801 AA749190 AI480223 BE327332 AI470017 AW628345 AI917472 AI972264 AI375571 AI652583 AI656167 AI983110 BE550378 AW015085 BE552318 AI631475 AI433447 AA534540 AI865480 AI468119 BF110875 AW512059 W58721 AA827482 R59357
35	455358 415204 425854	1160035_1 1865508_1 2638_3	AW370493 AA923304 AI660828 AA502611 BI017370 AA039704 W65393 BE938514 W65295 BF919626 BI759440 BI838879 AA336207 F12441 BF171187 BE185031 T74062 AW904410 AA280078 BF919629 AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176555 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361 AA193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 AI620346 BG986374 BE706521 C02691 AI596834 F31902 F26078 AA670099 BF475555 F30818 F37524 AJ346558 F28050 F19333 F31637 C03413 AI092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546 AW821260 BE162466 BE161168
40	411188 417529 417527 451385 436740 419630 400149	1072487_1 3302462_1 2431831_1 85022_1 1239008_1 37310_5 16458_1	AA203634 AA203524 W88451 AA019761 AA017656 AA017374 AW975133 AA805813 AA729943 BF223647 AA204668 AA256086 BF574707 W57756 AA249070 BI906494 AA248011 BC003160 NM_001610 X12548 BG386685 BI760866 BI559619 BG323829 AU135543 BI834101 AU142120 AU124511 AU124889 AI558171 AU117286 BI824000 BG386610 BI753285 BI223475 AU134828 BM126369 BE206493 BF751498 AL544274 AY007137 BI828921 BE870130 BF771242 BI835451 BI765655 BI220955 BI223344 BG015924 BI759894 AL527413 BF310588 N31870 N23974 BE514914 I48863 AW860257 BF334625 AA883860 AU141668 AA442562 AU159491 AU148353 AA564123 AU148667 AI377256 AW664004 AI871712 AI141486 AI323351 AI339094 BE206109 AW519033 AI817729 AI332490 AI149455 AI857411 AI763154 AI751608 AI377222 AI081956 AW664229 AI275872 AW168546 AA975270 AI367408 AI687729 AI269164 AW105344 BM193081 BE550930 AI082116 AA854691 AI056249 AI221062 AI290113 D51818 AA732409 BG055125 N85878 AU156121

BF093671 AA053070 T28548 AL570460 BI006862 BI007207 AA373520 W95069 AA629136 AA708164 AI014886 AW168697 D51623 AA577168  
 AI094208 AA028946 AA975078 R16815 BG151132 AI276297 D51676  
 BC014081 NM\_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL555882 AL541576 AL550654 BI283519  
 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470  
 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429  
 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404  
 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220  
 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184  
 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619  
 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256  
 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601  
 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586  
 AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239  
 AA074615 AI291059 AI681053 AA702355 BF439899 AW055165 AI096957 BF223853 AL119659 AI692209 BM312961 AI869297 BE466252 AI292024  
 AA402764 AI214620 AA765312 BF380770 AA442682 AL519746 AW295039 AI037878 AW473433 AI499437 AI401618 AI130831 AA427406 AI042138  
 BG272488 AI828769 AI828764 AI189390 W84635 AA398496 AA761672 AA699520 AI200406 N68093 AI143913 AA993133 AA613306 AI050971  
 AA661905 AA722687 AI749977 AA829345 BG057324 BF001339 AA910169 AA765133 AI360722 AI701849 AI365083 H95974 AI830377 AI312866  
 AI370491 BE858907 N62185 AA705746 BE379632 W93803 AI440333 AW367670 AW367640 N77131 BF993216 AI858263 W52329 N68106 R83113  
 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851  
 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 AI073567 AA004957 AI539585 N95093 H99798 H95072 H96853 AA215712  
 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 AI693577 BE181027  
 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H55903 H17591 R20167 AA310039 R58734  
 R58506

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36461
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84974-85125
405036	7543748	Minus	121957-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420923	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
418854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	AI093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microseminoprotein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	54.6
428398	AI249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7

5	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
10	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
15	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 lina-1 pr	39.3
	416585	XS4162	Hs.79386	leiomodulin 1 (smooth muscle)	39.0
	447726	AL137638	Hs.19368	matrilin 2	38.6
20	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
25	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415539	AI733881	Hs.72472	BMP-R1B	34.9
30	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
35	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AI918950	Hs.123642	EphA3	32.7
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sera domain, immunoglobulin domain (Ig),	32.4
40	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
	408380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytostatin)	31.4
45	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H777 transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
50	442993	BE018682	Hs.166196	ATPase, Class I, type BB, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	29.2
55	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023630	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
60	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
65	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442670	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
	403047			NM_005656:Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
70	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AI267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens prostelin mRNA, complete cds	26.4
75	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
	400292	AA250737	Hs.72472	BMP-R1B	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
80	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59822	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448106	AI800470	Hs.171941	ESTs	25.5
	415992	CO5837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW967646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	24.5
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
5	418396	AI765805	Hs.26691	ESTs	24.1
	412088	AI689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abl-interacting protein ArgBP2	24.0
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
10	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	22.9
	440260	AI972667	Hs.71130	copine IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-ek	21.9
20	450642	R39773	Hs.71130	copine IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	21.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
	416655	AW958613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
40	408912	AB011084	Hs.48924	KIAA0512 gene product: ALEX2	21.1
	445133	AW157646	Hs.153506	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420511	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
50	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
	424897	D53216	Hs.153684	frizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263*:HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	20.3
	429918	AW873986	Hs.119383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
	441690	R81733	Hs.33106	ESTs	19.9
65	423690	AA329648	Hs.23804	ESTs, Weakly similar to PND099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
	431556	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
70	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	LIM domain only 4	19.2
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
80	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latexin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

	445929	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
5	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	18.7
	418819	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443966	Hs.31595	ESTs	18.4
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
20	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439589	AW602166	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424682	AW604804	Hs.151717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
	431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
30	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (tr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium Intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
45	421823	N40850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.159983	ESTs	16.9
	432966	AA650114	Hs.325198	ESTs	16.9
55	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:mp12d11.s1 NCL_CGAP_Pr3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF085833	Hs.135624	ESTs	16.8
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
60	442054	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocan	16.4
	443801	AW206942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
70	409060	AI815867	Hs.50130	necln (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30098	ESTs	16.0
75	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW089181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AJ093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AI418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor I	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	15.4
	443674	AI081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418693	AI750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase	15.1
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	lumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432305	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AI699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/HE (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336695	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AJ026838	Hs.30120	ESTs, Weakly similar to NUC1_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	14.5
75	410339	AI916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2831	protein kinase C, mu	14.5
	424432	AB037821	Hs.145858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5



	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
	416836	D54745	Hs.80247	cholecystokinin	14.4
5	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
10	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	A1927288	Hs.195779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob)	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
	433332	A1367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
15	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	14.1
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
20	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	13.9
	418848	A1820961	Hs.193465	ESTs	13.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
25	439518	W76326		gbzcd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
	447384	A1377221	Hs.40528	ESTs	13.9
30	444880	AW118683	Hs.154150	ESTs	13.9
	433409	A1278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
35	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
40	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
45	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
50	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
55	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	A1497778	Hs.20509	HBV pX associated protein-8	13.6
	410001	AB041036	Hs.57771	kallikrein 11	13.6
60	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965*:Homo sapiens phosphoglucomuta	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	13.6
65	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
70	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN III	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
	447082	T85314	Hs.42644	thioredoxin-like	13.5
75	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypolheti	13.3
	433517	AW022133	Hs.189838	ESTs	13.3
80	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (	13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226527	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
10	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.156880	ESTs	13.2
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68796	Hs.237731	ESTs	13.1
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI362575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
25	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
30	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
35	417315	AI080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW296451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothi	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
40	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
50	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI568801	Hs.71721	ESTs	12.6
55	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (I	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
60	427078	AI676082	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
65	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
70	432205	AI806583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965*:Homo sapiens phosphoglucomuta	12.4
75	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI459306	Hs.24908	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
80	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	12.2
	400880			NM_000611*:Homo sapiens CD59 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odz (odd Oz/en-m, Drosophila) homolog 1	12.1
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
15	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	435169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164226	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984625	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730045	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	426981	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AI472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	11.5
	412677	AW029508	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI038316		gb:ox48c08.x1 Soares_tota_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428829	RI4050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoiet	11.4
	456804	AI421645	Hs.139851	caveolin 2	11.4
75	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3

	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476*gil12737279[ref]XP_012163.1	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
10	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
	436758	AW977167	Hs.155272	ESTs	11.2
	409401	A1201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
15	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	A1739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
20	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T86534	Hs.14372	ESTs	11.1
	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
25	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	11.1
	452598	A1831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
30	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
	412622	AW684708	Hs.171959	ESTs	11.0
	450353	A1244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
35	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104696	KIAA1324 protein	10.9
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
45	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.156110	immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
50	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	A1623752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	10.8
55	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	H22953	Hs.137551	ESTs	10.8
	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
60	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
65	450206	A1796450	Hs.201600	ESTs	10.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
70	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
75	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW975944	Hs.237396	ESTs	10.7
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198699	eukaryotic translation initiation factor	10.7
80	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA: cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

	433923	AI823453	Hs.146625	ESTs	10.7
	418196	AI745649	Hs.26549	KIAA1708 protein	10.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
5	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	AI754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmegin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)-like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	AI801098	Hs.151500	ESTs	10.6
	449685	AW296669	Hs.66095	ESTs	10.6
	441111	AI806867	Hs.126594	ESTs	10.6
15	436671	AW137159	Hs.146151	ESTs	10.6
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
	424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	AI694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	451900	AB023199	Hs.27207	KIAA0982 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037766	Hs.146085	KIAA1345 protein	10.5
35	402076			C5002020:gil1082876[pir][S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	AI380429	Hs.172445	ESTs	10.5
	443684	AI681307	Hs.55098	ESTs	10.5
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyclin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-67	10.5
	416182	NM_004354	Hs.79069	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293798	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
75	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
	451593	AF151879	Hs.26706	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	10.2
5	446553	AB021179	Hs.15299	HMB-A-inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
15	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
25	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
30	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
35	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (K0X 4, clone HF.1	10.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA053564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
55	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
	441054	AA913591	Hs.126480	ESTs	9.9
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31584	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8



	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
5	404571			NM_015902: Homo sapiens progesterone induce	9.7
	444427	H25094	Hs.293563	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278526	Arg/Abl-interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A45010 X-link	9.7
15	417171	BE613486	Hs.81412	tipin 1	9.7
	421709	AA159394	Hs.107056	CED-6 protein	9.7
	415155	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523939	Hs.165258	ESTs	9.6
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.5641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	9.5
	408915	NM_016651	Hs.48950	hepaticellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H46008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	436497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AI636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulon 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crik avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
65	412446	AI768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncollin	9.4
	421689	N87820	Hs.106826	KIAA1695 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW288235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
80	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
5	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
	428465	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D86960	Hs.3610	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ111011	9.2
	401558			ENSP00000220478*:SECRETORANIN III.	9.2
15	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
20	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
25	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	9.1
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
30	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
35	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
40	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
45	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
50	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [Hsapli	9.0
	405523			C8001409*:gil7441226 pir  S31212 collage	9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
55	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.9
60	414917	C04863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
65	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
70	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502663	Hs.145037	ESTs	8.9
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
75	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
80	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97111.s1 NCL_CGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	necdin 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	AI743880	Hs.12876	ESTs	8.8
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW080798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypolheti	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA564489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3506519, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:d127e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypolheti	8.7
40	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275*Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60	425907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

	434747	AA837085	Hs.220585	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
	450813	AI739525	Hs.203376	ESTs	8.5
5	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypothe	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
10	432620	AA777749	Hs.5978	LIM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	S-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
25	421622	AB037748	Hs.106204	KIAA1327 protein	8.4
	431160	AW971174	Hs.324330	ESTs	8.4
	449567	AI990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	8.3
30	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425692	D90041	Hs.155956	N-acetyltransferase 1 (aniline N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431952	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	toll-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433615	AA732982	Hs.269507	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	AI799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450:Homo sapiens four and a half L	8.3
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothe	8.3
	453121	AI988264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434C0921 (f	8.3
50	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (f	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	8.2
	432695	D63480	Hs.278634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell c3 93	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALU7_HUMAN IIII	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypothe	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypothe	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	AI824719	Hs.328700	ESTs	8.2
75	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 59B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
		AW848214
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
418866	179788_1	T65754 AA229857 AA229658
418876	179960_1	AA740616 AA654854 AA229923
419536	185688_1	AA603305 AA244095 AA244183
419544	185760_2	AI909154 AA526337 AA244193 AI909153
423800	232161_1	AA331156 AA331157 AA331155
426413	266650_1	AA377823 AW954494 AI022688
429163	300543_1	AA884766 AW974271 AA592975 AA447312
430848	324621_1	AW021726 AA487752 AA488085
431121	328275_1	AW971157 AA492575 AA492520
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
434415	385931_1	BE177494 AW276909 AA632849
434579	38916_1	T55958 T57205 AF147346
439518	47334_1	W76326 AF086341 W72300
443161	561305_1	AI038316 AI344631 AI261653
447974	745643_1	R76886 AI453674 R77049

TABLE 59C

Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
Nt_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	Nt_position
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401785	7249190	Minus	165776-165995,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
402076	8117410	Plus	128316-128627
402812	6010110	Plus	25026-25091,25844-25920
402855	9662953	Minus	59763-59909
403047	3540153	Minus	59793-59968
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403149	9799833	Plus	25034-25185
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404571	7249169	Minus	112450-112648
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of prostate tumor to normal adult body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	56.6
419526	AI821895	Hs.193481	ESTs	56.2
420154	AI093155	Hs.95420	JM27 protein	44.0
432441	AW292425	Hs.163484	ESTs	41.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothe	37.9
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	36.0
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
400298	AA032279	Hs.61635	slx transmembrane epithelial antigen of	30.0
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222896	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	AJ918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H7?? transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_0011172:Homo sapiens arginase, type II	24.5
	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AJ267700		ESTs	20.2
	407709	AA456135	Hs.23023	ESTs	20.0
15	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.55145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
20	410929	H47233	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656*:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AJ765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AJ694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	AJ972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AJ202703	Hs.152414	ESTs	14.4
	450893	AW450461	Hs.203965	ESTs	14.4
40	431548	AJ834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.3
	430187	AJ799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AJ970672	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450542	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
50	434656	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AJ127076	Hs.306201	hypothetical protein DKFZp55401278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
55	453861	AJ026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	12.3
	428398	AJ249368	Hs.98558	ESTs	12.2
	421059	AJ654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	12.2
	443960	AJ093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	latexin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.278595	Homo sapiens prostein mRNA, complete cds	11.9
70	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AJ821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp55401278	11.6
75	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218885	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AJ277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.5
80	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
15	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021965*:Homo sapiens phosphoglucomula	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
50	440774	AI420611	Hs.153934	ESTs	8.7
	420120	ALD49610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJD10901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid	8.2
65	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	426330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X76592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453160	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6



5	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AI750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI088489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homeo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AU077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
50	439492	AF086310	Hs.103159	ESTs	6.8
	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI732230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
60	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB039670	Hs.9728	ALEX1 protein	6.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA861697	Hs.120591	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystokinin	6.6
70	447033	AI357412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
75	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
	421077	AK000061	Hs.101590	hypothetical protein	6.4
80	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoeiti	6.3
	453390	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.3
	433610	AA805822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AI922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
	425465	L18964	Hs.1904	protein kinase C, tota	6.2
15	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AI800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
20	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
	437323	AA371145	Hs.194397	leptin receptor	6.1
25	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
30	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmegin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
	431359	AW993522	Hs.292934	ESTs	5.9
45	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	405523			C8001409:gi 7441226 pir S31212 collage	5.9
50	448807	AI571940	Hs.7549	ESTs	5.8
	404642			NM_021965:Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414528	AA148950	Hs.188836	ESTs	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50856	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AI739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970976	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_AW1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	AI241733	Hs.43871	ESTs	5.4
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AI459306	Hs.24908	ESTs	5.4
	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
15	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
20	428354	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	AI27483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
	412677	AW029608	Hs.17384	ESTs	5.3
25	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	AI829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 ferri	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	AI278802	Hs.25661	ESTs	5.3
	441102	AA973905		intermediate filament protein syncoilin	5.3
35	453387	AI990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	AI823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
	447574	AF162666	Hs.18895	lousled-like kinase 1	5.2
40	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	5.2
	429467	NM_004477	Hs.203772	FSHD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	tol-like receptor 5	5.2
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA889120	Hs.110637	homeo box A10	5.2
55	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446795	AI797713	Hs.156471	ESTs	5.1
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 83	5.1
60	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	5.1
	453293	AA382267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409643	AW450866	Hs.257359	ESTs	5.1
65	427723	AJ355260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068658	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	AI358957	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
	433023	AW864793	Hs.87409	thrombospondin 1	5.0
	433862	D86960	Hs.3610	KIAA0205 gene product	5.0
80	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	AI734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659305	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
15	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	4.9
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
20	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	I-box and leucine-rich repeat protein 4	4.8
	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410258	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA453208	Hs.28274	RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*:SECRETORANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.7
	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALU8_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403046			NM_005656*:Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	4.6
80	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6

	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
5	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
10	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
15	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
	433507	AI817336	Hs.191791	ESTs	4.5
20	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
	419745	AF042001	Hs.53005	slug (chicken homolog), zinc finger prot	4.5
25	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
	414272	AI651603	Hs.46988	ESTs	4.5
30	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb:xc28c12.x1 NCL CGAP_Co18 Homo sapiens	4.5
35	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476"-gjl12737279reflXP_012163.1]	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	4.4
40	433517	AW022133	Hs.188838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076535	Hs.50984	sarcoma amplified sequence	4.4
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
45	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 fertilin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
	434384	AA631910	Hs.162849	ESTs	4.4
50	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
	448766	AI473827	Hs.31793	ESTs	4.4
55	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisogu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
	434022	R18374	Hs.117956	ESTs	4.4
60	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
65	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
70	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
75	435023	AI692552		gb:wd73f12.x1 NCL CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.63883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
	420405	AA743396	Hs.189023	ESTs	4.3
80	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155694	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
5	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629666		ESTs, Weakly similar to S64054 hypothe	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
10	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulon 3	4.2
	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
15	450546	AA010200	Hs.175551	ESTs	4.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
20	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449685	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
25	450377	AB033091	Hs.74313	KIAA1265 protein	4.2
	419647	AA348947	Hs.91816	hypothetical protein	4.2
	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW969657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
30	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
35	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.1
	447752	M73700	Hs.105938	lactotransferrin	4.1
	402855			NM_001839: Homo sapiens calponin 3, acid	4.1
	443161	AI038316		gb:ox48c08.x1 Soares_tota fetus_Nb2HF8_	4.1
	415827	H17462	Hs.23079	ESTs	4.1
40	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418355	AW014345	Hs.161690	ESTs	4.1
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AJ335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
45	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239499	KIAA0185 protein	4.1
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
50	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.1
	428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
55	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.0
	443273	AJ042063	Hs.132156	ESTs	4.0
	428055	AA420564	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AJ457338	Hs.29894	ESTs	4.0
60	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
65	409705	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
	418594	AJ732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
70	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
75	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW277121	Hs.254881	ESTs	4.0
	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213559	ESTs, Weakly similar to KIAA1357 protein	3.9
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
	400695			C11002514:gil11280151[pil]E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.s.a	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

	428852	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
5	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0982 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.9
	442320	AI287817	Hs.129636	ESTs	3.9
15	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:aa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280699	ESTs	3.8
	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
35	443484	AI091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.8
	430968	AW972830		gb:EST384925 MAGe resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48804	DKFZP434B168 protein	3.8
50	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW105663	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
	448207	AI475490	Hs.170577	ESTs	3.7
65	450628	AW382884	Hs.204715	ESTs	3.7
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
70	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
	408312	AF263613	Hs.44198	intracellular membrane-associated calci	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.7
75	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
80	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7



	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (I	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.7
	445941	AI267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.6
	412533	AA679863	Hs.69606	ESTs	3.6
10	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AI475858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
15	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	3.6
20	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.6
	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN IIII	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
	433887	AW204232	Hs.279522	ESTs	3.6
25	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
30	435703	AW630133	Hs.83313	GK003 protein	3.6
	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GC81 Homo sapiens	3.6
	411552	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazarus	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA529399	Hs.165258	ESTs	3.5
	410762	AF226053	Hs.66170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exosomosis (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.5
55	420390	AA330047	Hs.191187	ESTs	3.5
	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
60	413950	AA249096	Hs.32793	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
70	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
75	432589	AL135725	Hs.131708	ESTs	3.5
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460.1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
5	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
10	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AJ969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synthase	3.4
	434966	AA657494		gb:nt66f04.s1 NCL CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902: Homo sapiens progesterone induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
20	436374	AA400709	Hs.95716	ESTs, Weakly similar to T17210 hypotheti	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*: Plasma membrane calcium	3.4
25	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AI655662	Hs.197698	ESTs	3.4
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
30	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
35	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
40	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21517	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
45	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
50	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
55	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
60	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
65	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
70	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
75	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*: HSPC213.	3.3
80	433404	T32582	Hs.102720	ESTs	3.3
	422546	AB007959	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:cx10e09.r1 Soares_t0tal_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
15	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
	432363	AA534489		gb:m176g11.s1 NCI_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288584	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI93046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulin 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chain	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75812	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein veza2in; hypotheti	3.2
80	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
15	408784	AW971350	Hs.63386	ESTs	3.2
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig), Target Exon	3.2
	405558			ESTs	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
25	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheli	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		ghzo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
	438979	AW976218	Hs.32565	ESTs	3.1
70	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
75	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
5	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW529223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gbnc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
15	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
20	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
30	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	426695	AJ355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242759	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIKE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Pkey: Unique Eos probaset Identifier number

CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
5	411479	1247077_1 AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	411667	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	414372	143909_1 AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
10	414680	147525_1 AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	415989	156454_1 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416288	1585983_1 H51299 H44619 H46391 R86024 H51892 T72744
	416882	162718_1 AI633044 AW016212 AW241143 AA766058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
15	416913	163001_1 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161005 BE162499
	417379	167238_1 AA196390 AA507837 AA196468
	418304	173658_2 AA215702 AA368006 AA215703 BE066555 BE006876
	418647	177521_1 AA226198 AA226513 AA383773
20	418866	179788_1 T65754 AA229857 AA229658
	419536	185688_1 AA603305 AA244095 AA244183
	419544	185760_2 AI909154 AA526337 AA244193 AI909153
	423412	228001_1 AF109300 AI299378 AI202654
	423800	232161_1 AA331156 AA331157 AA331155
25	426226	262918_1 AA769045 AA372590 AW963633
	426413	266650_1 AA377823 AW954494 AI022688
	426503	268283_1 AA380153 AA380233 AW963529
	426775	271683_1 AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
30	426991	27415_1 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
	428342	290035_2 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
	429163	300543_1 AA884766 AW974271 AA592975 AA447312
	429220	301384_1 AW207206 AW341473 AA448195 AI951341
35	429258	301917_1 AA448765 C04967 C03045 AA658293
	430935	325772_1 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430968	326269_1 AW972830 AA527647 AA489820 AA570352
	431429	33313_1 AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T59596 BE618035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
40	432093	341283_1 H26383 AW972670 H28359 AA525808
	432125	341776_1 AW972667 AA526539 AI057032 AW167842
	432189	342819_1 AA527941 AI810608 AI620190 AA635266
	432340	345248_1 AA534222 AA632632 T81234
45	432363	345469_1 AA534489 AW970240 AW970323
	432600	350959_1 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432810	354375_1 AA863400 AI991439 AW016017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA626033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542
	434579	38916_1 T55958 T57205 AF147346
50	434966	396504_1 AA657494 AI582663 AI581639
	435023	398093_1 AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	437866	44433_2 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
55	438147	45074_1 AW250553 L07876 Z36843 R30693 AI190097 AW965317
	439092	468554_1 AA830149 AW978407 M85983 AW503637
	439518	47334_1 W76326 AF086341 W72300
	439904	479942_1 AW892676 AA853877 D44747
	440840	50357_2 AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
60	441102	509604_1 AA973905 AI299888 AA917019 H63235 T90771
	442562	54500_2 BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492830 AI376090 AI472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130896 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D62102 AI0007
65	443161	561305_1 AI038316 AI344631 AI261653
	445808	65133_1 AV655234 AW966332 AA340239
	447082	707248_1 T65314 AI360684 T85528 T91254
	448212	755099_1 AI475858 AW969013
70	449625	8113_1 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 N40087 H12925 AA460778 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
	450580	83929_1 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
75	450582	83933_1 AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW795099 AI833027 AI765395 AI763029 AI758228
	452260	9074_1 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
	452598	92338_2 AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AI138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI16834 N25206 AA828301 AI084555 AI302816 AW026905 AA77255
80	452815	93255_1 AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
	453802	981589_1 AL134757 AW079131
	455100	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853\_1 AW974811 AA651634 AA650072

5 TABLE 60C

10 Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

35

40

Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

45 Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue  
 R2: Ratio of prostate tumor to normal prostate tissue

50

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263:HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	della (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
425018	BE245277	Hs.154195	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	6.1	6.1
437147	AL049954	Hs.8358	hypothetical protein FLJ20356	2.6	6.0



5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	3.3	5.9
	431548	AI834273	Hs.9711	novel protein	15.7	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
10	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
15	451684	AF216751	Hs.26813	CDA14	3.9	5.4
	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
20	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
25	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
30	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.35598	ESTs	5.4	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
35	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464	Hs.159993	gbt108f04.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476:gil12737279[ref]XP_012163.1]	4.6	4.6
40	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111802	ESTs	4.8	4.5
45	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
50	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
	428826	AL048842	Hs.194019	atractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
55	429900	AA450421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gbztd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
60	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
65	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433887	AW204232	Hs.279522	ESTs	4.1	4.1
	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443646	AI085198	Hs.164226	ESTs	4.1	4.1
70	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
75	444755	AA431791	Hs.113823	CipX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoacipale aminotra	3.9	3.9
80	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
10	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7	3.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AI571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
15	451009	AA013140	Hs.115707	ESTs	4.1	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AI357412	Hs.157601	ESTs	7.7	3.6
20	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
25	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.2	3.5
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AI918950	Hs.123642	EphA3	16.5	3.5
	429302	AI076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
30	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGalNAc beta 1,3-galactosyltr	2.1	3.4
35	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
40	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
50	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
55	444489	AI151010	Hs.157774	ESTs	3.2	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
	453078	AF053551	Hs.31584	metaxin 2	2.1	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
60	434804	AA649530	Hs.348148	gbns44f05.s1 NC1_CGAP_Alvi Homo sapiens	2.1	3.1
	445840	AI277811	Hs.146291	ESTs	3.1	3.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
65	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
70	420154	AI093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
75	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	AI356867	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
80	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	A1628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AJ582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisou	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 feri	2.9	2.9
5	428600	AW853261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129536	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451796	AL133019	Hs.27038	Homo sapiens mRNA: cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
15	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor TII, polype	2.8	2.8
	433865	N29862	Hs.44104	ESTs	2.8	2.8
20	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654650	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
40	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436589	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
55	433419	AI830342	Hs.211272	ESTs	2.9	2.6
	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A45010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191060	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
70	431474	AL133990	Hs.190642	ESTs	9.3	2.5
	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO05	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656: Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ111344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubitinuclein 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.322250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gi4507689jref[NP_003298.1] tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478:SECRETOGRANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	tol-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
5	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
10	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008:gi7303957 gb AA59000.1  (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
15	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
20	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothei	2.1	2.1
	452959	AI933416	Hs.189674	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
35	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
40	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
80	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 618

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AJ141054 AW194991 AA252147 AA319500 A1184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AJ748815 AI763294 AJ333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AJ040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
15	424036	23460_1	AA770588 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290558 C15404
	426413	266650_1	AA377823 AW954494 AJ022688
	429258	301917_1	AA448765 C04967 C03045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AJ014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA253370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI98402 T613
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
40	Nt position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt position
	401197	9719705	Plus	176341-176452
	401519	6649315	Plus	157315-157950
	401558	7139678	Plus	103510-104090
45	402802	3287156	Minus	53242-53432
	403047	3540153	Minus	59793-59968
	404641	9795810	Minus	32247-32362
	405685	4508129	Minus	37956-38097
50	406068	9114084	Plus	382-543

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
65	R1:	Ratio of prostate tumor to normal prostate tissue

  

Pkey	ExAccn	UnigeneID	Unigene Title	R1
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	26.5
427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
420729	AW964897	Hs.290825	ESTs	15.8
412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
424247	X14008	Hs.234734	lysosome (renal amyloidosis)	12.6
401197			ENSP00000229263:HSPC213.	12.6
426793	X89887	Hs.172350	HiR (histone cell cycle regulation defec	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
443271	BE568568	Hs.195704	ESTs	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	stl (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.105768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	della (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002357	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AJ080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
20	425174	D87450	Hs.154978	KIAA0261 protein	8.6
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AJ934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AJ984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	435962	AW377314	Hs.5364	DKFZP5641052 protein	7.9
	450313	AJ038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153584	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AJ590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AJ796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AJ300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AJ971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AJ350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AJ499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418195	AJ745649	Hs.26549	KIAA1708 protein	6.1
80	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9



	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	5.9
	431548	AI834273	Hs.9711	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	sialyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
15	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	luberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CD44	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103261	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
	403851			C5002154".gij7299015[gb]AAF54217.1] (AE0	5.3
40	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
55	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
60	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
65	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
70	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	Inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96896	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476:gij12737279[ref]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419455	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE366283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:ztk85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ty	4.3
	426827	AW067805	Hs.172655	methyltetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_008732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b5?	4.2
	439518	W76326		gb:ztd60d04.r1 Soares_fetal_heart_NbH:119W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AA58213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567659	Hs.40342	putative nuclear protein	4.1
	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	VW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (tr	3.9
	444755	AA431791	Hs.113823	CipX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoacidipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axd)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122669	KIAA0264 protein	3.8
	403100			C2001027:g[7296271]gb AA51562.1  (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432353	AA534489		gb nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304505	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmnb33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75958	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350.gij6578126jgb AAF17706.1 AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446418	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M50721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb y12c04.r1 Soares infant brain 1N1B H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb yv59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
75	401744			Target Exon	3.4
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

	432741	AJ732358	Hs.185118	ESTs, Moderately similar to A37413 calbi	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AJ207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428466	AF151063	Hs.184456	hypothetical protein	3.4
5	447397	BE247676	Hs.18442	E-1 enzyme	3.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
10	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000165	Hs.288809	hypothetical protein FLJ20159	3.4
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
15	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
	403389			C3001393*gi 3327090 dbj BAA31613.1  (AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
	410494	M36564	Hs.64016	protein S (alpha)	3.3
20	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
25	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
30	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
35	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
	426848	H72531	Hs.36190	ESTs	3.3
	439553	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
40	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
	430280	AA361258	Hs.237688	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081* KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
50	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
55	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
60	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
65	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
70	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	424273	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
80	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:CVO-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
20	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
30	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNAX-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
40	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	414527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S55657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e06 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	3.0
	442420	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
80	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA: cDNA DKFZp564O1262 (f	3.0
416882	AI633044		typtophanyl tRNA synthetase 2 (mitochon	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
		AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
		AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
		AA708749 AA644620 AA652769 AA242975 AA151074 T19890
		R17236 R52580 F11642
		AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
		AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
		AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
		N59027 AA314694 N53937 R08100
		R06054 AA378789 AW956453
		AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
		AW972830 AA527647 AA489820 AA570362
		BE157283 BE157287 AA502438
		AI685464 AW971336 AA513587 AA525142
		AW972667 AA526539 AI057032 AW167842
		AA534489 AW970240 AW970323
		AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
		AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
		AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
		AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
		AW979177 AA846994 AA829672
		W76326 AF086341 W72300
		NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW795099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400479	8439786	Minus	115388-116348
400658	8118459	Minus	73525-73544
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-85469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39624-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75<sup>th</sup> percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of normal prostate tissue to prostate tumor tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	AJ738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	AI791314		gb:ae46g f2.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AI280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936.gij3746443[gb]AAC63969.1[AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N1B H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2



	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AJ218950	Hs.125461	hypothetical protein FLJ11539	4.1
	425094	AI955956	Hs.21417	ESTs	4.1
5	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AI028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
	404260			Target Exon	4.0
10	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
	449233	BE048401	Hs.196511	ESTs	3.9
15	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
	409679	BE250521		ras homolog gene family, member A	3.8
20	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
25	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gij6679124[ref NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
30	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gij12654691[gib AAH01185.1]AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
	436524	AA922236	Hs.221037	ESTs	3.7
35	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
40	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
	442097	AW015799	Hs.128474	ESTs	3.6
45	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
	400749			NM_003105*:Homo sapiens sortilin-related	3.6
50	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCI_CGAP_GCB1 Homo sapiens	3.5
	405704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
55	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.126326	ESTs	3.4
60	445045	AI652676	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KGA1578 protein (Fragm	3.4
	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
	444286	AI625304	Hs.190312	ESTs	3.4
65	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gij2695979[emb CAA70854.1] (Y0	3.4
	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
70	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
	418672	L44284	Hs.12915	ESTs	3.3
75	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
	458539	AI733837	Hs.145661	ESTs	3.3
80	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
5	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
10	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
15	451686	AA059246	Hs.110293	ESTs	3.1
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: hles3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
20	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	3.1
	402490			Target Exon	3.1
25	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
30	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
	419386	AA236667		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
35	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
40	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
45	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
50	449245	AI636539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
55	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
60	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
65	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	2.9
	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
70	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
75	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:zi199b10.s1 Soares_testis_NHT Homo sap	2.8
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
80	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

5	426481	AW963941	gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656		Target Exon	2.8
	407269	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.8
	435754	AA700752	ESTs	2.8
	433565	AA599763	ESTs	2.8
10	451004	AA044957	gb:z53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770		NM_002362:Homo sapiens melanoma antigen,	2.8
	456227	T84239	ESTs	2.8
	454445	AW749432	gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
15	419494	W01060	ESTs	2.8
	427639	AW444530	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	ESTs	2.7
	406337		C14000021:gil7242973[dbj]BAA92547.1] (AB	2.7
	401884		Target Exon	2.7
20	406881	D16154	gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	ESTs	2.7
	450044	R66444	ESTs	2.7
	403630		C3001708*:gil4758028[ref]NP_004360.1] co	2.7
	445514	AI241280	ESTs	2.7
25	446362	AW612481	ESTs	2.7
	432492	AW275110	ESTs	2.7
	430889	U22491	G protein-coupled receptor 7	2.7
	434316	AW411330	annexin A6	2.7
	413155	BE067952	gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
30	433329	AF015041	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	sarcolipin	2.7
	449923	BE258051	gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
	453826	AL138129	gb:DKFZp547F152_r1 547 (synonym: hibr1)	2.7
	405678		CX001454:gil8393794[ref]NP_058681.1] myo	2.7
35	432789	D26361	KIAA0042 gene product	2.7
	455791	BE090689	gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
	439255	F01143	zinc finger 1111	2.7
	415984	R19046	gb:yg21f11.r1 Soares infant brain 1N1B H	2.7
40	402844		C1000118*:gil9951913[ref]NP_062832.1] pr	2.7
	456666	AA452512	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	ribosomal protein S14	2.7
	404979		Target Exon	2.7
	412318	AW936911	hypothetical protein MGC11082	2.7
45	424361	AK001551	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	ESTs	2.7
	441975	AW173248	EST	2.7
	457021	AW968934	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	BCL2-like 1	2.7
50	439204	AF087987	EST	2.7
	415642	U19878	transmembrane protein with EGF-like and	2.7
	446847	T51454	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
	443359	AI792583	ESTs	2.7
	447336	AW139383	ESTs	2.7
55	449045	BE072483	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	OKFZP434B172 protein	2.7
	436030	R02287	ESTs	2.7
	449589	AW752437	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AI345995	ESTs	2.6
60	415054	AI733907	gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	ESTs	2.6
	410483	BE163567	gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083	wee1 (S. pombe) homolog	2.6
65	426629	AI203933	ESTs	2.6
	415831	H15145	ESTs	2.6
	412281	AI810054	ESTs	2.6
	434898	AW500458	KIAA0460 protein	2.6
	422229	AF134414	ABO blood group (transferase A, alpha 1-	2.6
70	447518	T80061	gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215667	ESTs	2.6
	438648	AA813125	ESTs	2.6
	450399	AW511049	ESTs	2.6
	420833	R47948	ESTs	2.6
75	453903	AW296606	ESTs	2.6
	443650	AI698330	ESTs	2.6
	427419	NM_000200	histatin 3	2.6
	423741	AA330362	gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	ESTs	2.6
80	441358	AW173212	ESTs	2.6
	402706		Target Exon	2.6
	436054	AI076262	ESTs	2.6
	402749		Target Exon	2.6
	442472	AW806859	gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872	gb:oo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564		Target Exon	2.6

	406003		Target Exon	2.6	
	459584	AI910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.6
	445060	AA830811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gil403440[gb]AAA73168.1 (M817	2.6
	416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypothe	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA225522		gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	Hs.170058	ESTs	2.6
20	441063	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	AI125263	Hs.170410	ESTs	2.5
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AI693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yl79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.5
45	404678			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429906	AL080137	Hs.193743	ESTs	2.5
	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
50	438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048462_1	AW176091 H24234
	408432	1058667_1	AW195262 R27868 AW811262
	409579	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
65	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
	411829	1260309_1	AW865749 BE179419 BE179492
70	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
	415054	151827_1	AI733907 AA159708 AI732614
75	415098	1522174_1	D59687 D59694 D59656 D59589
	415131	1523680_1	D61119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35594 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237056 AA354236 AW957759 H08951
	419896	1888662_1	Z99362 Z99363
	420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599
			CO2215 AI6525
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
15	436190	41555_1	AK001059 AA633055
	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
20	447518	724787_1	T80061 AI382804
	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
25	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090698 BE090698
	455887	1380836_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
50	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
65	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
	403649	8705159	Minus	27141-27247
75	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
80	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

5	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079,102261-102443,102895-103202
	405564	2114222	Minus	16766-17344
	405678	4079670	Plus	151821-152027
	405735	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

15

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

20

TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

25	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to normal adult body tissue		
30	Pkey	ExAccn	Unigene ID	Unigene Title
	420154	AI093155	Hs.95420	JM27 protein
	425747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen
	419526	AI821895	Hs.193481	ESTs
	432441	AW292425	Hs.163484	ESTs
35	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheri
	407202	N58172	Hs.109370	ESTs
	432101	AI918950	Hs.123642	EphA3
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen
	425075	AA506324	Hs.1852	acid phosphatase, prostate
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1
	410929	H47233	Hs.30643	ESTs
	400287	S39329	Hs.181350	kallikrein 2, prostatic
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr
45	415989	AI267700		ESTs
	428336	AA503115	Hs.183752	microseminoprotein, beta-
	450693	AW450461	Hs.203965	ESTs
	400298	AA032279	Hs.161635	six transmembrane epithelial antigen of
	407168	R45175	Hs.117183	ESTs
50	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport
	454119	BE549773	Hs.40510	uncoupling protein 4
	428819	AL135623	Hs.193914	KIAA0575 gene product
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278
55	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheri
	433444	AW975324	Hs.129816	ESTs
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL
60	401424			NM_001172:Homo sapiens arginase, type II
	432435	BE218886	Hs.282070	ESTs
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1
65	407275	AI364186		gbqw34h07.x1 NCI_CGAP_U14 Homo sapiens
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma
	432473	AI202703	Hs.152414	ESTs
	410330	AW023630	Hs.159425	ESTs
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH
70	452792	AB037765	Hs.30652	KIAA1344 protein
	418848	AI820961	Hs.193465	ESTs
	400292	AA250737	Hs.72472	BMP-R1B
	433647	AA603367	Hs.222294	ESTs
	453160	AI263307	Hs.239884	H2B histone family, member L
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624
	431474	AL133990	Hs.180642	CEGP1 protein
	429220	AW207206		ESTs
	428134	AA421773	Hs.161008	ESTs
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA
80	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu
	434792	AA649253	Hs.132458	ESTs
	433466	AA508353	Hs.105314	relaxin 1 (H1)
	439176	AI464444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr
	428398	AI249368	Hs.98558	ESTs

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
	429918	AW873986	Hs.119383	ESTs	9.1
5	440260	AJ972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450642	R39773	Hs.7130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55899	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.145625	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoi	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AJ799909	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415785	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site faml	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
10	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
15	434485	AI623511	Hs.118567	ESTs	5.8
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA18703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902: Homo sapiens progesteron induca	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449525	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo	5.5
	426581	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	448715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	M83941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW843046		gb:IL3-CT0214-150300-Q85-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0



	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
5	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.0
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100:gi5852342[gb]AAD54015.1] (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	5.0
10	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
15	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
20	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AJ939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
25	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AJ692689		gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AJ345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	4.7
30	452843	AJ796769	Hs.208320	ESTs	4.7
	458229	AJ929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
35	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AJ792628	Hs.133273	ESTs	4.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AJ831190	Hs.166676	ESTs	4.6
40	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
45	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
50	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AJ760833	Hs.293971	ESTs	4.5
55	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78958	Hs.14411	ESTs	4.5
60	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
65	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
75	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*-PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW958065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
5	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
	420111	AA255652		gb:zs21h11.1 r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001664:gil12698061 dbj BAB21849.1  (AB	4.3
10	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
15	420905	AA521307	Hs.186651	ESTs	4.2
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
20	450597	AI701635	Hs.207077	ESTs	4.2
	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
25	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
30	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
35	436714	AA728964	Hs.293399	ESTs	4.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
40	445206	AI350199	Hs.269990	ESTs	4.1
	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449507	AA004825	Hs.103281	ESTs	4.1
	430487	D87742	Hs.241552	KIAA0268 protein	4.1
45	448152	AI741053	Hs.170770	ESTs	4.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125763	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
	400746			Target Exon	4.1
50	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypothe	4.0
55	442338	AI761976	Hs.156080	ESTs	4.0
	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
60	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
65	421312	AA824627	Hs.291670	ESTs	4.0
	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partia	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
70	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
	452221	C21322	Hs.288057	hypothetical protein FLJ2242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
75	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
80	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothe	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
5	435878	R08330	Hs.20152	ESTs	3.9
	446862	AV660697	Hs.282700	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403			Target Exon	3.9
10	448779	BE042877	Hs.177135	ESTs	3.9
	420533	AI809510	Hs.118971	ESTs	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	423453	AW450737	Hs.128791	CGI-09 protein	3.9
15	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AWB48047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	Hs.190325	ESTs	3.9
	421129	BE439899	Hs.89271	ESTs	3.9
20	424332	AA338919	Hs.101615	ESTs	3.9
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	3.9
	447033	AI357412	Hs.157601	ESTs	3.9
	439306	BE220199		WD40 protein Clao1	3.8
	410352	AW969725	Hs.150444	KIAA0373 gene product	3.8
25	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	3.8
30	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE617907	Hs.97635	ESTs	3.8
	438379	N23018	Hs.171391	C-terminal binding protein 2	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
35	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	Hs.97266	protocadherin 18	3.8
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	Hs.191791	ESTs	3.8
	437718	AI927288	Hs.196779	ESTs	3.8
40	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	426981	AL044675	Hs.173081	KIAA0530 protein	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
45	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	3.7
50	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	423096	AA732684	Hs.278428	progesterone induced protein	3.7
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420564	Hs.101760	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	453293	AA382267	Hs.10653	ESTs	3.7
	436671	AW137159	Hs.146151	ESTs	3.7
60	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	Hs.44743	KIAA1435 protein	3.7
	420092	AA814043	Hs.88045	ESTs	3.7
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	Hs.5722	hypothetical protein FLJ23316	3.7
65	419875	AA853410	Hs.93557	proenkephalin	3.7
	431231	AA653552	Hs.116532	ESTs	3.7
	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
70	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	Hs.145037	ESTs	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
80	450630	AA010429	Hs.191939	ESTs	3.6
	411057	AI681006	Hs.71721	ESTs	3.6
	436326	BE085236		aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
10	425465	L18964	Hs.1904	protein kinase C, iota	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517":g[4758712]ref[NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
15	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
	427304	AA761526	Hs.163853	ESTs	3.5
20	434763	AA648618		gb:ns07a11.1.r1 NCL CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
25	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769":BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
50	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
65	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
70	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
80	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
5	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
15	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
20	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
	423595	R82826	Hs.220702	ESTs	3.2
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhiHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338*:gll7459502 prij74665 outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.65731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI456682		gb:tk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
75	423855	AA331761	Hs.254859	ESTs	3.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:zab2d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
10	418658	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	407349	AA825449	Hs.83332	ENSP00000233779~Hypothetical 68.0 kDa p	3.1
	410869	AW808361		Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
15	425354	U62027	Hs.155935	gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425480	AB023198	Hs.158135	complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346	KIAA0981 protein	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
20	459324	AW080953		ESTs	3.1
	433852	AI378329	Hs.126629	gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.0
	448658	H71739	Hs.200227	ESTs	3.0
	452242	R50956	Hs.159993	ESTs, Moderately similar to A53959 throm	3.0
	424690	BE538356	Hs.151777	glycosyltransferase	3.0
25	405264			eukaryotic translation initiation factor	3.0
	407253	AA411175	Hs.141939	NM_030813~Homo sapiens suppressor of po	3.0
	452234	AW084176	Hs.223296	ESTs, Moderately similar to S65657 alpha	3.0
	434497	AI821803	Hs.136580	ESTs, Weakly similar to I38022 hypothe	3.0
	420355	AW968263	Hs.123126	ESTs	3.0
30	403481			Target Exon	3.0
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	Hs.115838	ESTs	3.0
	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
40	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
45	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
50	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-ii	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	Hs.194397	leptin receptor	3.0
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
60	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
65	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.162898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retrovru	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410790	1221131_1	AW803357 AW803423 AW812233 R06814
410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
		AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
		AW808704 AW808558 AW808714 AW808420 AW8
411436	1245660_1	AW846433 AW846159 AW846377 AW846528

5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355085 Z43062 R13213 H14422 H51299 H44619 H46391 R86024 H51892 T72744 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AJ333114 AI277384 AI088297 AI468477 AI824624 AW189506 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597 AA215404 AI950909 BE464132 AW271459 N74332 AI262061 T65754 AA229857 AA229658 AI217097 AW886090 W38035 W38792 AA232835 AW936043 AA603305 AA244095 AA244183 AA255652 AA280911 AW987920 AA262684 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AF109300 AI299378 AI202654 AA337221 AA336756 AW966196 AA377823 AW954494 AI022688 AA380153 AA380233 AW963529 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA418703 AA418711 BE071915 BE071920 BE071912 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340 AA884766 AW974271 AA592975 AA447312 AW207206 AW341473 AA448195 AI951341 AW968485 AW968670 AA480922 BE350425 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339 AJ003429 AJ003367 AA564825 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA648618 AW974389 H51771 N73895 AJ001872 BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281 AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706 AW270601 AW873282 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW502574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188 AA830149 AW978407 M85983 AW503637 BE220199 W01813 AF086118 N70760 BE221405 AW628666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877 AA910403 AI815593 W58361 AW162520 AI816550 N99828 BE079873 AI110738 AF074645 AV653771 BE089370 AI458682 H24240 R14537 R18426 AW867082 AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053 AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467 H00789 R76925 AW1828 AA001793 AA001871 NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AI692689 R14223 R18395 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816692 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AA495800 AA495737 AA010736 AA654716 AA640726 BE173515 BE173560 AI902860 T79703 T96307 AL079725 AW998716 AW022148 N68020 AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW753456 AW753036 AW854868 AW854862 AW835767 AW835537 BE160187 AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464 AA493662 AW897396 BE154814 AI911066 AI933734 AI680888 AJ003599
---	--------	-----------	---

TABLE 64C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NI\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
------	-----	--------	-------------

	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
5	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9955004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
35	R1:	Ratio of BPH tissue to prostate tumor tissue			
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	428134	AA421773	Hs.161008	ESTs	9.4
	446336	AW815036	Hs.151251	ESTs	9.3
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	400533			ENSP00000209376:-PRED65 protein (Fragmen	8.7
	418310	AA814100	Hs.86693	ESTs	8.7
	404592			NM_022739:Homo sapiens E3 ubiquitin lig	8.1
45	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
	400080			Eos Control	7.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
50	418387	R18085		gb:yg16b12.r1 Soares infant brain 1N1B H	7.2
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
	404967			Target Exon	6.9
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
	412988	BE046680		gb:hm42h03.x1 NCI_CGAP_RDF2 Homo sapiens	6.8
	400440	X83957	Hs.83870	nebulin	6.6
60	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
	400086			Eos Control	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
65	419015	T79262	Hs.14463	ESTs	6.3
	453789	AA628517	Hs.118502	ESTs	6.2
	424940	AA985308	Hs.283902	ESTs	6.1
	403667			Target Exon	6.1
	429014	AI800518	Hs.118158	ESTs	6.0
70	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter	6.0
	419999	AI760942	Hs.191754	ESTs	6.0
	405348			C7001664:gi12698061 dbj BAB21849.1  (AB	6.0
	404003			Target Exon	5.9
	453200	AA033832	Hs.212433	ESTs	5.7
75	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432319	AW510770	Hs.128386	ESTs	5.7
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
	443361	AI792628	Hs.133273	ESTs	5.6
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	5.6
80	439079	AF085937	Hs.38348	ESTs	5.5
	422081	AW136820	Hs.196011	ESTs	5.5
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
	423529	T87318	Hs.120411	ESTs	5.5



	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
	454958	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
15	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
20	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	450317	AI692689		NM_002518*:Homo sapiens neuronal PAS dom	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gi 4758712 ref NP_004659.1  al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
55	439752	T78968	Hs.14411	ESTs	4.5
	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stratagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
	441620	R59595	Hs.26675	ESTs	4.2
70	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	408500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	430124	AW204994	Hs.253450	ESTs	4.2
80	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
5	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo	4.0
10	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW569118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
15	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
20	454806	AW872430	Hs.273743	ESTs	3.9
	429056	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
25	407834	AW084991	Hs.26100	ESTs	3.9
	400398	AF137396	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482:gij9790241[refJNP_062628.1] S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized Infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NCL_CGAP_P2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AI637649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AI470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Refina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455057	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
5	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517:gij4758712[re]NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	HB6374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769:BG153O3.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410651	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI39732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
50	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA069050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-r06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothe	3.2
	418986	AI123555	Hs.81795	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501:gij129092[sp]P23270[OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429559	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA577981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AI754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
15	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
25	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
30	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypothe	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AI939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	418948	AI217097		gb:q43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140*:Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AI381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

## 55 TABLE 65B

Pkey:		Unique Eos probeset identifier number	
CAT number:		Gene cluster number	
Accession:		Genbank accession numbers	
60	Pkey	CAT Number	Accession
	408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 AW810325 AW810443 AW8
65	409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
	410559	1208283_1	AW754192 W00554 AW857797 AW754203 AW754197 AW754193
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
70	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411518	1248692_1	AW850246 AW850251 AW850302
	411552	1249255_1	AW851255 AW851432 AW850955
75	412701	1322288_1	AW984757 AW984797 AW984734 AW984745
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
80	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	418059	171879_1	AA211586 F35799 AA211641 F29720 AW937387 AW937408
	418387	174731_1	R18085 AA219028 R17712 Z44345
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW052757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228589_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW935217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

45

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probe set
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nl position:	Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	Nl_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
65	403305	8099945	Plus	114632-114805
	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	105655-108050
	403433	9719511	Minus	72225-72437
	403481	9965004	Plus	93496-93633
70	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442, 1545-1697
	403805	8140491	Minus	51483-51742, 53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
75	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034, 25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
80	405321	3419846	Minus	44654-45210
	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
445336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:zw34h07.x1 NCI_CGAP_U14 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-05 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431457	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PREDE65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AI968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (f	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.128075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to 138022 hypothe	5.3

	423101	M83941	Hs.123542	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
5	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
10	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71885 Ste20-lik	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
15	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420633	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
20	457374	AA493682		gb:nh05d12.s1 NCI_CGAP_Tth1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
	450497	H64159	Hs.15328	ESTs	4.8
25	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H28882		ESTs	4.8
30	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
35	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	405348			C7001664.gij12698061dbj BAB21849.1  (AB	4.6
40	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123542	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
45	449821	AI671141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
50	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
55	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
60	420111	AA255652		gb:zs21h11.1 NCI_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
65	432765	AI003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	458912	AI911066		ESTs	4.2
70	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	450597	AI701635	Hs.207077	ESTs	4.1
75	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
	435136	R27299	Hs.10172	ESTs	4.0
5	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, moto	4.0
10	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
15	412988	BE046680		gb:hn42h03.x1 NCL CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
20	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	440450	AI333129	Hs.156147	ESTs	3.8
25	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	407198	H91679		gb:vv04a07.s1 Soares fetal liver spleen	3.8
30	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
35	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	432101	AJ918950	Hs.123642	EphA3	3.7
40	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-r03 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	435345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
55	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
65	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44099	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
	426917	AA913814	Hs.172854	DKFZP58680923 protein	3.6
70	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
75	401132			C12000517*:g 4758712 ref NP_004659.1  a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCL CGAP_Ew1 Homo sapiens	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5



	430665	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
5	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429543	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
10	404848			ENSP00000240769:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
20	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AA57449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170685	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW511703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321			Target Exon	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	433444	AW975324	Hs.129816	ESTs	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
	415861	Z43123	Hs.144513	ESTs	3.1
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.1
10	432527	AW975028	Hs.102754	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	417958	AA767382	Hs.193417	ESTs	3.1
15	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	405548			Target Exon	3.1
	423595	R82826	Hs.220702	ESTs	3.1
	412533	AA679863	Hs.69606	ESTs	3.1
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.1
25	405264			NM_030813:Homo sapiens suppressor of po	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-004 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
30	435021	AA922192	Hs.54709	ESTs	3.0
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087		ESTs	3.0
	432319	AW510770	Hs.128386	ESTs	3.0
	453713	R20640	Hs.79133	cadherin 8, type 2	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
35	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp7620076	3.0
40	404995			ENSP00000251890:Monocytic leukemia zinc	3.0
	444794	AI419991	Hs.145225	ESTs	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	420133	AA426117	Hs.155543	ESTs	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338	ESTs	3.0
50	449745	AI668593		gb:y138a05.x5 Soares breast 3NbHbSt Homo	3.0
	428412	AA428240	Hs.126083	ESTs	3.0
	428200	AI039624	Hs.98388	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
55	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 66B

60	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
65	Pkey <sub>i</sub>	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
			AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
			AW808704 AW808558 AW808714 AW808420 AW8
70	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411479	1247077_1	AW846047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
			AW848905 AW848214
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
75	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
80	424200	236595_1	AA337221 AA336756 AW966196
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912

	428342	290035_2	A1739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085530 AA731340 AW968485 AW968670 AA480922 BE350425 AJ003429 AJ003367 AA564825 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA648618 AW974389 HS1771 N73895 AJ001872 AA830149 AW978407 M85983 AW503637 BE220199 W01813 AF086118 N70760 BE221405 AA910403 AI815593 W58361 AW162520 AI816550 N99828 BE079873 AI110738 AF074645 AV653771 BE089370 AI458682 H24240 R14537 R18426 AW867082 AA001793 AA001871 AI668593 AI820774 R86205 H39971 H22177 H26241 AI692689 R14223 R18395 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AA495800 AA495737 AA010736 AA654716 AA640726 BE173515 BE173560 AI902860 T79703 T96307 AL079725 AW998716 AW022148 N68020 AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW753456 AW753038 AW854868 AW854862 AW812866 AW812746 AW812747 AW812884 AW812763 AW812722 AW835767 AW835537 BE160187 AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 AW854538 AW854418 AW854412 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464 AA493662 AW897398 BE154814 AI911066 AI933734 AI680888 AJ003599
5	430635	319643_1	
	432765	353907_1	
	433523	368873_1	
	434763	392847_1	
	436295	41733_1	
	439092	468554_1	
	439306	47088_1	
10	440947	505904_1	
	442481	543588_1	
	445432	63943_1	
	448044	747196_1	
	449570	81018_1	
15	449745	814534_1	
	450317	831956_1	
	450580	83929_1	
20	450582	83933_1	
	450687	84327_1	
	452462	918580_1	
	453682	977454_1	
	454037	996287_1	
25	454096	1007449_1	
	454171	1049240_1	
	454457	1207274_1	
	454665	1228599_1	
	454860	1237732_1	
30	454968	1247029_1	
	455067	1252050_1	
	455276	1272541_1	
	455646	1348557_1	
	455710	1352368_1	
35	457374	328758_1	
	458912	823104_1	

TABLE 66C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 Rt: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin)-prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M33119	Hs.89584	insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449825	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	della (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFP434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
	432101	AI918950	Hs.123642	EphA3	9.1
10	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypol	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
15	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	8.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.5
20	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
25	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0666 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
30	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91652	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	429505	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	432586	AA568548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
	450377	AB033091		KIAA1265 protein	6.6
60	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AJ297436	Hs.20166	prostate stem cell antigen	6.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP56680846 protein	5.8
5	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.7
10	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
15	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	5.4
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-8 protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
25	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
30	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
35	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptotagmin 2	5.0
	403046			NM_005656*:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
	450164	AJ239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AJ378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
50	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.105778	ATPase, Ca transporting, type 2C, member	4.7
	431724	AA514535	Hs.283704	ESTs	4.7
60	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75745	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22527	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to J05238 galactosy	4.5
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
75	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
80	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S6B401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8959	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
5	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AJ694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheli	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
10	442501	AA315267	Hs.23128	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
15	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
20	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
	432363	AA534489		gbm176g11.s1 NCL_CGAP_Co3 Homo sapiens	4.1
25	447574	AF162666	Hs.18895	lousled-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
30	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228699	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	438825	BE327427	Hs.79953	ESTs	4.0
35	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.282070	ESTs	3.9
45	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
50	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417057	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
55	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432675	AI791855		ESTs	3.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
60	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
65	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
70	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
75	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	calcinurin-binding protein calsarcin-1	3.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
80	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

5	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synthase	3.6
	422424	AI186431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
10	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
15	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
20	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
25	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
30	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
35	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
40	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
45	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
50	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
55	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
60	433891	AA613792		gb:ne97h03.s1 NCI_CGAP_Py2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
65	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
70	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
75	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*:gij12737279[ref]XP_012163.1]	3.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
80	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upt3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2



	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteoneclin, cwcw and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
15	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
	436278	BE396290	Hs.5097	synaplogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	438705	AJ049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278952	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA: cDNA DKFZp564N0763 (f	3.0
45	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AJ298501	Hs.211192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429638	AJ916662	Hs.211577	kinectin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.292833	ESTs, Weakly similar to t38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10569	ESTs, Weakly similar to T00050 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78106	phosphodiesterase 8B	2.9
	412826	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
80	431683	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

5	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferm	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
15	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
20	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
25	418166	AJ754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
30	425320	U29344	Hs.83190	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
40	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA058901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
45	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulf	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
55	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
70	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
	409650	T08490	Hs.28969	HSCARG protein	2.7
75	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
80	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

5	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	niban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
15	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulon 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
20	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
30	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
40	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRV (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
50	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
55	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AJ373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
60	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW981400	Hs.333526	HER2 receptor tyrosine Kinase (c-erb-b2,	2.5
70	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC087 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450628	AW382884	Hs.204715	ESTs	2.5
75	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
80	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
	414556	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
10	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.5
	443837	AI934625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
	435021	AA922192	Hs.73952	ESTs	2.5
15	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	426976	C75094	Hs.334514	NG22 protein	2.5
20	449458	AI805078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.181444	hypothetical protein	2.5
	424369	R87622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.5
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.5
	427515	T79526	Hs.179516	integral type I protein	2.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5
30	TABLE 67B				
	Pkey: Unique Eos probeset identifier number				
	CAT number: Gene cluster number				
	Accession: Genbank accession numbers				
35	Pkey	CAT Number	Accession		
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153		
			BG285837 AI720344 BF541715 AA355086 AA172236		
40	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259		
	412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514		
			AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538		
			BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721		
			AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815		
45	433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341632 BE222503 N71836 AI026061 AW953116 AW083132 AI979261		
			AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421		
			N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433		
	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526		
			BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360		
50	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307		
			AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991		
			AA084581 AA033610 AV742510 AV735788 R08336		
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756		
			AW779380 AA608979 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727		
55	437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010		
			N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860		
			AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742		
			AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA68546 AI262504 AI452782 AA554458 AA807080		
			AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744		
			T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422		
60	432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548		
	438869	52134_1	AF075009 R63109 R33068		
	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695		
			BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768485 AW512118 AA479302 AW770384		
			AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699		
65			AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398		
			BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866		
			AI699181 N73808 H08164		
	436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970		
70	428342	6712_1	N40094 N28596 AA884747 AA512890 BG436593		
			AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BI469629 AW968804 AA425658		
			AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361		
			AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040		
			AI392620 Z40708 AI885564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036987		
			AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166		
75	424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377		
			AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096		
			BM045465 AL531028 BG437151 BE868021 AA179427		
	450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846		
			AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192		
80	451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901		
			BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333		
	432363	1234917_1	AW970240 AA534489 AW970323		

5	422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE046820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW195918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 DH1142 C15616 AI538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 FD4161 T87230 R40898 AW204071 BI819428 AA683393 AA583376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
	417379	1610005_1	AA196390 AA507837 AA196488
10	407819	7392_2	AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
	419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
15	432675	1237917_1	AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610
	447620	687223_1	AI973051 AI400921 AI796154 AW241817 AW230951
20	409151	4123_1	NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435620 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
	409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF505938 AW266868 AI268977 BI168133 BM352065 AI262769 BF941976 AI056920 BI254740 BE732690 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
25	433891	647290_1	AW182329 AA613792 T05304 AW858385
	414922	1563_2	BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AI562079 AI700926 AI700561 BF063058 AW196387 AI132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827
30	414222	18695_1	BC021085 AI527872 AI526296 AL557087 BI255090 AU143499 AI560356 BG823170 BE736988 AU141388 AI580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H57776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U03761 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219705 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI420449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI727535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AI564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106
	426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG507710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
45	434194	62680_1	AF119847 AA437261 AA436987 AI132965
	432908	452541_1	AF150424 AI861896 AA570057 AV738855
50	412652	18858_2	AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI1668953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
	437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA338371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA717919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AI917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
55	418166	18858_1	AK055915 BE867252 AI523348 AA765350 BF468658 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI068810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI860060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732
	431416	120918_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974
60	447881	44623_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI438339 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32995 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
	407192	2200202_1	AA602964 AA609200
70	434747	117643_1	AW976537 AI033582 AA837085 AA745261 AA648395
	410297	2990_1	BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI37842 AI433809 BE222392 AA602308 AA28261 AI60355 AW662760 AI888087 AI342098 AA722418 W78151 AA64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA561791 BM474307 BI911169 BG575154 AW953303 T33504 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N99799 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AI418710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI855262 R55325 AI468927 R34681 H96211 Z39807 BF954386
75	424339	50559_1	NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833

445636	8561_5	BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090572
419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961054 AI018062 H80618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA594211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322 AI041403 Z49148
406789	0_0	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358395 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AI568301 AI567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
400263	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562865 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF669652 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW495536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859,56389-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165995,166189-166314,166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833,5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AI821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
5	400292	AA250737	Hs.72472	BMP-R1B	31.4
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	30.3
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	29.6
10	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.1
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	27.5
15	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.4
	403047			NM_005656*:Homo sapiens transmembrane pr	25.7
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.0
	428336	AA503115	Hs.183752	microseminoprotein, beta-	24.9
	401424			NM_001172:Homo sapiens arginase, type II	24.7
20	407709	AA456135	Hs.23023	ESTs	24.6
	407122	H20276	Hs.31742	ESTs	23.2
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.1
	415989	AI267700		ESTs	22.7
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.6
25	437052	AA861697	Hs.120591	ESTs	22.5
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	21.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	20.8
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.5
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
30	427958	AA418000	Hs.98280	polassium intermediate/small conductance	19.8
	431548	AI834273	Hs.9711	novel protein	19.4
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.3
	426501	AW043782	Hs.293616	ESTs	18.9
35	413597	AW302885	Hs.117183	ESTs	18.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.0
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	17.9
	429220	AW207206		ESTs	17.6
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.3
	418961	AW967646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	16.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.3
	428398	AI249368	Hs.98558	ESTs	15.8
	419078	M93119	Hs.89584	insulinoma-associated 1	15.4
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.2
45	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	14.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.7
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.6
	448519	AW175665	Hs.276695	Homo sapiens protein mRNA, complete cds	14.5
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.4
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.3
	418848	AI820861	Hs.193465	ESTs	14.2
	429918	AW873986	Hs.119383	ESTs	14.1
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
55	418278	AI088489	Hs.83937	hypothetical protein	13.9
	408000	L11690	Hs.196689	bullous pemphigoid antigen 1 (230/240kD)	13.3
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.1
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	12.7
60	412446	AI768015		ESTs	12.6
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.5
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.4
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.2
	453160	AI263307		H2B histone family, member L	12.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	della (Drosophila)-like 1	11.9
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.7
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.3
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.2
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.1
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.0
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
5	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
10	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975844	Hs.237396	ESTs	10.0
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
	443180	R15875	Hs.258576	claudin 12	9.5
20	406964	M21305		FGENES predicted novel secreted protein	9.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
25	440594	AW445167	Hs.126036	ESTs	9.4
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
30	437124	AA554458		KIAA0666 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
	438669	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
35	418836	AI655499	Hs.161712	ESTs	8.8
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
40	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	8.7
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
45	416239	AI038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP5641052 protein	8.4
	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420611	Hs.153934	ESTs	8.3
50	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
55	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
60	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
	447476	BE293466	Hs.20860	ESTs, Weakly similar to I38022 hypothe	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	7.7
65	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
70	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	7.6
	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2



5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
	412350	AJ659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
10	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
15	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
20	420297	AJ628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
25	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
30	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	lalexin protein	6.3
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
35	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
40	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
45	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
50	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
60	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
65	435706	W31254	Hs.7045	GLD04 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
70	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	5.5
	403046			NM_005656*:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
75	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
80	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
5	417318	AW953937	Hs.240845	ESTs	5.3
	429467	NM_004477	Hs.203772	F5HD region gene 1	5.3
	416276	U41060	Hs.79136	UV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
	450832	AW970602	Hs.105421	ESTs	5.1
15	448807	AJ571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
20	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
25	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	HA0164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635385	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489		gb.m176g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.7
50	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Stralagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X65724	Hs.2839	Norie disease (pseudoglioma)	4.7
	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538225	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
75	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433555	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
5	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
10	417958	AA767382	Hs.193417	ESTs	4.4
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	A1923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
20	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
30	432675	AJ791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI248720	Hs.114390	ESTs	4.2
	410297	AA148710		lumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301199	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340805	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	teptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476:gil12737279[ref]XP_012163.1	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGalNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ublnuclein 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

5	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	AJ681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AJ249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
15	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426891	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AJ186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429586	AJ871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA305342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AJ861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AJ806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*:HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulin 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
55	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
60	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.6
	409096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
75	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	AJ049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AJ093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.286906	WW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gbno97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA: cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300295	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439509	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427451	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
70	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_016569	Hs.267182	TBX3-iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to t38022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase 1	3.2

5	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	A1023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	A1382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275:Homo sapiens keratin 15 (KRT1	3.2
10	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypothe	3.2
	422173	BE385828	Hs.250619	phorbol-like protein MDS019	3.2
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
15	419829	AJ924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371:Homo sapiens hydroxysteroid (1	3.2
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
20	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
25	437179	AA393508		serologically defined colon cancer antig	3.2
	418700	AJ963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
30	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638:Homo sapiens hypothetical prot	3.2
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
35	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
40	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AJ187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
	448044	AJ458682		gb:tk13e01.x1 NCL CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
45	421254	AK001724	Hs.102950	coat protein gamma-coop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
50	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
	439864	AJ720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105964	ESTs	3.1
55	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
60	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437295	AA350994	Hs.20281	KIAA1700	3.1
	452627	AJ122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
65	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
70	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
75	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
80	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypothe	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445596	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
15	408298	A1745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	ALD49977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	A1452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	A1584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	A129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	A1675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:zn24c08.s1 NCI CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.26661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	A1200281	Hs.123910	ESTs, Highly similar to B34087 hypothe	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	nilan protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749865		ESTs, Weakly similar to I38022 hypothe	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AJ015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	A1373544	Hs.331328	intermediate filament protein syncollin	2.8
	433312	AJ241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF176265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	A1984625	Hs.9884	spindle pole body protein	2.8
75	418196	A1745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
80	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AJ557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
	440080	AW051597		ESTs	2.8
15	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10500	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
25	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
50	432745	AI821926		ghnl78f05.x5 NCL CGAP_Pr3 Homo sapiens	2.7
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(fh	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000081	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron of trichorhinophalangial syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AB23987	Hs.182285	ESTs	2.7
	411950	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	TS3519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7



	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	436682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
15	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain Interacting p	2.7
	404913			NM_024408*-Homo sapiens Notch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
35	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.6
	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	429825	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
50	417327	NM_004922	Hs.81954	SEC24 (S. cerevisiae) related gene famil	2.6
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47357	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
60	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
	434551	BE387162	Hs.260858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin; beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410645	Hs.164649	hypothetical protein DKFZp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
75	458946	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Aubergier b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-HRNA synthetase	2.5
	431836	AF178532	Hs.271411	bela-site APP-cleaving enzyme 2	2.5
15	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-HRNA synthetase-like	2.5
	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
25	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W05656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [Hs	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AJ023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AJ951341 AA969259	

449625	249224_1	B1918168 AW779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG886750 N45526 BG986917 T61382 R49391 R45432 A1203107 R35004 F07491 R25094 R35350
412446	63467_1	BC021735 A1669212 A120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF950659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 B1035538 BF908052 BF908057 BF090026 BF943158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 A1633838 AA617929 BF947001 B1035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 A1702161 AW341832 BE222503 N71836 A1026061 AW953116 AW083132 A1979261 AV725377 A1423288 A1640707 AW675518 A1032611 A1818044 A1295508 A1911386 A1270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF080433
453160	6028_5	BC009612 NM_003526 B1597616 AV761592 AV760377 AL601008 B1604131 BE645918 BG187760 BG181525 BG210634 BG192999 A1263307 AA344186 AW952956 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 A1143991 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R24557 A1337047 AA948360 A1638005 AA459950 A1624915 A1638047 A1467856 A1521826 AA860305 A1932315 AW003092 AW271756 AW779380 AA609879 A1634791 A1493770 A1565211 Z41145 A1627952 AA303734 BE349457 AW196765 AA255527 BE089727
437124	59408_1	AL1050013 BG939500 AW969191 AA769925 A1377973 A1625545 AA811365 AA521114 N24705 A1379579 AA424899 A1684671 AA829715 A1453010 N35401 AA677452 AA504340 A1209149 AA883574 A1379062 A1084455 A1280147 AA644327 BF432508 N27873 A17364 N34880 A1147024 T85860 A1219716 AA960926 H25544 B1857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 A1292318 AA829886 N95742 A1218758 H25588 N36282 AA024987 N36687 B1919187 N49471 AA889970 AW166152 AA68546 A1262504 AA52782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 A1016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 B1756612 AA508234 R49885 BF850422
438669	52134_1	AF075009 R63109 R63068
428342	6712_1	AK056315 A1015524 AA724079 B1713519 A1377728 AW293682 A1928140 A1092404 A1085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 A1332765 AW500888 AW576556 A1859571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 AW070509 A1521500 AL042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 A19392620 Z40708 A1985564 AW263513 AA913892 A1693486 AW263502 A1806164 AW291137 B1051872 B1059498 AA134476 AW084888 AA036967 AW370823 T55262 B1002756 AA489664 BF827261 W74741 BF963166
450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 A1819354 AW974068 A1393635 A1580846 A1024796 AW020098 B1491127 A1393644 N74993 AW7472959 BM478854 B1597437 H12165 A1458612 BE543192
432586	6633_1	BC022881 AU150944 BG50783 AW754175 AW857737 A1911659 A1050036 AA554053 A1826259 AA568548
450377	12109_1	AB033091 AL502743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 A1679751 A1873695 BG700891 B1553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 A1857643 A1768486 AW512118 AA479302 AW770384 AW072470 A1041596 A1049699 AW592865 AA978261 BE879747 BG114119 AW183811 AA909938 BF671621 BF350794 BF351375 BE925699 A1050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 B1036602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW1950540 A1693720 AA743364 A1915793 N48185 A1573107 AA043474 A1351615 A1969490 A1910763 R50866 A1699181 N73808 H08164
436063	5483_1	AK000028 AA494483 A1298674 AA720773 AV761529 A1884670 A1936202 AW294235 D61652 BF881184 A1711384 N27154 A1926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
424036	6226_1	NM_033445 BC001193 A1858781 BF794032 AA476620 AA810906 AA810905 A1291244 A1885097 A1359708 A1335629 H97396 A1344589 AA300377 AA457566 AW771833 BE465621 A1364068 A1364452 A1648505 A1918342 A1928670 AA886580 AL531029 AA886344 A1186419 B1932096 BM045465 AL531028 BG437151 BE668021 AA179427
407819	7392_2	AK056626 A1800896 BF939022 BE644718 A1954754 BE218177 BE348567 A1962406 AW293122 A1968798 A1457321 BE327228 BG913531 AW933055 T30280 R54166 Z43366 BG819153 BF033119 BE646274 BF940881 R18246 R42185
409151	4123_1	NM_004892 AF047442 BE275338 BF724863 B1917206 BE276933 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 A1002726 AA354813 B1092644 BG778400 B1260001 BG007325 A1267455 AA426574 A1160782 A1472186 AA256500 AA434006 BG435520 A1356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW968448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
422890	61426_1	AK057805 AW162343 A1190479 A1093318 BE048820 A1198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z42566 AW572911 AW964436 AW04030 A1632565 BE502530 B1792383 BF056928 AA449241 A1651825 AA805324 A1264863 A196918 A1948267 A1953735 A1263703 BF056387 AW594171 A1867447 AA319159 A1903440 AW956110 A1366013 A1867923 BG911906 D81142 C15616 AL538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 B1819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
451752	10408_5	AB032997 A141678 AW978722 BE467119 A1761408 BF727385 AW237035 A1934521 BF436248 A1479668 Z40632 AA832081 AW295901 BF057835 BE465977 A1621269 BE465983 A1756369 N74056 A1817896 AA716567 AA934774 H62600 H09497 BF943762 BE395333 BE883333
432363	1234917_1	AW970240 AA534489 AW970323
417379	1610005_1	AA196390 AA507837 AA196468
414922	1563_2	BG107484 AA632009 A1432670 A1656660 A1650884 A1521919 A1264653 AW150793 AW611894 A1917098 B1091245 A1551454 BF434889 A1580286 A1880735 BE301995 A1392959 AW613965 BM023628 AW515374 A1460102 BM023318 BE328188 A1952820 A1581363 AA557165 A1695577 AL562079 A1700926 A1470561 BF063058 A196387 AU132984 B1064046 A1970157 R02122 H55924 A1521721 AA808206 AA725223 A1766003 AW339821 AA805951 A1287969 AW664827
419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 A1951970 AW663548 A1139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 A17188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF587723 H28581 AA249370 BF726598 BE841554 B1045099 T84625 AW129578 BG770826
432675	1237917_1	AW973834 A1791932 A1791855 A1732640 AA558833 AA559897 A821610
410297	2990_1	BC013939 B1494690 B1491211 A1928393 AA843540 BG938644 AU185628 B1495842 AW173255 BM052709 A1743999 A1690144 A1922209 A1740907 AW340368 AA928759 AW118737 BF513970 A1707807 BF435295 A1339463 A1373842 A1433809 BE222392 AA602308 AA428261 A1460355 AW662760 A1888087 A1342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 A1150479 A1016166 AA779515 AA661791 BM474307 B1911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 B1602483 BE889592 AW954311 BM052986 B1962893 A1989299 Z42328 BF029504 T35668 BG402602 A10185770 A1023271 AA147719 A1434079 A1569000 A1276488 AA992453 AA342821 AA648303 A194364 A1051008 AA926941 AA350894 AW071451 N22249 A1784138 AA083847 N22258 AW440825 AA651570 AA376687 AA659125 A1356299 R70463 A1383586 AA827189 B1494872 AW021094 B1494871 AA905500 AA460923 B1492041 AW028965 A1624611 BG271780 A1497723 H88862 D59858 N89979 AA658425 N81154 D62341 A1274437 N66697 H96993 A1370663 A1728850 H05232 R59374 H12223 A1935759 A1362553 D60006 N29572 A1916833 N75273 AA148710 B1597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA52342 AW965441 W19723 R32966 BE883841 R61003 A1910374 A1865262 R55325 A1458927 R34681 H96211 Z39807 BF954386
447620	687223_1	A1973051 A1400921 A1796154 AW241817 AW290951
407192	2200202_1	AA602964 AA609200
434194	62680_1	AF119847 AA437261 AA436987 A1132965
448663	16112_4	BE966763 AA659765 A1961656 A1520918 AA761743 AA281477 N66431 BE463652 AA281329 AW272944 AA058687 BM145087 AA045516 AW341820 AA112515 AA258766 A1886639 AA714133 AA768245 AA035533 A1630459 T20165 AW971268 BE966269 AA522722
429163	1238297_1	AW974271 AA592975 AA447312 AA884766

	426991	29771_1	AK001535 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AI353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI265642 BG108520 AU150719 AW510354 AI554256 AI353968 AA191092 BF132635
5	432908 433891 409960	452541_1 647290_1 39576_1	AF150424 AI861896 AA570057 AV738855 AW182329 AA613792 T05304 AW858385 BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA080246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
10	414222	18695_1	BC021085 AL527872 AI526296 AL557087 BI255090 AU143499 AL560356 BG823170 BE736988 AU141388 AI580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AI564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI200449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AI564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW348877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA076106
15			AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI668953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
20			AI005915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AI133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375590 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732 AW976537 AI033582 AA837085 AA745261 AA648395
25	412652	18858_2	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R96631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 AW867082 AI458682 H24240 R18426 R14537
30	418166	18858_1	NM_015720 AF219137 AL534420 AL524055 AI537346 AI538442 BG765888 AL530054 AI525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF080256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI919246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833 BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
35	434747 437179	117643_1 12239_1	BI009308 BI009893 BF922023 BF922809 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA173730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF080855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF79374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680 AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974 AL079283 BF792538 AA744861 AI871888 AI478580 AI720775 AI888937 AI808966 BE463436 BF725510 AW675767 BF589111 BE855951 AW197232 AW272173 AI480335 BF589044 AA443540 AI420128 AI056029 AI650755 AW274589 AW183510 AI401098 AI271801 AW080345 AW189506 AW008293 AA884731 AA579802 AI968645 AI620822 AI222117 AA677146 AI346296 BI792788 AA446615 AI183488 AA697113 AW271851 AW241299 W90134 AA482921 AI049496 AA492010 AA846639 AA983603 AA969293 AI890036 BI254992 AA465313 AA476659 AW673442 AL557763 AA868312 H28886 AA787711 AA081838 AI989340 AL557762 N99654 Z28545 N28847 AA442388 AW887818 AW663156 BG252539 BG501262 BG714174 BG499052 AA058524 BE881198 C75278 R59648 AI829311 AA037656 AW026747 N64518 AW103253 BF529731 AW241677 AW194855 AA917531 R462278 H94036 AA856665 T10342 AW439112 AI090044 AA661591 N71704 AI474928 AU152235 D53426 N21634 R59590 R51072 R96601 H06171 AA084440 H84172 AW118714 C04928 W90092 AA039267 AA136445 R52391 T66024 BG778916 AA428153 N41394 AA283539 R96600 H94122 BF743684 AA147009 T65867 Z19487 BF697478 AW971213 AA493925 AA493567 AA876839 AA934462 T69981 T69924 AA078476
40	448044 424339	111791_1 50559_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019369 BF928776 AWB13409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H66845 H95592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
45	418259	133853_1	AA761668 AA573621 R09670 R92814 BI918715 BF594193 AI073494 AI363077 AI656655 AA121979 BF983131 AA491795 BG152545 AI350401 BF939121 AI479401 BI493099 BF057693 AI970550 BF111919 BF448282 BI493100 AW043768 AW006202 AI564010 BF433292 AI458202 AI954746 BE220962 AI375411 AI361048 AA115853 AI364474 AI669815 AA133407 AI928647 AW016610 AA133334 AA504948 AI291629 AI161208 AA837042 AI867138 AA987255 AI830219 AU150404 AI680674 AW969901 AW976442 AA743319 AA766420 BG180003 AW975741 AW749865 AA731828 AA731829 AW974812 AI821822 AI821820 AI821075 AI821073 AA651643 AA651662 BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777 W01360 N94710 H87957 AW051597 AI733052 AI167287 AI732999 AI566918 AI476787 AI791542 AA887204 AW025394 AA863338 AI240285 AI791393
50	411089	5597_6	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA355626 Z44571 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618
55	431416 434974	120918_1 77302_1	AA761668 AA573621 R09670 R92814 BI918715 BF594193 AI073494 AI363077 AI656655 AA121979 BF983131 AA491795 BG152545 AI350401 BF939121 AI479401 BI493099 BF057693 AI970550 BF111919 BF448282 BI493100 AW043768 AW006202 AI564010 BF433292 AI458202 AI954746 BE220962 AI375411 AI361048 AA115853 AI364474 AI669815 AA133407 AI928647 AW016610 AA133334 AA504948 AI291629 AI161208 AA837042 AI867138 AA987255 AI830219 AU150404 AI680674 AW969901 AW976442 AA743319 AA766420 BG180003 AW975741 AW749865 AA731828 AA731829 AW974812 AI821822 AI821820 AI821075 AI821073 AA651643 AA651662 BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777 W01360 N94710 H87957 AW051597 AI733052 AI167287 AI732999 AI566918 AI476787 AI791542 AA887204 AW025394 AA863338 AI240285 AI791393
60	431155 409927 447881	235742_1 2333801_1 44623_1	AW051597 AI733052 AI167287 AI732999 AI566918 AI476787 AI791542 AA887204 AW025394 AA863338 AI240285 AI791393 AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA355626 Z44571 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618
65	437050 436823 457733 453912	1240141_1 MH1660_153 119160_1 32562_3	
70	443009 412719	2142268_1 1634_2	
75	437050 436823 457733 453912	1240141_1 MH1660_153 119160_1 32562_3	
80	440080 419175	517737_1 35068_1	

			AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI634143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
5	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AL567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL535876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957657 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AI581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896 BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322 AI041403 Z49148
10	441128	20932_1	AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG142719 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL563737 BG029709 W52836 AI439658 BE551237 AA283724 BF109630 AI457096 AI080592 BE467736 AA693467 AI697593 AI887863 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AI418634 T31585 AA436630 AI366472 AA706191 AI422304 AI204899 AI041169 AA211402 AW827081 AA788593 T32736 AI767935 AA747914 T03534 AW959843 AI119527 BE327307 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113 AA658826 AI821926 AI791191 AA635129 AA564492 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769205 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084 BG256892 H10532 NA6614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W06152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298 BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R86953 R96989 R39707 BE867593 AA090310 AA090672 N27807 AA256634 BE276324 AF263306 BF951698 T66089 F11783 F11794 H29379 R19493 H18042 AL133995 AW134660 AI299437 AA057405 AA917450 AI002692 T09262 R43839 H29290 T65008 N78357 AI221207 AI659856 AA913591 AI220302 NM_000786 U23942 BI010150 BG773455 BI561558 BI460206 BG714348 BM126447 AU129411 AU129401 AI119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 AI217668 AA399409 BE182318 BM128040 AI693998 AW615411 AW070426 AI124550 AW778736 AA477781 AW263013 AI459619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA504786 BF432722 BI916393 BM470755 BI333211 AA095636 BI256415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48858 T91611 H42019 BI869421 BG502073 BG425943 W37290 W31363 BE004451 BF208311 BI048717 N78122 AA226597 AI525334 AI953821 AA657925 AA935436 AW957068 BC000222 AL136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI227161 BG820180 AA454463 AA255685 N31549 AA326504 BC019924 BG257230 BI092368 BI869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF686779 AI755222 AA452272 AW241170 AU156565 F28259 T16319 AA362508 N45153 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 AI922439 BE270975 AL119339 BF956085 AI565178 AL1554305 AL573240 AL572917 AI129627 AL546640 BE392285 AI092843 AI371057 BE302410 AI608753 AW674261 AI750057 AI052649 N47822 AL516249 AI589903 BG258439 AI123662 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 AI051112 AI783806 AL569622 AA070466 BF229936 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 AI361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 BI262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 BI085685 AA564566 AI221630 D52045 C14510 AA029390 W60153 H98743 AI682641 H28485 AA723093 AI081730 AA641309 AA587083 BI224818 AW204722 AI309186 AI215122 AI200785 BE467373 BM352502 AI304400 AI193071 AI742483 AW003408 AI400201 AI656740 AW665173 AI215120 AI147599 AI803429 AI076110 AI754349 AW205103 AI262491 AI808243 AI281007 AI051273 AI004801 AW768918 AW103289 AI474637 AI264446 AI699509 BE704420 AA989278 AA918256 AA830956 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94863 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 AI813809 AA933607 AA129695 AA548261 AA714393 AA775005 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51696 D55942 D52740 AI000118 AL516304 AL534259 N54940 AL579194 AI669399 AI342925 BE939201 AA633000 BI222963 AI519676 AW190306 BF035010 AW087897 AI864969 T57243 R48211 AA113880 R26594 C14467 C14444 BI195459 BE856346 BE270780 AL568073 BG389833 BE891549 BI223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA903841 BF752571 BE731304 AI380443 AI240179 AA977516 AA848643 AW079380 AW294316 AI913755 AI864320 AI685770 H25135 AI972654 AI538592 AI174783 R12271 R83569 AI274757 AI558500 AW022192 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D50181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60556 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769205 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
15	406789 410099	0_0 16732_1	
20	432745 400263	112643_1 18977_1	
25			
30	411605	10026_3	
35	445636	8561_5	
40	441054 429925	2641490_1 33135_1	
45	434976 440191	121716_1 MH790_2	
50			
55			
60			
65	440409 444610 446091 431843	588375_1 2145292_1 515091_1 445334_1	
70	400262	18977_1	
75			
80			

TABLE 68C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56389-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104, 152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624: Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931: Homo sapiens NADPH oxidase 4 (	2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AJ750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90808	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
438729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*: CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
15	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gbryb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
40	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
45	406506			Target Exon	1.97
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaplojanin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	mutimerin	1.85
	445727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414785	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiotensin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.76
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endothe	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.65
70	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL036668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94



5	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82952	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.109706	hematological and neurological expressed	1.65
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs;similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypothe	2.33
45	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
50	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406964	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
60	408989	AW361666	Hs.49500	KIAA0746 protein	1.43
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420255	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-rel simian leukemia viral oncogene hom	2.25
70	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AI066548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI597655	Hs.49265	ESTs	3.08
	422424	AI186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession



5	453085	10017_1	BC017336 BG16430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745542 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI288436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AAD43217 BE219784 AI799814 AA129575 AI671727 AW70033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AW273200 C06123 BF057147 AA627686 AA157944 AI990245 AA562517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136558 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI965583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773486 BE773474 BE773473 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242858 AW197954 BE905184 AA722026 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751088 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961685 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068278 AW976385 AL121194 AI767324 BM054718 AW366882 AA155151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
---	--------	---------	--

45	TABLE 69C
	Pkey: Unique number corresponding to an Eos probeset
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
	Strand: Indicates DNA strand from which exons were predicted.
50	NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	402463	9796896	Minus	8818-8952
	400494	9714719	Plus	169845-170272
	401234	9929642	Plus	120173-120337
55	406506	7711374	Minus	6843-8077
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
	406666	8118496	Plus	17982-18115,20297-20456

60	TABLE 70A:
	Pkey: Unique Eos probeset identifier number
	ExAccn: Exemplar Accession number, Genbank accession number
65	UnigenelD: Unigene number
	Unigene Title: Unigene gene title
	R1: Ratio of the mean of the vessel AI's to the mean of the HUVEC AI's

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
70	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	0.99
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06
	412636	NM_004415		desmoplakin (DPI, DPII)	1.25
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.36
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.50
75	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.55
	414572	AU077174	Hs.288181	cathepsin H	1.64
	415314	N88802	Hs.5422	glycoprotein M6B	1.70
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	1.75
	406973	M34996	Hs.198253	major histocompatibility complex, class	1.88
80	456974	M12529	Hs.169401	apolipoprotein E	1.90
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.91
	406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of m	1.97
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	1.99

5	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	AI193115	Hs.16611	tumor protein D52-like 1	2.27
10	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudodysostosis)	2.38
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.39
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
15	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
20	426716	NM_006379	Hs.171921	sera domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
30	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
35	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
40	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
45	429123	AB011099	Hs.196547	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425822	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
50	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
55	414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
	424651	AI493206		ESTs	3.17
	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone H1409 unknown mRNA	3.20
60	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin(OSF-2os)	3.24
	447384	AJ377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
65	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
70	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI091195	Hs.65029	growth arrest-specific 1	3.35
	451529	AI917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
75	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.8615	myosin regulatory light chain 2, smooth	3.41
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
80	407938	AA905097	Hs.85050	phospholamban	3.48
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	Integrin, alpha 8	3.52
	404277			NM_019111*:Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AJ017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AJ769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.85
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
	434868	RS0032	Hs.159263	collagen, type VI, alpha 2	3.90
15	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
20	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW539251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78065	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.88
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
45	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probe set identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 B438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW365566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI06306 BG990973 BI040954 BF919911 AU140155 AI951765 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF073593 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG988845 AA131128 AA099891 W39488 CD4715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI558096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA126330 BG681425 BE705078 R20904 BG880059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE057786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI668869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247695 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

5	454042	30254_1	BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177785 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 AJ420458 AI018523 AA708886 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570 AW964381 BG007409 BM314056 AA465642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267360 N64249 W67500 F07962 AA322394 BI489987 BE644965 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280 BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA635644 AI493206 AA669979 BE245127 BG986430 BG986529 BF665973 BG030157 BG622575 AA766495
10	440820	3091_1	
15	424651	46029_5	

## TABLE 70C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404277	1834458	Minus	91655-91946

## TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	75th percentile of ewing sarcoma to 85th percentile of body map

Pkey	ExAccn	UnigeneID	Unigene Title	R1
104659	AW969769	Hs.105201	ESTs	70.3
101447	M21305		gb:Human alpha satellite and satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6
110278	AF061573	Hs.19492	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008583	Hs.91622	neuronal pentraxin receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5
121362	AF050147	Hs.97832	chondromodulin 1 precursor	34.7
131291	NM_004350	Hs.170019	runt-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylser	28.7
122651	AW975398	Hs.293836	ESTs	28.0
100299	D49493	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
123619	AA602964		gb:nc97602.s1 NCL CGAP_P12 Homo sapiens	26.1
124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi)	23.1
116301	AW969706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN III	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	21.3
131313	R96290	Hs.75874	ribosomal protein L44	20.8
116790	AW161357		microtubule-associated protein tau	18.7
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1594	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW292315	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126789	AW753865	Hs.74376	olfactomedin related ER localized protein	16.3
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	15.5
107160	AA314490	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40665	Hs.31564	ESTs	13.8
	106498	AJ221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calsynenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
10	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
15	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104968	AI249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033084	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
	123049	BE047680	Hs.211869	diclkopf (Xenopus laevis) homolog 2	10.6
25	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-in	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
	110730	N67655	Hs.26411	ESTs	10.3
30	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AI204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-in	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown [H.sapi	8.8
55	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AI347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Se-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AI823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP586D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (	7.6
	118036	AA711862	Hs.196008	Homo sapiens cDNA FLJ111723 fis, clone HE	7.6
	131170	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
15	101050	AJ077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
	118013	AJ674126	Hs.94031	ESTs	6.9
	120147	AJ917116		hemoglobin, beta	6.8
30	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIc, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AJ373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AJ078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
55	106383	AA447453	Hs.27850	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
60	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yl32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AJ088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.8
70	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R55841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI458004	Hs.278956	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AJ034467	Hs.34650	ESTs	5.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gbxn98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
5	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
	106668	R49390	Hs.254129	KIAA1678	5.4
10	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
	131185	BE280074	Hs.23960	cyclin B1	5.4
15	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
20	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothi	5.2
	120830	AI568170	Hs.96885	ESTs	5.2
30	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	AI089560	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothi	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	116814	H50834	Hs.77899	gb:yp86a10.s1 Soares fetal liver spleen	5.0
50	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	125769	AA083456		gb:zn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
70	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALLUS_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcdonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

	113974	AW959756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
5	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
10	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothe	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
15	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
20	106489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypothe	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
25	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
30	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
35	115167	AA749209	Hs.43728	hypothetical protein	4.3
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
40	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
45	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
50	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
55	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	4.2
	130832	AW836006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
60	125960	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-IRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
65	123729	AL039779	Hs.278572	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73964	EphA4	4.2
	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
70	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothe	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
75	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
80	129948	AJ537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1



	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid)	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovirus	4.0
5	127153	AJ732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128559	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
10	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo)	4.0
	126965	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	4.0
	103100	NM_005574	Hs.184585	UIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
15	128797	NM_002975	Hs.105927	stem cell growth factor, lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
20	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M82843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_	4.0
25	126522	W31912	Hs.21168	gb:zc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
30	105808	AJ133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
35	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
40	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	3.9
	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
45	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
50	105476	AL117352	Hs.77196	Human DNA sequence from clone RPS-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
55	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.8
	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
60	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA296874	Hs.77494	deoxyguanosine kinase	3.8
65	127262	AA828125		gb:od71a09.s1 NC1_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UJ-H-BI3-ala-a-12-0-UI.s1 NC1_CGAP_Su	3.7
	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126862	R12014	Hs.20976	ESTs	3.7
70	116203	AW137166	Hs.87306	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
75	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AJ241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
80	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW654072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (I	3.6
	114118	F01598	Hs.175930	ESTs	3.6
	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypothe	3.6
15	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_Nb:HH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X18866	Hs.333497	cytochrome P450, subfamily IID (debrisq	3.6
	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
20	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypothe	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1N1B H	3.5
	117265	AA451966		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	AJ002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	105918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI639429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	Insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
60	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	105367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.195008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AJ076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
80	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N53753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
5	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	108650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal cleft	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares infant brain 1N1B H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:tk3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T65813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	3.3
	123284	AA488888	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14205 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
5	133761	AF041430	Hs.75922	brain protein I3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
10	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
15	109517	AJ631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AJ769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN IIII	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA928960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
30	132305	AJ806090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
35	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
45	134964	AJ803516	Hs.272891	hippocampin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease H1, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group 1, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AJ652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
60	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12850	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW283689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AJ908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AJ914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
75	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
80	123485	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hn88a05.x1 NC1_CGAP_Kd11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
15	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator corla	3.0
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.59423	ATP-dependent RNA helicase	3.0
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133666	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	3.0
40	122219	AA436002	Hs.183161	ESTs	3.0
	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp5640043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	129659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:ae38104.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	126887	H20832		gb:ym48d03.s1 Soares Infant brain 1N1B H	3.0
70	117950	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

80 Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey CAT Number Accession

108451 13766\_2  
 107908 46987\_1  
 5 123619 371681\_1  
 131495 142008\_1  
 10 101445 1650\_5  
 100944 25682\_2  
 117265 10421\_1  
 117297 647718\_1  
 108859 137143\_1  
 15 125165 1852047\_1  
 116790 19864\_1  
 20 103038 15024\_1  
 25 103038 15024\_1  
 30 103038 15024\_1  
 35 103038 15024\_1  
 40 126086 1606216\_1  
 126098 1629789\_1  
 125464 168460\_1  
 126127 1205826\_1  
 125558 1703083\_1  
 126426 110687\_1  
 45 118644 81501\_1  
 50 118644 81501\_1  
 55 118644 81501\_1  
 60 127262 231725\_1  
 127315 37938\_1  
 103898 187213\_3  
 126769 119008\_1  
 120147 386607\_2  
 128080 1540039\_1  
 104590 44964\_1  
 65 127262 231725\_1  
 127315 37938\_1  
 103898 187213\_3  
 126769 119008\_1  
 120147 386607\_2  
 128080 1540039\_1  
 104590 44964\_1  
 70 127496 340470\_1  
 126872 142696\_1  
 75 126887 1572189\_1  
 128132 177108\_1  
 126967 169750\_1  
 120325 166688\_1  
 112511 17406\_2  
 80 127496 340470\_1  
 126872 142696\_1  
 126887 1572189\_1  
 128132 177108\_1  
 126967 169750\_1  
 120325 166688\_1  
 112511 17406\_2

106012	95214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02658 AA035018 R75957 AI803329 R27528 R35203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909584 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R88588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
5	127705 966283_2 127728 3398_5 129012 22280_4	AJ003322 AJ003324 AW404061 R09654 T67160 N50566 N53259 R81936 D78695 D78806 D78780 C17009 AA004406 AA122102 R70625 AA148932 H59583 H81146 H03878 H49863 H21182 H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R21924 H01290 H01283 H42464 W31947 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AA492481 AA088608 R69918 R36334 H80281 N58483 AI075154 AI086754 AA595787 H81051 H01187 AI057251 T66992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 AI088338 AI373324 H66992 R96235 AI494132 R16678 AA088178 AA705356 AA962143 AA148933 R09231 AI160937 R70525 T46980 AI200046 H02301 AA367587 R35968 T97106 D78703 N78072 D78668 D63268 R28197 AA085579 R3766 R92415 W00998 R80766 R67875 R27583 R09343 H13646 R27682 T89007
10	106498 245223_1	AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI92961 AI361526 F04002 AA452141 T23551 AI472655 AI193667 AI341984 N92658 T32870 R52664 N50428 AW089291 AI934175 AI242373 D60665
15	120934 177521_1 115197 42406_1 129706 81501_1	AA226198 AA226513 AA383773 R18656 AW968014 AA262288 AW968002 X93079 AJ002788 R51324 AI381600 D80031 AW500520 AW593740 F09382 AA810597 AA262174 AA810595 AA810596 AA443241 R23784 R67255 R00047 AI457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864 AI953638 R31669 AW769278 R82399 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605 AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W33671 R99823 R77956 H61601 R98785 R09738 H78317 H53537 H81056 T53780 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI070230 R30775 H68996 AI014957 AA369082 AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453 H00188 R21233 H03055 R53822 AA367588 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H60972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R82759 C19002 H01715 W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N99687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805255 AI458777 AA974369 AI8665929 AI886032 AI823925 AI823566 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI355825 AI2668 AA894603
20	131019 223488_3	AW105585 AI824555 AW339175 D20479 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
25	131170 8113_1	AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 AI093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 AI673095 AA599106 AW601545 AI538739 AI538730 AI521786 AW366369 AW021010
30	123470 8785_29	AA362576 AI289927 AA382592 AA608733 T74884 AA620552 U42359 N57493 H01052
35	123532 genbank_AA608733 125032 genbank_T74884 123808 genbank_AA620552 102398 entrez_U42359 118129 genbank_N57493 109841 genbank_H01052 118922 220560_1	AW206193 AW137594 AI953685 AI919143 AI24371 AW007698 AW025681 AI954289 R40438 AW070364 AI679653 AI679081 AI623213 AI652310 AI631411 AI565384 AI566734 AA149597 AI538172 AI040831 AI770021 AI914287 AA279311 W73001 AI493117 AI693374 AI802007 AI990645 N29752 R94559 AA806475 AA806828 R90998 R94558 AW300112 W24097 AW003016 N91920
40	113119 genbank_T47910 104799 genbank_AA029703 113560 genbank_T91015 129794 39565_1	T47910 AA029703 T91015 AF093097 AI869509 T27070 AA326718 AA024743 W23922 AA479593 AI765668 W23908 U92986 AA081632 N50578 AA065245 AW365046 AW365014 AA961091 AA150231 H53426 AA234651 N50522 T79343 T87399 N91858 H41179 AW009453 AA024744 T27069 AI346379 H88431 AA152289 R45373 AA477432 AI745607 AI807602 H41152 AA065244 AI242569 AI091032 AI251849 F03857 H88369 AI174488 AI002696 H53427 T87293 N91869 W35270 AA453723 AA453705 AW071829 AI393866 AW071807 W23592 AI342074 D31158 AA833756 AI991896 AA447791 AI864125 AW377239 AA295365 AI687970 R34076 F07607 AA521310
45	124250 314220_1 101447 entrez_M21305 117357 genbank_N24829 103392 entrez_X94563 135029 H58818_at 105225 genbank_AA211777 121292 genbank_AA401807 105909 82840_1	AW499865 R94584 R21283 AA350256 H68126 M21305 N24829 X94563 H58818 AA211777 AA401807 AA195191 AA190578 AI632307 AA195227 AA743633 AI823408 AI832203 AI653114 AA205307 AW021913 AI687980 AI674198 AI675563 AI417935 AA707350 AA135157 AI434721 AI151038 AI038305 R52643 AA780141 AW207645 D19691 AI474370 AA401739 N22905 N70378
50	100237 entrez_D30715 114988 genbank_AA251089 123423 genbank_AA598484	D30715 AA251089 AA598484
55		
60		
65		
70		
75		

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigena Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigena number
	Unigena Title:	Unigena gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

Pkey	ExAccn	UnigenelD	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932	Seq ID No B1 & B2
	410102	AW248508	Hs.279727	Seq ID No B3 & B4
	101104	AW862258	Hs.169266	Seq ID No B5 & B6
	447761	AF061573	Hs.19492	Seq ID No B7 & B8
	428183	AW969726	Hs.98381	Seq ID No B9 & B10
10	439221	AA737106	Hs.32250	Seq ID No B11 & B12
	121619	AA528339	Hs.178062	Seq ID No B13, B14, & B15
	104559	AW969769	Hs.105201	Seq ID No B16
	105782	H09748	Hs.57987	Seq ID No B17 & B18
	129977	NM_000399	Hs.1395	Seq ID No B19 & B20
15	100299	D49493	Hs.2171	Seq ID No B21 & B22
	116301	AW969706	Hs.293332	Seq ID No B23 & B24
	106533	AL134708	Hs.145998	Seq ID No B25-B27
	131313	R96290	Hs.75874	Seq ID No B28 & B29
	105316	AI671245	Hs.24835	Seq ID No B30 & B31
20	113003	AW292315	Hs.7215	Seq ID No B32
	102836	U94320	Hs.158330	Seq ID No B33 & B34
	102745	AW753865	Hs.74376	Seq ID No B35-B40
	123308	C14187	Hs.157208	Seq ID No B41 & B42
	120147	AI917116	Hs.211869	Seq ID No B43
25	123049	BE047680	Hs.211869	Seq ID No B44 & B45
	119082	AF252297	Hs.91546	Seq ID No B46 & B47
	105301	AW352357	Hs.7457	Seq ID No B48 & B49
	128478	AA708205	Hs.100343	Seq ID No B50-B53
	106111	AW875398	Hs.6451	Seq ID No B54 & B55
30	131307	NM_000025	Hs.2549	Seq ID No B56 & B57
	120830	AI568170	Hs.96886	Seq ID No B58 & B59
	127664	AA806164	Hs.116502	Seq ID No B60
	102725	AB026187	Hs.159156	Seq ID No B61 & B62
	132520	AA257992	Hs.50651	Seq ID No B63 & B64
35	130637	AA356764	Hs.17109	Seq ID No B65 & B66
	117602	N35020	Hs.44685	Seq ID No B67 & B68
	128797	NM_002975	Hs.105927	Seq ID No B69 & B70
	129703	BE388665	Hs.179999	Seq ID No B71 & B72
	125770	AA143045	Hs.81665	Seq ID No B73 & B74
40	414761	AU077228	Hs.77256	Seq ID No B75 & B76
	420462	AF050147	Hs.97932	Seq ID No B77 & B78
	410268	AA316181	Hs.61635	Seq ID No B79 & B80
	104691	U29690	Hs.37744	Seq ID No B81 & B82
	416836	D54745	Hs.80247	Seq ID No B83 & B84

Table 72B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
50	131307	3138_1
	131313	93372_1
		NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
		R95290 U02411 C18327 AA367588 AA367557 H89632 C17954 AA568860 AI752983 AA699451 H04260 AI128118 AW193364 N94503
		AA029995 T40536 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226
55		AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R65618 H73711 R58545 D79189 AW265710
		R77664 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H63662
	116301	52669_2
		AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807206 AW663917 AA454645
		AA489238 BE241958 AA743491
60	103080	17092_1
		AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880
		BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077
		W05266 AI824103 AI499061 AA642944 AI042556 AA906539 W60380 AI571777 AI135581 AA112340 N75459 AA592929 AI085348 AI278890
		AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160603 AI074344 AI344561
65		AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI659596
		AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779
		AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H66084
		AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077
		AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141
70		BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329
		BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W46412 AW771113 AI700678 AA502628 AA133137 BE274186
		BE396090 BE613371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970
		AW298822 AW080962 AI073747 W24123 AA577596 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347
		AA589485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162
75		W49709 AW514883 AA100676 AI366087 AA069474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333594 AI289794
		AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI660881 AI366117 AA403090 AI272818
		AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079958 AI752231 AA076431 AA113245
		AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535500 AA064665 AA705388 AA064623 AA962503 AI924926 AW131206
		AW275281 AI280632 T29597 W48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 N72201 AW510563 AW079132
80		AA207064 AI143740 AW440672 AA632154 AI290288 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526
		AA487486 R92970 AA934071 AI080448 AA063257 C05786 N99099 R42969 AA807065 AA662686 AA533833 AA662304 H51748 BE539444
		AI382164 AI814595 BE537043 AI168307 BE408935 AA453606 R89428 AA936527 AA936890 AW369618 AW264602 R18074 AI474189
		AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086552 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692



5	132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW838107 AW838105 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE000988 AA131806 BE180577 AW838269 AL039831 A1754380 C06051 AA131737 AW838239 A1767465 A480134 AA610312 AW838190 AA379252 AW838282 AA484077 A1423413 A1685064 BE328307 A1241857 AW838281 AW838284 A1671267 A1814928 AA828367 A1476306 A1270180 AA622352 A1076497 A1635919 A1444994 A194028 A1669159 A1928131 AA448853 A1350143 AW079289 AW467807 AA480442 AA522935 BE180570 AW380087 AW380109 A1081015 A1690818 A1589485 A1698510 AA642019 AA714366 A1580430 AA985527 A1740475 C21398 AA257993 A1302393 A1689018 AW770194 AW753750 A1079164 BE550338 AA559851 T16108 A1864822 A1932827 AA045095 AA045062 A1954225 AA768569 AA709308 AW958363 N35020
10	117602	10565_4	AB026187 NM_014522 U79247 F13304 AA224524 F10602 R39431
	102725	11582_1	AW753865 F07644 F11280 F06355 F08136 U79299 F07459 F08750 F12419 F12842 F06488 F08585 F13403 F05921 F05512 F11683 F05416 F12841 F12810 F05418 F12850 R24551 F06276 H11803 H10237 H11542 H22894 R59563 H19351 H18722 F11237 F08507 H23123 R61595 F07796 F06201 F12289 F07107 T78113 F08734 F13344 F05760 F11784 F08780 F05835 R20588 F07739 F11497 R17410 H17414 R20440 T66090 R25292 T66236 T78766 T79908 R25286 R60071 C14761 AW905192 AA331914 AW965291 H09000 F05212 F08313 F05825 H06399 H15135 H11378 R66424 R61541 AA235405 A1205041 R59564 H23124 H18638 R37359 A1571275 R41780 T66174 T66159 R54102 W07657 H10794 R52337 R42890 H14354 R40952 T17391 H12068 R56797 R51000 R60011 R37617 R39434 H29286 T16403 H09129 R49114 H15161 H11729 R39160 H10458 H24454 H11432 R54433 H08768 H24042 H09511 H17281 H15292 R37849 A1991965 R52815 R2650 T17390 T16438 T17388 T16285 R48963 R50782 R44247 R46729 R59558 R40696 R43575 R44420 T17403 R37754 R46637 R51039 R40513 T23785 F10433 T16350 H10191 R43688 T23543 H08591 R44351 R37575 R49508 F04379 F04056 F05067 F02010 F09158 F10036 F08900 F02559 F09914 F09434 F05034 H17415 F02644 H10650 F10451 H14589 F10444 T16440 R44517 R46643 F03993 F10443 F02170 F03343 F10414 F04794 F11122 F04997 F03894 AW005932 F02767 F10941 F01777 R45260 F03386 R45261 T65009 F10990 F08942 F01673 H23253 F04533 F02082 F01669 F03689 H09568 R40763 H06400 R50958 N80570 A198226 T23763 AA814486 AW015823 A1886272 A1886271 A1886270 A1886269 F10049 A1984267 A1886279 AA558516 F02071 A1783843 A1804884 F01468 AA730438 AF035301 R38389 R41440 R59468 R14437 T89036 R43560 H10821 R52850 R56722 R14559 T09299 H10467 R25829 F13546 R56796 R51151 D82657 T32952 T66257 H06569 F12430 T74326 H08489 R34430 R13083 H23364 R21134 T77098 AW957157 H24150 H11403 R52336 F12830 T77173 T74281 T77663 T74736 H10649 H12067 R20092 T74735 R54530 R17552 R59557 R54529 H17280 T75171 H14694 T74975 H15291 R18574 R54157 R13446 H15221 R35120 R35031 R21277 R19632 R35820 R50899 R13923 R36771 R26485 R33061 R20100 H24426 H09184 H15958 R19253 H15916 H09510 R36032 R19691 H14402 H14885 T17068
15			AF252297 N27888 F13415 R34552 R14377 AA323962 AW611514 AW614097 AW195487 A1026040 A1097663 AA012834 AW969885 AA988198 R49069 AW873673 R37774 F08840 AA484668 AW873664 AA170805 AA170825 AA585275 AA585280 AA012833 U94320 NM_006174 U66275
20			AA143045 AW271802 A1017093 AA450183 W93694 A1885044 A1890068 AW264522 AW073559 A1355325 A1051302 A1567686 A1143554 A1457891 AW468784 A1567693 AW884460 A1424892 AA401298 AW244098 A1122936 N24824 AA552932 AA873164 A1308810 N26098 H81852 N20798 AW263947 A1696267 AA449422 AW877967 A1917116 AA633698 A1580389 Z39483
25	119082	34131_1	AW292315 A1090408 AW517041 A1928695 A1092060 AA716741 N98235 T23629
30	102836	25380_1	AW969769 AA484137 A1291362 N64753 A1133784 AA007153 BE046923 D59990 C15166 D59991 D60194 AA648108 N76160 D61027 D60630 U29690 AF272890 AA708166 AA010748 R23839 H59572 R23383 A1625747 AA011176 AW665324 H02674 H59573 AA757931 H12502 R66851 AA702310 AA748431 AA749352 C01127 A1003679 T96352
35	120147	386607_2	AW352357 AA852419 T80568 AA332510 AW149659 AA341609 AA809550 A183690 AA730875 T31719 AW565361 AA779709 T05461
	113003	420161_1	AA564806 A1142536 A1553857 D53384 D53747 D54101 D55112 AW071935 A1082447 A1290911 AW168872 AA199743 A1091646 A1246702
	104659	82594_1	AZ71662 AW117296 A1032138 A1741489 A1538705 AA233541 A1682685 AW136268 A1689641 AA599916 A174443 A1432175 A131328
	104691	41308_1	AW136277 AA852418 AA243035 T03902 C15651 D52660 H08108 AA844525 A1420648 A1282445 AW068986 AW497637 AA779042 AA298564 BE262936
40	105301	27795_5	A1571245 D81062 A1085879 A1193252 A1870535 N23132 H97661 H18098 AA552173 AA233924 AA503379 H19618 D60732 F04762 H11343 AW590283
45	127664	394361_1	AA806164 AA678564 AW978234 AW023951 AA651859 A1699785 AA913686 AW974569 A1681287
	106111	4671_1	AW875398 A1064861 NM_014138 AF090943 BE071887 BE547232 BE622599 A1345700 AA284315 AA147700 AW376340 BE220170 BE348475 AA025037 AA057284 AA025038 T16193 AW130196 AW594516 A1989991 A1139091 AW675747 AA830435 A1924977 A1670778 A1051887
50	128478	370722_2	AA912574 AW130213 A1828335 A1570587 A1332760 A1313115 AA804653 AA477920 AA147645 A1916912 AW768839 AA715098 AA292723
	105782	246361_1	AA732421 T33122 A1631560 A1698686 A185386 R43829 AA421638 AA961400 C00503 AA604025 AA554026 AA553885 BE172244 R24040
	120830	244476_1	A0708205 H15963 R20851 L13829 A1934608 A1950163 H28993 A1267243 N66614 H28983 R42031 H06198 AA468628 H92779 L13828 T34896
	128797	20410_1	H09748 R61554 AA350215 R40551 A1568170 AA731212 AW294848 AW466878 AA568908 A1281804 A1923633 AA347885 A1718854 AA714940
55	106533	305354_1	NM_002975 AF020044 AB009244 BE620464 AA541683 AW000991 AW089850 AW664612 A1636676 A1627854 A1885823 A1864548 A1554122 A1499582 A1570905 A1376008 A1871364 A1074230 A1363719 AA905016 AA977446 AA844732 T78922 AW244007 A1924747 A1986230 A1824575 A1999224 A1569490 AW379856 AW292314 A1016874 AW292037
	121619	284072_1	AL134708 AW206610 AW665919 AW594227 A1917093 A1498361 AA635141 AA453786 D54178 D53224 A1804341 D53111 M78885 AL134707
	123049	30801_1	AA453903 A1278054 A134339 A1380496 AW235939 D60373 D60993 D81246
60	129703	64196_1	AA528339 A1017218 AA416911 BE047680 AF177395 NM_014421 AB033208 AB035181 W55979 A1093106 A1863392 AA715452 AA300480 AW022313 AA648103 AA720544 D61856 AA481794 AA737112 AW316551 AA714937 AW974378 A1370632 A184289 A1333962 AA714945
65			BE388665 AA740614 A1394542 AA484451 AW070575 AA877654 A1360981 A1475799 BE349560 A1037351 N29437 A1246453 AW083444 AA844441 A1150871 A1440477 A1889061 AA682422 AA680053 AA740212 A1858728 AA490589 AW243692 A1249450 A1304448 AA534421 A1500317 A1273337 AW027729 A1979132 C06120 A1860916 AW591923 A1803174 A1559264 BE250500 AW675522 AA883284 T71033 A1346838 A1066754 A197913 AA931979 AA427559 A1304730 A1285159 A1273325 A1038450 A1033760 N74972 AA135517 A1304446 A1262652 AA401348 AW514617 A1361795 AW514389 N30307 N93439 AA190775 BE349902 A1342114 A1186831 AA039628 H74242 A1914825 A1955761 A1343851 AA693856 T71096 A1498539 AA778995 AA084278 A1274678 A1022673 AW339621 AA704929 AW089735 AA041252 AA161337 A1185333
70			AW189397 A1160990 A1082392 A1935848 A1144404 A1141633 AA447987 AA642421 A1342103 AW026118 AA834025 AW664459 AA603777 AA630752 AA115450 N49944 AW166071 AW769795 AA991877 AA873609 AW083441 H99130 AA910538 AA486199 AW083358 AA151767 A1161193 N54945 AA180193 A123477 A1188387 A1608747 N58900 A1038449 A1136852 AA565913 A1180502 H61741 AA701125 A1127678 AA278541 R76523 AA666187 H85083 Z24755 R77729 AA135137 BE250395 R76239 AW794625 AW794404 H61957 AA308197 AW996031 AA345524 N52726 AA354360 AA177975 N57375 R16447 AA160645 W21481
75	100299	2801_1	D49493 NM_004962 D49492 AA948479 AA938343 AA017558 AA992567 AA912897 A1185363 AA018254 N93253 AA297544 T19187 R53287 AA069337 AA297489 N62906 AW023929 AA018253 AA017615 W25110 R52085 R52633 W16549 H88916 H89134 AA069338 NM_000399 AA018140 AF139463 J04076 AW390694 AW361756 AL079830 A1190587 AA731059 AA742743 A1635915 AA878209 A1262612 A1264201 AA446300 AA715016 AA446027 A1274101 AA593330 AA593338 AW015388 A1681724 A1347984 AL045275 AA970069 AA018188 AW014396 AW769445 A1588869 AW338296 A1801548 A1367702 A1888410
	123308	322009_1	C14187 AA496211 D80456 AA484051 D80455 AA528446
	101104	26442_2	AW862258 L07615
80	130637	7040_1	AA356764 NM_004867 AF038953 W16828 R50284 A1929589 R01594 AA010474 W37917 N64212 N78175 R57511 AA329322 W77834 AA169869 AA285240 AA356670 T93146 AA325779 AA357064 AA328151 AA308939 AA306801 N31260 AA306202 AA312530 BE242703 AA354371 N42259 AL021786 H50965 H38038 A1655965 A1566732 A1953952 AW972835 A1077300 A1948482 A1760966 AA648335 W72197 N32815 AA768073 AW338181 AW001742 A1819896 A1015666 N58011 A677584 A1183750 AW105514 W37875 AW301679 AA775257

5			AA730357 AI128690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087 AA773947 AA469192 AI199289 AI127085 H89232 N30719 AI028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061 N59622 AI360625 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407 AA736720 AA664587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60546 AA483039 AA507705 AA480448 AI768654 AA658955 AA730803 AA330312 AW021127 BE172031 AW961052 AA339070 AA648172 BE172892 AA174175 AA492012 AA491590 AW118733 AA484130 AA730783 AA730510 D62577 D62828 AI469294 AI801343 N53447 AA740226 AI831983 AA516146 D79799 AI758212 AA484040 H38039 AI038772 AI039410 AA528387 AA730576 AA527231 AA748111 D62946 U38439 AA721708 H22130 AA559229 H51620 AA283355 AA730970 R01595 N72450 AA469123 AA579389 AA480477 AA283306 AA347822 AA328013 AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA664359 AI91039 AA084598 AA081641 AA316181 BE439545 AC005053 AF186249 AW386101 AC004969 AA730199 AA032221 AI686139 AI167942 AA809228 AI184070 AI394674 AW969977 AA032279 AW079284 AA513174 AA888312 AI453179 AA483363 AA528432 AA579511 AU077228 U61145 AL044256 AA206185 AL044975 NM_004456 X95653 AW890805 AA332806 AW965453 BE299226 U52965 BE275009 AA428252 AA769212 AA312778 AA810901 AA461315 AI969286 AI953668 AW296248 AI291422 AA704747 Z44716 BE541235 AW608806 AA588583 AW403788 AW408386 AA053521 T87571 AA581163 BE183241 T97906 R89149 AI808196 BE618521 AI970278 AI652680 AW130143 AI970272 AW197254 BE550449 AI628403 AA010143 AW005107 AA251815 AA805836 N53459 AA055309 AA643678 AI345616 AI345618 AI635728 AI871286 AI018437 AI262514 H75287 AI033155 AI203388 AA205802 AI475265 AW594186 AI696059 AI333312 AW264710 AA876764 AA864892 AA173156 AI292066 T79837 W93995 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T89364 AI090913 N55098 AA101673 AA626665 AA251840 N68857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310 BE244495 AI365179 T99536 AI203088 Z40549 AW139858 AA599627 R91847 AA483681 AW068982 H51746 AA091201 H13030 AA459732 T99430 AI051764 R45991 D54745 AU077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571 H19813 AI745597 AI769202 AI205982 AW205841 R64324 AI201975 H46993 C18067 R71189 N29729 AI799838 AI091209 H87455 R82443 AW970995 AW072136 N40841 H13148 AI219052 N30191 T28007 AI817428 AA503602 AF050147 NM_007015 AB006000 AB005999 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194 BE222414 BE046984 AW470357 AW339338 C02526 AW590220 AI298082 AW296998 AI333135 AI867816 AA730514 BE348513 AA405500 AW136179 AA327834 BE327350 BE327366 AW969726 AA424028 AI266636 AI271571 AA423988 AI266634 AA702780 AA452037 AI424866 AA742931 AA483361 AA737106 N35765 N35779 AF086045 N30152 AW374028 AI478237 AA923562 AI382236 AA846668 AI627389 AI371709 H98083 H95983 H26576 H95984 AA745021 AA639180 H26575 AF061573 NM_002590 AA780138 AW135620 AI197884 AA483348 R05468 AW969724 H29216
10	410102	117657_1	
	410268	11897_1	
	414761	14860_1	
15			
20	416836	16233_1	
25	420462	19379_1	
	428183	287965_1	
	439221	46993_1	
30	447761	7355_1	

Table 73: Sequences

Seq ID NO: B1 DNA sequence  
Nucleic Acid Accession #: NM\_053056.1  
Coding sequence: 210..1097

5	1	11	21	31	41	51	
	CACACGGACT	ACAGGGGAGT	TTTGTGTAAG	TTGCAAAATC	CTGGAGCCTC	CAGAGGGCTG	60
	TCGGCGCAGT	AGCAGCGAGC	AGCAGAGTCC	GCACGCTCCG	GCGAGGGGCA	GAAGAGCGCG	120
10	AGGGAGCGCG	GGGCAGCAGA	AGCGAGAGCC	GAGCGCGGAC	CCAGCCAGGA	CCCACAGCCC	180
	TCCCCAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCCAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAATGT	GTGCAGGAAG	360
	AGGTCTGCCC	GTCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCCAGGAAC	420
15	AGAAGTGCGA	GGAGGAGGTC	TTCCCGCTGG	CCATGAACTA	CCTGGACCGC	TTCTGTGCGC	480
	TGGAGCCCGT	GAAGAGAGAG	GCCTGCAGC	TGCTGGGGGC	CACITGTCATG	TTCTGTGCGC	540
	CTAAGATGAA	GGAGACCATC	CCCTGACCG	CCGAGAAAGT	GTGCATCTAC	ACCGACAAC	600
	CCATCCGGCC	CGAGGAGCTG	CTGCAATGG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTGGA	660
	ACCTGGCCGC	AATGACCCCG	CACGATTTC	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
20	CGGAGGAGAA	CAAAACAGATC	ATCCGCAAA	ACGCGCAGAC	CTTCGTTGCC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCATTTC	AATCCGCCCT	CCATGGTGGC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCAAG	CCTGAACCTG	AGGAGCCCCA	ACAACCTCCT	GTCTACTACT	CGCCTCACAC	900
	GCTTCCTCTC	CAGAGTGATC	AAGTGTGACC	CAGACTGCCT	CCGGGCTGCG	CAGGAGCAGA	960
	TCGAAGCCCT	AAGGAGCCCG	AGCCTGCGCC	AGGCCCGAGC	GAACATGGAG	CCCAAGGCCG	1020
25	CCGAGGAGGA	GGAGAGGAG	GAGGAGGAGG	TGGACCTGGC	TTGCACACCC	ACCGACGTGC	1080
	GGGACGTGGA	CATCTGAGGG	CGCCAGGCAG	GCGGGCGCCA	CCGCCACCCG	CAGCGAGGGC	1140
	GGAGCGCGCC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCAGA	1200
	AGGGAAGCT	TCATTCTCCT	TGTTGTGGT	TGTTTTTTCC	TTTGCTCTTT	CCCCCTTCCA	1260
	TCTCTGACTT	AAGCAAAAGA	AAAAGATTAC	CCAAAACTG	TCTTTAAAG	AGAGAGAGAG	1320
30	AAAAAAGAAA	TAGTATTGCG	ATAACCTGTA	GCGGTGGGGG	AGGAGGGTTG	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TGTTTTTTAT	ATTAATGTAC	TTGTTTCTCT	1440
	GTTGTAAGAA	TAGGCATTAA	CACAAAGGAG	GCGTCTCGGG	AGAGGATTAG	GTTCCATCCT	1500
	TTACGTGTTT	AAAAAAAGC	ATAAAACAT	TTTAAAAACA	TAGAAAAATT	CAGCAAAACA	1560
	TTTTTAAAGT	AGAGAGGGT	TTAGGTAGA	AAAACATATT	CTGTGCTTT	TCCTGATAAA	1620
35	GCACAGCTGT	AGTGGGGTTC	TAGGCATCTC	TGTACTTTGC	TTGCTCATAT	GCATGTAGTC	1680
	ACTTTATAAG	TCATTGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAACC	TCTTCACCTT	1740
	ATTCTATGGT	GAAGTACACT	CTTGGTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCCTT	1800
	TGCGCCTGTG	ACCAACACCC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
	TGCGGCACCA	GAGAGCGTAG	CAGGGTGGGG	AAAGGCCACC	TGTCCCACTC	CTACGATAGC	1920
40	CTACTATAAA	GAGAAGACGA	AATAGTGACA	TAATATAATC	TATTTTTATA	CTCTTCTCTAT	1980
	TTTTGTAGTG	ACCTGTTTAT	GAGATGCTGG	TTTTCTACCC	AACGGCCCTG	CAGCCAGCTC	2040
	ACGTCCAGGT	TCAACCCACA	GCTACTTGGT	TTGTGTTCTT	CTTCATATTC	TAAACCAATT	2100
	CCATTTCCAA	GCATTTTCAG	TCCAATAGGT	GTAGGAAATA	GCGCTGTTTT	TGTTGTGTGT	2160
	GCAGGGAGGG	AGCTTTTCTA	ATGGAATGGT	TTGGGAATAT	CCATGTACTT	GTGTTGCAAGC	2220
45	AGGACTTTGA	GGCAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGCCAG	TCAAGAGAAA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCTT	2340
	TTCCCTTTCT	TTAAAGAAAGT	TGAAGTTTAG	GAATCCTTTG	GTGCCAACTG	GTGTTTGAAA	2400
	GTAGGGAGCT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGGTTAT	CTTAGATGTT	2460
	TCACACCGCA	AGGTTTCTTA	ACACTAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
50	ATTTATTGCA	GAGGATGTTT	ATAAGGCCAG	TATGATTTAT	AAATGCAATC	TCCCTTGAT	2580
	TTAAACACAC	AGATACACAC	ACACACACAC	ACACACACAC	AAACCTTCTG	CCTTTGATGT	2640
	TACAGATTTA	ATACAGTTTA	TTTTTAAAGA	TAGATCCTTT	TATAGGTGAG	AAAAAACCAA	2700
	CTGGAAGGAA	AAAAACCCACA	CAAGACATT	GATTACGCCCT	GTGTTGGCGTT	TCCAGAGTCT	2760
	ATCTGATTGG	ACAGGCATGG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTCGGTTCC	2820
55	GATGAATTCT	TATCCCTCTC	CCCTTCTCTT	AAAAAATCTA	GTGACAAAT	AGACAATTG	2880
	CACATCTTGG	CTATGTAATT	CTTGTAATTT	TTATTTAGGA	AGTGTGTAAG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGGAGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGCTC	3000
	CCGAGGGGAA	GGGGCGGTGC	CCACACCGGG	GACAGGCGCG	AGCTCCATTT	TCTTATTGCG	3060
	CTGCTACCGT	TGACTTCCAG	GCACGGTTTG	GAATATTCCA	CATCGCTTCT	GTGTATCTCT	3120
60	TTACATATGT	TTGCTGCTAT	TGGAGGATCA	GTTTTTGTG	TTACAATGTC	ATATACTGCC	3180
	ATGTACTAGT	TTTAGTTTTT	TCTTAGAACA	TTGTATTACA	GATGCCCTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATTTC	CAAAAAGGTT	3300
	GCTGTTTTC	AATACCTCAT	GCTTCACTTA	GCCATGGTGG	ACCCAGCGGG	CAGGTTCTGC	3360
	CTGCTTTTGC	GGGCAGACAC	GCGGGGCGGA	TCCACACACG	GCTGGCGGGG	GCGGGCCCCG	3420
65	AGGCGCGGTG	CGTGAGAAC	GCGCGGTGT	CCCCAGAGAC	CAGGCTGTGT	CCCTCTTCTC	3480
	TTCCCTGGCG	CTGTGATGCT	GGGCACITCA	TCTGATCGGG	GGCGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATTCTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	CGGCTTGTGA	CCTGTAGGAC	TCTCATTGCG	3660
	GATGATTGGA	ATAGCTTCTG	GAATTTGTTT	AAGTTTGGGG	TATGTTTAAT	CTGTTATGTA	3720
70	CTAGTGTCTT	GTTTGTATT	GTTTGTGTTA	TTACACCATA	ATGCTAATTT	AAAGAGACTC	3780
	CAAAATCTCA	TGAAGCCAGC	TCACAGTCTC	GTGTGCCCCG	GTCACTAGC	AAGCTGCCGA	3840
	ACCAAAAGAA	TTTGACCCCC	GCTGCGGGCC	CACGTGGTTG	GGGCCCCGCC	CTGCGAGGGT	3900
	CATCCTGTGC	TGAGAGGCCA	TCTCGGGCAC	AGGCCCAACC	CGCCCCACCC	CTCCAGAACT	3960
	CGGCTCACGC	TACCTCAAC	CATCCTGGCT	GCGGGTCTG	TCTGAACCA	CGGGGGGCTC	4020
75	TGAGGGACGC	TTTGTCTGTC	GTGATGGGGC	AAGGGACAA	GTCTGTGATG	TGTGTGTAT	4080
	CGAGAGGCCA	AAGGCTGGTG	GCAAGTGAC	GCGGCACAGC	GGAGTCTGTC	CTGTGACGCG	4140
	CAAGTCTGAG	GGTCTGGGCG	GCGGGCGGCT	GGGTCTGTGC	ATTTCTGTGT	GCACCGCGGC	4200
	GCTTCCACGC	ACCAACATGT	AACCGGCATG	TTTCCAGCAG	AAGACAAAAA	GACAAACATG	4260
80	AAAGTCTAGA	AATAAACTG	GTAAAAACCC	AAAAA			

Seq ID NO: B2 Protein sequence  
Protein Accession #: NP\_444284.1

1 11 21 31 41 51

MEHQLLCCEV ETIRRAYPDA NLLNDRVLRA MLKAEETCAP SVSYFKCVQK EVLPSMRKIV 60  
ATWMLLEVCEE QKCEEEVFPL AMYLDRLFLS LEPVKKSRLQ LLGATCNFVA SKMKETIPLT 120  
AEKLCIYTDN SIRPEELLQM ELLLVNKLKW NLAAMTPHDF IEHFLSKMPE AEENKQIIRK 180  
HAQTFVALCA TDVKFISNPP SMVAAGSVVA AVQGLNLRSP MNFLSYRLT RFLSRVIKCD 240  
PDCLRACQEQ IEALLESSLR QAQNMDPKA AEEEEEEEE VDLACTPTDV RDVDI

Seq ID NO: B3 DNA sequence  
Nucleic Acid Accession #: XM\_044166  
Coding sequence: 1..1576

1 11 21 31 41 51  
CTTTTGTTC GCCATGCTTA GTCTAGTGGT ATCTGGAATA ATGGAAGAA ATGGGGGCTT 60  
TGGAGAACTA GGATGTTTCG GGGGAAGCGC TAAGGACCGA GGGCTGCTGG AAGACGAGCG 120  
CGCCCTTCAG CTGGCTCTCG ATCAACTCTG CCTCTGGGT TTGGGGGAGC CCCCAGCCCC 180  
CAGGCGGGGC GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCGCGGAGC CGACAGCCCC 240  
CCGCGAGCGG GCGCGGCGGC CGCGCGCGGC CCCCCACGCG CCCCCAGCGC CGACGCGCCC 300  
CGCAGCGCAG ACGCCCCAGC CCCCCACGCG CCCCCAGCGC CCCCCAGCGC CGACGCGCCC 360  
CGCTCTCTAC AAAGAGGCGG AGCTGCGCCT GAAGGGCAGC AGCAACACCA CGGAGTGTGT 420  
TCCGCTGCGC ACCTCCGAGC ACGTGGCGGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA 480  
GGCCTTGAGG GCCAAGACCA ACACCTACAT CAAGACACCG GTGAGGCGGC AGGAACCACT 540  
GTTTCATGGT ACAGGGCGAC GGGAGGACGT GGCACACGCG CGCGGGGAAA TCATCTCAGC 600  
AGCGGAGCAC TTCTCCATGA TCCGTGCGCT CCGCAACAAG TCAGGCGCGC CCTTTGGTGT 660  
GGCTCCTGCT CTGCCCCGCC AGGTGACCAT CCGTGTGCGG GTGCCCTACC GCGTGGTGGG 720  
GCTGGTGGTG GCGCCCAAGG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA 780  
CATTATCACA CCAAGCGGTG ACGCGGACCC CGTGTTCGAG ATCAAGGGTG CCCCAGGCAA 840  
CGTGAGCGGT GCGCGCGAGG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT 900  
CGAGTACCAAC AATGAAACGC ACTTCTGGC GGGGAGCCCC GACGACGCAA TCGATAGCCG 960  
CTACTCCGAC GCGTGGCGGG TGCAACGACC CGGTGCAAG CCCCCTCCCA CCTTCGCGCA 1020  
GAACAGCGTG GCGTGCATCG GCGAGTGGCG AGTGGACTCT GGCTTTGAGG CCCCAGCGCT 1080  
GGGTGAGCAG GCGCGGAGCT TTGGCTACGG CCGGTACCTC TTTCCGGGCT ATGGCGTGGG 1140  
CAAGCAGGAT GTGTACTACG GCGTGGCGGA GACTAGCCCC CCGCTGTGGG CGGGCCAGGA 1200  
GAACGCCACG CCGACCTCCG TGCTCTCTC CTCTGCTCC TCTCTCTCT CCTCTTCCG 1260  
CAAGGCCCGC GCTGGGCCCC CGGGCGCACA CCGCTCCCTC GCCACTTCG CGGGACCGCA 1320  
GCTGGCGGTG CTCCCGAGGC GCGCGCGGG AGAGCGCGCT CAGGGCTTCT CTAAACTTGG 1380  
TGGGGGCGGC CTGCGGAGCC CCGCGCGGG GCGGGATTGC ATGGTCTGCT TTGAGAGCGA 1440  
AGTGAATGCC GCGCTGTGTC CCGTGGGACA CAACCTGTT TGCATGGAGT GTGCAGTACG 1500  
CATCTGOGAG AGGACGGGAC CAGAGTGTCC CGTCTGCCAC ATCAGAGCCA CGCAAGCCAT 1560  
CCGAATATTC TCCTAAGCCC CGTGCCCAT GCGTCCGGGG CCGACTCCAC TGGGCCACAC 1620  
CTGGAGCTGT TTCTCCATA AGCCTTTTGG AAAGCGGTGA TTTGAGGGG AAGGTGCTTA 1680  
GAGATACTCG CTGCTGGGG AAGGGGGGAG GGAGGCACTG GTGGCTGGAG GGTGCGCCAC 1740  
TTTCAGAGCC TGTGGTCACT CTGTCTGGA AAGATTGGA GGGGGCCAGA CTGAAATTTT 1800  
TACTAGAGTT ACAACTCTGA TACCTCAACA CACCTTAAAT TCTGGAAGCA GCTAAGAGAA 1860  
ACTTTTGTGT TGCCAGAGGT GGCCACTAAG GCATCTTGAC GCGCTCTGCC CACTTCCCC 1920  
GCTGTGTATC ACTCTCACCC TTCTTCCGAG GAGGGGGTGG GTAAAGGGA GAGGGAGAA 1980  
TACCACCTGT ATCTAGAGGT GCTCTTGA ATCCCTAAGC CCTCTGGTCC TGACCTCCGA 2040  
CCTCCAGCT CTGCTTGTCT CTTGTCTTCT GTCTTCTCT CCGTCCCCCT GCGCTGCCC 2100  
CTACCAGCCC AGCTTTGGGG ACACCATCCT TCTGGGGAGA AGTAGGGGGA GGAATATTGT 2160  
GATGGTCCCT CCATCTCTCT TCAGGCACTT GGAGGCCCTC TCCCCACTC CTCCAAAGAA 2220  
ACATCTCAAA TTAATGATG AATGTATCCC CATTCTCAGT GAAATGTGA GGAGGGGACT 2280  
AATACTGGG TAAAGGGTCA AACCCTCACC TTCTCACTA TGGGCATTAT ATTTAGGGAG 2340  
TAGTCTTGG GCTGGATTTT CTGGTTGTGG AAGTGGGGGC GCCAGAGTAG TGTGTCTGCT 2400  
ATTTAAAGGA GCAGGAAAGG GCGTGAGGCA GGAGGAGAGA CTGGTGAGG GAAGAGCTGC 2460  
TCTTCCCATC CAGTGCCCGA CTCCCTGCAC CCGTCTCAAC CTGACCTGAA CCTTTATTGA 2520  
ATCCTTATTA GCTTGAATCC TTATTAGCTT GAATCTCCA TGCAATCAT GGAGTCTGTG 2580  
TCCACCTTGA TGTGTTTGG GAGAAGCCAG GTCTTCAAAG AGGGGTGAGC CTGGGCAAAA 2640  
GCAGGACTGG GGGGAGGTGG GCAGCAGGCG CTATTCTGAG AATCAGATAT TGTACAGGCG 2700  
CTTGACCCCC CTTGTCTGCT TCCCTCTGCG TCATTGSGG CTGCCACAG CTCTCCACCC 2760  
TCTGGTTCCT GCTGGCGGG CCAAGAGAGG ATGGAGGGAT GGGAGTCCCA GAGATCCTT 2820  
GTAAATAGTG GGTGGGACT GTTCTGAGTG ATCACCAGAG CACTTAAAGC TCCAGAGTCC 2880  
CATTCTTCTT GATGAGGAG GGTGAGGTG CAGAGGGGAT TTCTCTCTCT CCTTCTCTCT 2940  
GTGAGAAATT AACACCTCTC CACAGCCTTC CCGTCCAGAA CACAGCCAG GGAGGGGTGG 3000  
GGAAGGAGGT CACAGCCAG AAAACTGCCC TGTGACGACT TCCCTCCTTC CCGCTATGT 3060  
GAGCCATCCT GAGATGTCTG TACAATAGAA ACCAAACCA ATGGGACACC TCGGTTGCCG 3120  
GGGGGCGAGT GGGGAGGGGG GTGGGAAGAA GGGATGTCTG TCTGTCTGCC CCGTCCCCCT 3180  
CTCCACTCTT TACCCACAAA GGCAGAGAC TGTACACTA GGGGGCTCAG CAAATTCAAT 3240  
CCCACCCCTA CCAATTGAGC CAAACCTAGA AACAAACACA AAACACGAAT AGTGAGAGAC 3300  
AAAATAGAGG AGAGAAAGAG AGCATGAGAG GGAGCGAGAC AGGCGACCA CACAGAGGAG 3360  
AGAAAACAAA AATAGCAAAA AAAAAAATAA AAAGCAGTTC TTTATAATT AATATTCTAT 3420  
TTTAATAAAG GCGTTTATTA CCAATAAAT GTAGCAAGA ACCTGGGCTA ATATGAA

Seq ID NO: B4 Protein sequence  
Protein Accession #: XP\_044166.2

1 11 21 31 41 51  
FCFAMPPLVV SGIMERNGGP GELGCFGGSA KDRGLLEDER ALQLALDQLC LLGLGEPPAP 60  
RAGEDGGGGG GGAPAQPTAP PQPAPPPPPA APPAAPTAP AAQTQPPPTA PKGASDAKLC 120  
ALYKAEALRL KGSSNTTECV PVPTSEHVAE IVGRQGCKIK ALRAKNTYI KTFVRGEEFV 180  
PMVTGRREDV ATARREIISA AEHFSMIRAS RNKSGAAGFV APALPGQVTI RVRVPYRVVG 240  
LVVGPKEGATI KRIQQNTNTY IITPSRDRDP VFEITGAPGN VERAREEET HIAVRTGKIL 300  
EYNNENDFLA GSPDAIDSR YSDANRVHOP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360  
GEQGGDFGYG GYLFPYGVG KQDVYGVAE TSPLWAGQE NATPTSVLFS SASSSSSSSA 420

KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQGFSLKG GGGLRSPGGG RDCMVCFESE 480  
VTAALVPCGH NLFQMECAVR ICERTDPECP VCHITATQAI RIFS

5 Seq ID NO: B5 DNA sequence  
Nucleic Acid Accession #: NM\_000909.1  
Coding sequence: 209..1363

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60
    GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATTG CAATATCGGG 120
    AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180
    ATAATCTATA ACAACCAAAC CAATCAAAT GAATTCACCA TTATTTTCCC AGGTGAAAA 240
    TCATTGATGC CACTCTAATT TCTCAGAGAA GAATGCCAG CTTCCTGGCT TTGAAATGA 300
15 TGATTGTGAT CTGCCCCTTG CCATGATATT TACCTTAGCT CTTCCTATG GAGCTGTGAT 360
    CATTTCTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAAC AAAAGGAGAT 420
    GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTGCGCAT 480
    CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540
    GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT 600
20 GGTTCCTATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660
    TAATAGACAT GCTTATGTAG GTATTGCTGT GATTTGGGTC CTTCCTGTGG CTTCCTCTTT 720
    GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGCTC CAAATGTAA CACTTGATGC 780
    GTACAAAGAC AAATACGTGT GCTTTGATCA ATTCCATCG GACTCTCATA GGTGTCTTA 840
25 TACCACTCTC CTCTTGGTGC TGCAGTATT TTGTCCACTT TGTTTATAT TATTTGCTA 900
    CTTCAGATA TATATACGCC TAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960
    TAAGTACAGG TCCAGTGAAA CCAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
    ATTTGCACTC TGCTGCTGCC CTCTACCAT CTTTAACAAT GTGTTTGATT GGAATCATCA 1080
    GATCATTGGT ACTGCAACG ACAATCTGTT ATTCTGCTC TGCCACTCA CAGCAATGAT 1140
30 ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGAAC AAAAATCTCC AGAGAGACTT 1200
    GCAGTCTTTC TTCAACTTTT GTGATTTCGG GTCTCGGAT GATGATTATG AAACAATAGC 1260
    CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCG 1320
    ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAATC TGAAACTACT TATAGCCTAT 1380
    GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
35 TCTCCCAAGG AATGGGGTTG AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500
    TTACTGCTTT TGTGTAGTGT GTCATAAATTA CATTTGGAAC AAAAGGTGTG GGCCTTGGGG 1560
    TCTTCTGGAA ATAGTTTGA CCAGACATCT TTGAAGTGCT TTTTGTGAAT TTATGCATAT 1620
    AATATAAAGA CTTTTATACT GTACTTATTG GAATGAAAT TCTTTAAAGT ATTACGATGC 1680
    GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCAATTG ATTGGGTCAT CTTGATTAGA 1740
40 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
    TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTG AGGAGCCGAA AGATAGTCTT 1860
    GAAGTCATTG AGAAGTGTTT TGAGGTTTCT GTTTTGTGGT GGTTTTGTGT TGTTTTITTT 1920
    TTTTTCACCC TTAAGGGAGG CTTTCATTTC CTCGCCACTG ATTGTCACTT AAATCAAAAT 1980
    TTAATAATGA ATAAAGAAC ATACTTCTCA GCTGCAAAATA TTATGGAGAA TTGGGCACCC 2040
45 ACAGGAATGA AGAGAGAAAG CAGCTCCCCA ACTTCAAAAC CATTTTGGTA CCTGACACAA 2100
    AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
    TATATTTGAT TGAATTGATG GTCAAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAGTGT 2220
    TTGTCAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280
    ACAAATATCG TTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTTCAATGTC 2340
50 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTTACCTAGC 2400
    AGGGAATAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAAT 2460
    GTGTGACTTG TGGGCTCTTA TAAATAATGC ACTGTARAGA TTACTGAATA GTTGTGTGAT 2520
    GTAATGTGTC CTAATTTTCA GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTGGAG 2580
    AAACATATAT TTAAGAACCA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640
55 TGTGTGATTT TAAAGGGCG GACATTTTAT TAAATCAAT ATTGTTTTTG CTTTTTCTGA 2700
    GGAGTCTCTT TCAGTTTCAT TTTTCTCAT CCCATGACTT CCTCCGATG GT
  
```

Seq ID NO: B6 Protein sequence  
Protein Accession #: NP\_000900.1

```

60 1      11      21      31      41      51
    |      |      |      |      |      |
    MNSTLFSQVE NHSVSNFSE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60
    LIIILKQKE MRNVNIIIV NLSFSDLLVA IMCLPFTFVY TLMHWHVFE AMCKLNPFVQ 120
65 CUSITVSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180
    DEFFQNVILD AYKDKYVCFD QPPSDSHRLS YTTLLLVLYQ FGPLCFIFIC YPKIYIRLKR 240
    RNNMMDKMRD NKYSSETKR INIMLLSIVV AFVAVCWPLPT IFNTVFDWNH QIIATCNHNL 300
    LFLLCILTAM ISTCVNPIFY GFILNKNFQPD LQFFPNFCDP RSRDDDYETI AMSTMHTDVS 360
    KTSLKQASPV AFKKNINDD NEKI
  
```

70 Seq ID NO: B7 DNA sequence  
Nucleic Acid Accession #: NM\_002590.2  
Coding sequence: 204..3416

```

75 1      11      21      31      41      51
    |      |      |      |      |      |
    GCTTCTGTAA GAGACGAGAA GGCGCAGAGT GAGGGCGGGT CCGCGCGTCC TCAGAGCCCG 60
    CTGAGGGCTC GGAGCTGCTA CCGCGAGACT TCTCCGCGAC AGGGCTCGCA AAGAGCGTGA 120
    TTCCGAGAGC CTGAGACTGA CGCCCGACTT GGAACCCAGA GAAGACTTCC TTAGCCTTTC 180
    GGATCGCACT TGAGGCTGGA GGCATGAGTC CTGTGAGGCG TTGGGGCAGC CCTTGCCCTT 240
80 TCCCTTGTCA GCTCTTCAGC CTCTGCTGGG TGCTCTCAGT GSCCCAGAGC AAAACAGTCC 300
    GATACAGCAC CTTGAGGAG GATGCCCCCG GCACGGTCAT CGGAGCCCTG GCCGAGGACC 360
    TGATATGAA AGTATCGGGT GACACAAGCT TCCGCTGAT GAAGCAATTC AACAGCTCTC 420
    TGCTCCGGGT GCGCGAAGCG GACGGGAGC TGACCGTGGG GGACGCGCGG CTGGACCGCG 480
    AGCGCTGTGT TGCCAGGCC CCGCAGTGGG TGCTGGCCTT CGATGTGGTC AGCTTCTCGC 540
  
```

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60

AGGAGCAGTT CCGCTGGTG CACGTGGAGG TAGAGGTGAG GGACGTCAAC GACCAACGGC 600  
 CGCGCTTCCC CAGGSCCCAG ATCCCGGTAG AGGTGTCCGA GGTGGCGGCA GTGGGCAAGC 660  
 GCATCCCTTT GGAGGTGCGG GTGGACGAGG ACGTGGGCGC CAACGGGCTG CAGACCGTGC 720  
 GCCTGGCCGA GCGGCACAGC CCCTTTGCGG TGGAGCTGCA GACCGGAGCG GACGGCGCTC 780  
 AGTGGCGAGA CCTGGTCTG CTGCAGGAGC TGGACCGGGA GAGCCAGGCC GCCTACAGCC 840  
 TGGAGCTGTT GCGCCAGGAC GCGGCGCGCC CGCGCGCTC CGCCACGGCT GCCTCAGCG 900  
 TGCCTGCTCT GGATGCGAAT GACCACAGCC CGGCTTCCC GCAGGGCGCC GTGGCCGAAG 960  
 TGGAGCTGGC GGAAGAGCGG CCGCTGGGCT CCCTGCTTCT CGACTGGAC GCAGCGGACC 1020  
 CCGACGAGGG ACCTAACGGC GACGTGGTGT TCGCATTTGG CGCCCGCACC CGCGCGGAGG 1080  
 CGCGCGCTCT TTTCGGCTT GACCCGCGAT CAGGCGCGCT CACCTTGGCC GGGCCCGTGG 1140  
 ACTACGAGCG TCAGGACACC TACGAGCTGG ACGTGGGCGC GCAGGACCGC GGACCCGGGC 1200  
 CCGCGCTGCG CACCTGCAAG GTCATCGTGC GCATCCGAGA CGTCAATGAC AACGCACCCG 1260  
 ACATCGCCAT CACCCGCTG GCGGCCCGAG GCGCGCCGCG AACCTCACCC TTGCGCGCTG 1320  
 CGCGCGCGCG CGCTGCATC GGGGAGCGG ACGCTAGCTC GCGCGCGGGA GCCGGGACGC 1380  
 CGGAGGCTGG TGCCACTTCG CTGGTGC0GG AGGGGCGCGC GCGCGAGAGC CTGGTGGCCC 1440  
 TGGTCAGCAG TCGGACAGG GACTCGGGCG CCAACGGGCA AGTGGCTGCG GCCCTCTATG 1500  
 GGCACGAGCA CTTCGGCTG CAGCGCGCTT ACGCGGCGAG CTACCTGGTG GTGACCGCGG 1560  
 CGTGGCTGGA CCGCGAAGCG ATCGCGGAGT ACAACTTGAC GCTGGTGGCC GAGGATCGCG 1620  
 GCGCGCGCCG GCTGCGCACA GTGCGGCCCT ACACGGTGGC TGTGGGCGAC GAGAACGACA 1680  
 ACGCGCGCTT CTTCAGCGG CCGGCTCATG AGGTGTGGGT GCGCGAGAAC AACCCGCCAG 1740  
 GCGCTACTCT TGCGACGCTG GCGGCCCGCG ACCGGGACCT GGGCGGCAAC GGCCAGGTCA 1800  
 CCTACCGGCT GCTGAGGCGC GAGGTGGGCC GCGCGGGGGG GCGCTGTCC ACTTATGTCT 1860  
 CGGTGGACCC AGCTACCGGA GCCATCTAGC CGCTGCGCAG CTTCGACTAT GAGACGCTGC 1920  
 GCCAACTCGA CGTTCGCATC CAAGCTAGCG ACGCGCGCTC CCCTCAGCTT TCCAGCAGCG 1980  
 CCTAGTGCA AGTGGCGCTG CTGGACAGA ACACCATGCG GCCAGTCCGT GTGCAACCCG 2040  
 CGCCAGCCAA TGGCTCCCTA GAAGTGGCGG TGCTGGGGCG CACCGCAAG GACACGGTTG 2100  
 TGGCCCGTGT GCAGGCGCGG GATGACAGCG AGGGAGCCAA CCGGAGCTG CGGTTCGAGC 2160  
 TGCAGCAGCA GGAGCGCGCG GAAGCCCTTG CCATCGCGCG CCGCACGGGG GAGATACTGC 2220  
 TCACCGGCGA CCTCTCGCAG GAGCCACCG GTGCGGTGTT CAGGGCGCTC CTGCTCATAT 2280  
 CCGAGCGGGG CCGTCCCCCG CTCACACCA CCGCAACTGT CAGCTTCGTG GTAACAGCAG 2340  
 GGGGCGGGCG TGGCGCGCTG GCGCTGCGCA GTGCAGGAAG CCGGAGCGGT TCCCGCCCCG 2400  
 CTGGCTCTCG GCTCGGGTGT TCCGGTGGG TGCTGCAATG GGACACGCGG CTGATCGTCA 2460  
 TCATCTGCTT GCGCGGGAGC TGCACGCTGC TGCTGGCCCG CATCATCGCC ATCGCCACCA 2520  
 CCTGCAACCG CCGCAAGAA GAGGTGCGCA AAGGGGGGCG CCTCGGGGAA GAGCGGCCCC 2580  
 GGGGCGGGCG CCGCGGAGCC TCGGCTCCCG GCTCCCCGGA GGAGGCGGCC CGGGGAGCCG 2640  
 GGGCCAGGCC CAACATGTTG GAOGTGTCTA CCTTCCCTGG CACCGGCAAA GCGCCCTTGT 2700  
 GCAGCCCCGC GCGGACGCGG CCTCCGCTG CGTCCGCGCG GCGCAAGTG CCGGGCTCAG 2760  
 AGGGCGGCGG CCGCCTCTGG GAAAGCGCCT GTCACTTCGA GGGGACGAG CCGCTCCGCG 2820  
 GCGCGCACCG CGAGCCCTAC GGTGCTTCCC CGGGTTTTGG AAAGGAGCCG GCGCCCCCTG 2880  
 TGGCGGTGTG GAAAGGACAC TCCTTCAACA CCATTTCTGG CAGAGAAGCA GAGAAGTTCA 2940  
 GCGCAAGCA CAGCGGTAA GGGGACAGTG ATTTCAACGA CAGCGATTCC GACATCAGCG 3000  
 GGGACGCTCT GAAAAAGGAT CTCATCAACC ACATGACAGG TGGACTGTGG GCGTGACCG 3060  
 CTGAGTGTA GATCCTGGGC CACTCTGACC GCTGCTGGAG CCCATCTGCG AGCGGGCCCC 3120  
 ACGCACATCC ATCGCCTCAC CCACAGGCC AGATGTCAAC CTTCGTGAAG AGCAGCTCAC 3180  
 TGCCTCGGGA TCCTCTGCGC AGGGACAATT ACTACCGGCC CCAGTGTCCC AAGACAGTGG 3240  
 GCGTGCAGG CGTCTATGAG AAAGTACTGC ACAGAGACTA TGACAGGACA GTCACTCTCG 3300  
 TCTCCCTCC CCGTCCAGGG AGGCTCCAG ACCTGCAGGA GATTGGAGTA CCCCTCTACC 3360  
 AGTCCCTCC TGGCAGGTAC CTGTCCCGGA AGAAGGAGGC CAATGAAAT GTGTAATCCC 3420  
 ATGCTGCATG TCCTCACACA TATACAGTCT ACTCGAGAA GCCCTAAGT TATTGACCGG 3480  
 TTTCAAGTGT GTATATATA ATATGCAAGA TGTGCCITAC AATGAAGTTG TTGGAAGCTA 3540  
 TTTCAATCA GTGTGTATG GTTGTGATT TGCAACAAA AATGTAGTTA ATGTAATTTT 3600  
 TATGAAATGT GTGCAATATT TAATTTTCT TATGCTATTG ACTTGTATT CAATTGCGGC 3660  
 TTGCCATTTT CTAGTGTGTT TTAACCTGTA CATTTGTGTA TGTAAATGTT GTATATAATG 3720  
 AAATTTGTT ATATTTTAT ATAATAAAG CTAAAGTGGG AGTTATTGCC AAAGGAAGTG 3780  
 TCTGTAGAG AAAAACAACA ACATGTTGGA ATTACTTAAT TGAATTTAT CTTCACCTG 3840  
 AAAACAACCTA GTGTTTGA GAATTTGCTT TGCCAAGTAT AACTGTGATA TCTTGACTCT 3900  
 GTGGTAGATT TCAAGTTCAA TGTTATTTAA TTACATTTGG TTTTCCGTAA ACCGTGTCAC 3960  
 TTATAAGCAC AGTAATAAAA GATTGTGCTAT GTGTTTGAAG AAAAAAAAAA AAAAAAAA 4020  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: B8 Protein sequence  
 Protein Accession #: NP\_002581.2

65  
70  
75  
80

1 11 21 31 41 51  
 MSPVRRWGSF CLFPLQLFSL CWLVSVAQSK TVRYSTFEED APGTVIGTIL EDLHMKVSGD 60  
 TSFRLMKQPN SSLLRVREGD QQLTVGDAGL DRERLCQAP QCVLAFDVVS FSQEQFRLVH 120  
 VEVEVRDND HAPFPRAQI PVEVSEGAIV GTRIPLEVPV DEDVGANGLO TVRLAEPHSP 180  
 FRVELQTRAD GAQCADLVLL QELDRESQAA YSLELVAQDG GRPPRSATA LSVRVLDAND 240  
 HSPAFPQGA AVAEVLAEDAF VGSLLLDLDA ADPDEGENGD VVFAFGARTP PEARRLFRLD 300  
 PRSGRTLAG PVDYERQDTY ELDVRAQDRG PGPRAACTKV IVRIRDNDN APDIAITPLA 360  
 APGAPATSPF AAAAAAALG GADASSPAGA GTPEAGATSL VPEGAARESL VALVSTSDRD 420  
 SGANGQVRCA LYGHEHFRLO PAYAGSYLVV TAASLRERI AEYNLTIVAE DRGAPPLRTV 480  
 RPYTVRVGDE NDNAPLETRP VYEVSVRENN PPGAYLATVA ARDRDLRNG QVTVRLLEAE 540  
 VGRAGGAVST YVVDPATGA IYALRSFDYB TLRQLDVRIQ ASDGGSPQLS SSALVQVRVL 600  
 QDNDAFVLV HPAPANGSLE VAVPGRTAKD TVVARVQARD ADEGANGELA FELQQQEPRE 660  
 AFAIGRRTGE ILLTGDLSE PPGRVFRALL VISDGGRPPL TTTATVSFVV TAGGGRGPA 720  
 PASAGSPERS RPPGSRGLVS GSVLQMDTFL IVIIVLAGSC TLLLAIIAI ATTCNRREKE 780  
 VRKGGALREE RPGAAGGGAS APGSPPEAR GAGPRPMFD VLTFFPTGKA PFGSPAADAP 840  
 PPAVAAAEV SEEGGSATGE SACHFEGQOR LRGAHAEPYG ASPFGKEPA PPAVAVWKHS 900  
 FNTISGREAE KPSGKDSGKG DSDFNDSDSI ISGDALKKOL INHMQSLWA CTAECKILGH 960  
 SDRCSWSPSCS GPNAPSPFHP PAQMSTFCKS TSLPRDPLRR DNYQAQLPK TVGLQSVYEK 1020  
 VLHRDYDRTV TLLSPPRPGR LPDLQBIGVP LYQSPPGRYL SPKKGANENV

Seq ID NO: B9 DNA sequence  
Nucleic Acid Accession #: AL121939.12  
Coding sequence: 185..1426

```
5 1 11 21 31 41 51
AGGGGAGTST CAGTGGCGAG CTCGGGTGTC TGTGGCCCGG CCTTGGCCGG GCGGCCTCCG 60
GCTCAGGCTG GCTGAGAGGC TCCAGCTGTC AGCGTCCCGC CCGGCTCTCT CGGGAGCTCT 120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAGGCTG GCAGGACAAA ATTAGAAGAT 180
CAAAATGGAA AATATGCTGC TTTGGTTGAT ATTTTTCACC CCTGGGTGGA COCTCATTGA 240
TGGATCTGAA ATGGAATGGG ATTTTATGTG GCACCTGAGA AAGGTACCCC GGATTGTCTG 300
TGAAAGGACT TTCCATCTCA CCAGCCCCGC ATTTGAGGCA GATGCTAAGA TGATGGTAAA 360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCAACT CCCAGCCTTT CTGAATTGGA 420
GGATTATCTT TCCTATGAGA CTGTCTTTGA GAATGGCACC CGAACCTTAA CCAGGGTGAA 480
AGTTCAAGAT TTGGTCTTG AGCCGACTCA AAATATCACC ACAAGGGGAG TATCTGTTAG 540
GAGAAAGAGT CAGGTGTATG GCACCGACAG CAGGTTGAGC ATCTTGGACA AAAGGTTCTT 600
AACCAATTTT CCTTTCAGCA CAGCTGTGAA GCTTTCACG GGCTGTAGTG GCATTCTCAT 660
TTCCCTCAG CATGTTCTAA CTGCTGCCCA CTGTGTTTCA GATGGAAGG ACTATGTCAA 720
AGGGAGTAAA AAGCTAAGGG TAGGTTGTTT GAAGATGAGG AATAAAGTG GAGGCAAGAA 780
ACGTGAGGT TCTAAGAGGA GCAGAGAGAG AGCTAGTGGT GGTGACCAAA GAGAGGGTAC 840
CAGAGAGCAT CTGCAGGAGA GAGCGAAGGG TGGGAGAAGA AGAAAAAAT TGCGCGGGG 900
TCAGAGGATT GCCGAAGGGA GGCCTTCCTT TCAGTGGACC OGGGTCAAGA ATACCCACAT 960
TCCGAAGGGC TGGGCAGGAG GAGGCGATGG GAGCGCTACC TTGGAATCA ACTATGCTCT 1020
TCTGGAGCTG AAGCGTCTC ACAAAAAGAA ATACATGGAA CTGGAATCA GCCCAACGAT 1080
CAAGAAATG CCTGGTGGAA TGATCCACTT CTCAGGATTT GATAACGATA GGGCTGATCA 1140
GTGGTCTAT CGGTTTTCGA GTGTGTCYGA CGAATCCAAT GATCTCCTTT ACCAATAYTG 1200
CGATGCTGAG TCGGCTCCA CGGTTCCGGG GGTCTATCTG CGTCTGAAAG ATCCAGACAA 1260
AAAGAAATGG AAGCGCAAAA TCATTGCGGT CTACTCAGGG CACCACTGGG TGGATGTCCA 1320
CGGGTTTCA AAGGACTACA AGTTGCTGT TCGCATCACT CCCCTAAAAT ACGCCAGAT 1380
TTGCTCTGG ATTCACGGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAAC 1440
AGGCGGTGT ATCACTTAAA TCACAGAGAA AACCAGCTCT GCTTACCGTA GTGAGATCAC 1500
TTCATAGGTT ATGCTCGGAC TTGAACCTG TCAATAGCAT TTCAACATT TTCAAAATCA 1560
GGAGATTTTC GTCCATTTAA AAAATGTATA GGTGCAGATA TTGAACCTAG GTGGCACTT 1620
CAATGCCAAG TATATACTCT TCTTACATG GTGATGAGTT TCATTGTAG AAAAATTTTG 1680
TTGCTCTTCT AAAAATTAGA CACACTTAA ACCTTCAAC AGGTATTATA AATAACATGT 1740
GACTCTCTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTGG 1800
TTGTGTAITA AATGTGAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAAGTTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGTCTAT 1920
GCCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTTAGTTT AGTTTTTTTG 1980
AAGAATTACA AATCAGAAGA AAAAGCAAGC ATTATAAACA AAACATAATA CTGTTTACT 2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCT 2100
ATGAAATAAA CCTAGTTTAA AATAGGGGAA GCTGAGACAT TTTAAGATCT CAAGTTTTTA 2160
TTTAACTAAT ACTCAAATA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCAAAAT 2220
TATGAATGAT CATGTGTGTA AAGCCACATT ATTTTATGCT ATACATTCTA TGTATGAGGT 2280
GCTACATTTT TAGGACAAAG AATCTGTAA TCTTTTCAA GAAAGAGTCT TTTTCTCCTT 2340
GACAAATCC AGCTTTTGTG TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTAGA 2400
TATGCTCTTT CCTAAAATG AATAAAATTT ATGAATATGA CTTAAAAAAA AAARWCGACG 2460
CGGCGCGGAA TTTAGTAGTA GTAGTCGACC CGGGAATTCG GACCGGTAC CTGACGGCGT 2520
ACCAGC
```

Seq ID NO: B10 Protein sequence  
Protein Accession #: CAC35071.1

```
55 1 11 21 31 41 51
MENMLLWLIF FTPGWTLDIG SEMEWFDMWH LRKVPRIVSE RTFHLTSPAF EADAKMMVNT 60
VQIECQKEL PPSLSELED YLSYETVFEN GTRTLTRVKV QDLVLEPTQN IITKGVSVRR 120
KRQVYGTDSR FSILDKRFLT NFFPSTAVKL STGCSGILIS POHVLTAARC VHDGKDYVKG 180
SKKLRLVGLLK MRNKGSGKKR RGSKRSRREA SGGDQREGTR EHLRERAKGG RRRKKSGRGQ 240
RIABGRPSFQ WTRVKNTHIP KGWARGMGMD ATLDDYDALL ELKRAHKKKY MELGISPTIK 300
KMPGGMHPS GFDNDRADQL VYRFSVSDS SNDLLYQYCD AESGSTGSGV YLRKDPDKK 360
NWKRIIAVY SGHQWVDVHG VQRDYNVAVR ITPLKYAQIC LWHGNDANC AY
```

Seq ID NO: 11 DNA sequence  
Nucleic Acid Accession #: NM\_002035.1  
Coding sequence: 108..1106

```
70 1 11 21 31 41 51
AGGCGCCCGC CCGCCGCGCG TGATTCTCGC CTCGCCGCGC CCGAGCCCTG CCGGCCCTTG 60
CGGCGCGGCC CCGCCGCGGC GCTCCGCGCC CCGGCCCGCG CGAGCGGATG CTGCTGCTGG 120
CTGCCGCCCTT CCTCGTGGCC TTGCTGTGTC TGCTGTACAT GGTGTCTCCG CTCATCAGCC 180
CCAAGCCCTT CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
GGAAGTGCAT TGCTATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGACAGAA 300
ATGAGGATAA GCTGCTGCGC GCAAGAAAG AAATTGAAAT GCACCTTATT AATGACAAAC 360
AGTGGTGTCT TTGCATATCA GTTGATGTAT CTCAGACTA TAACCAAGTA GAGAATGTCA 420
TAAACAACGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAATTTGT GCAGGAATGG 480
CAGTGTCTAG AAAATTTGAA GATCTTGAAG TTAGTACCTT TGAAGGTTA ATGAGCATCA 540
ATTACCTGGG CAGCGGTGAC CCCAGCCGGG CGGTGATCAC CACCATGAAG GAGCGCGGG 600
TGGGCAGGAT CGTGTGTTG TCTTCCAGG CAGGACAGTT GGGATTATTC GGTTCACAG 660
CTACTCTGCT TTCCAAGTTT GCCATAAGGG GATTGGCAGA AGCTTTGAG ATGGAGGTGA 720
AGCCATATAA TGTCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGCGCTTG 780
CGAAGAAAA CAGAACAAAG CCTTTGGAGA CTGACTTAT TTGAGACCC ACATCTGTGT 840
GCAACACAGA ACAGTGGGCC AAACAAATTT TTAAGATGTC CATAACAGA AATTTCAACA 900
```

5  
10  
15  
20  
25

```

GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960
CTTCTATTAC TGAGGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT 1020
TGTTTTACCT TGGAAGTTTT GACAGCATAG TTCGTGCTG CATGATGCAG AGAGAAAAAT 1080
CTGAAAATGC AGACAAAACCT GCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTITCCAAA 1140
TAATTTGAAC AGCTTGCTGC TAAATGGGAC CCAATTTTGG GCCTATAGAC ACTTATGTAT 1200
TGTTTTCGAA TACGTAGAT TGGACCACTG CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG 1260
CTAGAAGTTC ACCTCCTGAC AGTATTATTA ATACTATGCA AATATGGAAT AGGAGACCAT 1320
TGATTTTCT AGGCTTTGTG GTAGAGAGGT GAAGGTATGA GAATTAATAG CGTGTGAACA 1380
AAGTAAAGAA CAGGATTCCA GAATGATCAT TAAATTTGTT TCTATTATT CTTTTTGCC 1440
CCCTAGAGA TTAAGTCCAG AAATGTACTT TCTGGCAGAT AAAGAAATCT TGAGGACTTT 1500
GTTTAAACCT TCCATAAAAA AACAAATTTT GGTTCCTCGG GTTCTCTCTC TCTGTCTCTC 1560
TGTCCTCTG TCCTCTGTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCT TCTTTGTGTA 1620
TTTTATTCAA GATGAGTTGG ACCCATTTGCC AGTGAGTCTG AATGTCACTG ACAGCCCTGT 1680
GTGTGCTCA GGACTCACTC TGCTGCTGGT GGAAGCTCAT GGCTTCTCTC TCTCTTTGAT 1740
CCCATAAAGC TACGAGGGGG ACGGGAGAGG GCAGTGCAAT GGGAGTAAA GAGATATTTT 1800
CCAGTAAAGC AAGCAATGCT TTCTTGCTTT TAGACTCAAA TGCTTAGGGA ACGTTTCATT 1860
TCTCATTCAT GGGGAAAGGC AGCCTCCTTA AATGTTTTCT GAAGAGCGGT AAAATCTAGA 1920
AGCTTAAAGAA TTACAGTTTC CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCAT 1980
TAGCATCTA CTTGTTTTTC CCATCTCTTC CTTTCCAATT TTGCTTATAC TGCTGTAATA 2040
TTTTGTAAA AAAAAAATAA AAGGAAAAAA AAGACCAGCT AAAATTTTGG ACTTGACTTT 2100
TTAACTTAAC TCATGAATTA ATTAAGCAA ATGAAAAAAT TAAAAAGTGT GACTTTTTCT 2160
CGGAGCATAT ATGTAGCTTT TAGGAAAGGC TGATGATGGT ATAAAGTTTG CTCATTAAGA 2220
AAAAAAGACA AGGCTGATTT TGAAGAGAGT TGCTTTTGAA ATAAATGAT CA

```

Seq ID NO: B12 Protein sequence  
Protein Accession #: NP\_002026.1

30  
35

```

1 11 21 31 41 51
| | | | |
MLLLAAFLV AFVLLLYMVS PLISPKPLAL PGAHVVTGG SSGIGKCIAT ECKYQGAFIT 60
LVARNEDKLL QAKKEIEMHS INDKQVVLICI SVDVSDYDYNQ VENVIKQAE KLGPVDMLVN 120
CAGMAVSGKF EDLEVSTFER LMSINYLGSV YPSRAVITTM KERRVGRIVF VSSQAGQLGL 180
FGFTAYSASK FAIRGLAEAL QMEVKPYNVY ITVAYPPDIT TPGFAENRT KPLETRLISE 240
TTSVCKPEQV AKQIVKDAIQ GNFNSLSGSD GYMLSALTIC MAPVTSITEG LQQVVTMGLF 300
RTIALFYLGS FDSIVRRCMQ QREKSENADK TA

```

Seq ID NO: B13 DNA sequence  
Nucleic Acid Accession #: CAT Cluster

40  
45  
50

```

1 11 21 31 41 51
| | | | |
CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTAA TTTTAAAAAT 60
CGGCAAAATA TTGGTGCCCT TCCGAAATTT TGGTCCGGG CTCCCTTATA GGATAATTGG 120
TTTGGATTGG TTAAGTCCAA TTATTAAATG CTGGGTTTTC AAATTCAGC CTGGAAGGAC 180
CAACCATTTA AAAACCTTCA AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAATAAT 240
CCAGCATTGT GTTTGACATA TTCCAGAGC TCAATCTGCG AGTGTTCAC ATGCACATAC 300
AAGATCCAGA GTCTCATGTT AAAATCACTT ACATACCCAG AAAGACCACC ACTTTGCAGG 360
TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
AAGAACACAT AAGATGCCCT CTTCATCAA ATGCACCTGC TTGTGAATTA ATGCACCTGT 480
AAATGAACA ATGCATCAG TCTTTTATAA TGCACTGTTT CAATTTGAGAT TCAAGTATT 540
CTATTTCTTG GAAAAAATTT TAAGATCAA AATAAAGAA AATAAAAGT GCATACAGTT 600
AAACATTCCA AAAAAAAAAA AA

```

55  
Seq ID NO: B14 DNA sequence  
Nucleic Acid Accession #: XM\_086767.1  
Coding sequence: 276..611

60  
65  
70  
75

```

1 11 21 31 41 51
| | | | |
CTTGTTCATG GCATCCTTAG AAACAAACTG CAATTTTATT TCATTTCCTT GTCGTTTATA 60
CAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC 120
TGGCTGGGT TATCAAGCCA AGCTATTATA AGGTGTTTTA AAAGAAAGGA TGGAAAGGAAG 180
ACCTCTTAGG ACCACTGTGT TTTGGATAC AAGTGTGACA TATCCATTCT GTAGCCTATT 240
ATTTTGTCT CAGTATAAAT GTTCCAGATA AAATATGAT GGTATGGCTG TTTTCATTTA 300
AATTATTAAA TCAGCTTGGG ATGATTGAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT 360
TTTATAAAT TCAAGAAGTC AAGATTCTTG CTCAATTTTA TAATGACTTT GTAAATATT 420
CAAGCATGG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCCACA TGCACATACA 480
AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540
ATAATATTGT ACTTAAAGAC AGAGAGGGAAG TGTTCCTTAA TCCAAACACA TGTACACCA 600
AGAACACATA AGATGCCCTT TTCCATCAAA TGCACTTGCT TGTGAATTAA TGGACTTGA 660
AATGAACAA TGCAATCAGT CTTTATAAAT GCACGTGTCA ATTTGAGATT CAAGTATTTC 720
TATTTCTTGG AAAAAATTTT AAGAATCAA AATAAAGAAA ATAAAAATG CATACAGTTA 780
AACATTCC

```

Seq ID NO: B15 Protein sequence  
Protein Accession #: XP\_086767.1

80

```

1 11 21 31 41 51
| | | | |
MMDGSFSFKL LNQLGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNISS IGLTYFQSSN 60
LQSCSTCYKI QRLMLKSLTY PERPPLCRYN IVLKDREEVF LNPNTCTPKN T

```

Seq ID NO: B16 DNA sequence



Nucleic Acid Accession #: CAT cluster

```
1      11      21      31      41      51
5      |      |      |      |      |      |
      TTTTITTTT TTTTITTTT TTAAATGCAA AGGAGCAACA AAATTTATTG ACTGAATTAA 60
ACACAACAGT AAAATGGCAG TGTTGTAAAT TCATTTTCAG ATGTTTGAAT GGAACAAGAA 120
AAGTGCTATT AGCCCAAGCT TCTTACATTC ATTAAGAGAG TGACTATCAA AAACAGCAAC 180
ATGCACAATG GTACATATGC ACAAATGGA ATTATATCAA CAAATATACA AAATACCCAA 240
AATAAAATAT TTACAGGTTT AAAAATATAA ACATTGATTC CTCTATCCCA TTAAACCAAT 300
10     GGAGTGGAGA AAGGAGGAAA GACCCATTG CTATTAGAA TCCTTTTAA AACAAAGTTT 360
TAAACATAG AATTAGTTCT AGGAGACAAT TTTTGATGTT TTTCAGGGGT TTAAACATTCT 420
ATTATAAAAA TAACATCTAT AAACCTACTA ACAATTTTCC TCCTGTGCAC AAAAATAATA 480
CTGCCAAAC CTGTCCTCAA AGACATGCCT GACTTTCAGG AAAGCTAATT ATGGAAATGG 540
AGTTTCTCGT TTGGGTATC TTTGTTACTA TTTTCAAATA ACCAGCACT CCCTATATTA 600
15     CACTGAGATA CTTTATATAA ATAACTGGG CGAAACCTGA AGTTCACAAT GAGCCTGCTA 660
GGTAGCTGGT TCAAGTACA AATGATAGGA ATTGACTTTG CCAACAACAT CAAAAGCATT 720
TTCCCTGATA TTCTGTATAG ACCTACCACT ATCAGATCCT CCATATTCAA TAAGATTTAT 780
CCTGGAAGCA ATGAAATGT TAAATATTAC TTTGCTAGAG TTCTCTCTCC TTTATTAGA 840
20     AATAAATGTG TAGTGGGGAC CAGTGGTTGT AATGTAGATA CTTGAGAAGT TTCATTGATT 900
CCTTCAGACC CATGCCG
```

Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM\_022898.1

Coding sequence: 268..2739

```
25     1      11      21      31      41      51
      TTTTCTTGCT TTCTTCCCT TTTTCTTCT TTTGCAACA AAACAAAAA CAGCATAGAA 60
GAAAGAGCAA AATAAGAGAG AAGAAGAGGA GGAAGAGAGG GAAAGAGAGG AAGGGAAGAA 120
AAACACCAAC CCGGGCAGAG GAGGAGGTGC GCGCGCGCGG CCGCGCGCGG CAGCGCGCGG 180
AGCGCGCGGG CCGCGGCTCG GACCCCTCC CCGGCTCCC CCATCAGTG CAGCTCTCG 240
GGCGATGCCA GAATAGATGC CCGGCAATG TCCCGCCGCA AACAGGSCAA CCGCGCAGAC 300
TTGTCCAGA GGGAGTCAT CACCCAGAG GCTGACCATG TGGAGGCGCG CATCTCGAA 360
GAAGACGAGG GTCTGGAGAT AGAGGAGCCA AGTGGCTCGG GGCTGATGTT GGTGGGCCCC 420
GACCCCTGACC TGCTCACCTG TGGCCAGTGT CAAATGAATC TCCCTTGGG GGACATCCTG 480
GTTTTATAG AGCACAAAG GAAGCAGTGT GCGCGCAGCT TGGGTGCTG CTATGACAA 540
GCCCTGGACA AGGACAGCCC GCCACCTCC TCACGCTCG AGCTCAGGAA AGTGTCCGAG 600
CCGGTGAGGA TCGGGATCCA AGTACCCCC GACGAAGATG ACCACCTGCT CTCACCCACG 660
AAAGGCATCT GTCCCAAGCA GGAGAACATT GCAGGTAAAG ATGAGCCTTC CAGCTACATT 720
TGACACAACT GCAAGCAGCC CTTCAACAGC GCGTGGTTCC TGCTGCAGCA CCGCGAGAAC 780
ACGCAAGGCT TCCGCACTCA CCGGAGCCC GGGCGCGCCA GCAGCTCGCT CACGCGCGG 840
CTCACCATCC CCGCGCGCTG CCGCGCGGAG GCGCTGGGCG AGTCCCGGCT CATGAATTTC 900
CTGGGCGACA GCAACCCCTT CAACCTGCTG GCGATGACGG GCCCATCCT GCGGAGCCAC 960
CCGGGCTTGG GCGAGGGCGG CCGCGCGGCT TCTTCAGTCC CCGCGCGGCG 1020
CACCACCTGG ACCCGCAGCG CCGCTGCTGC GAGGAGATGG GGCTGCTGCG CCAGCAGCCC 1080
AGTGCCTTAG CGCGAGTCTA GCGCTGAAC CCGATGGCCA TCGACTGCGC CGCATGAGC 1140
TTCTGCGGCG GCTTCCGCGA GCTGCGGCGC AACAGCTCCA CCGCGCGGCG CCGTCTCCCG 1200
GGCGCGGCGA ACCCTATGCA CCGCTCTCTG AACCCCTTCC AGCCAGCCCG CAGTCCCGG 1260
TTCTGAGCA CCGCGCGCTG GCGGCCATG CCGCTGCGG GCAAGCGGCG CCGCGAGCGG 1320
CCAGCCAGGA GCAAGTCTGT CGAGTTCTGC GGCAAGACCT TCAAGTTCCA GAGCAATCTC 1380
ATCGTGACCT GCGCGAGTCA CCGGCGGCGG AAGCCCTACA AGTGCCAGCT GTGCGAGCAC 1440
GCGTGTCTCG AGCGCAGCAA GCTCAAGCGC CACATGAAGA CGCATATGCA CAAAGCGCGC 1500
TGCTGGCGCG GCGGCTCCGA CGAGCGGCTC TCGGCGGCGA GCTCCCGGCA GCGCGGACCC 1560
AGCGAGCTGG CCGGCGAGGG CCTCAAGGCG GCGGAGCGTG ACTTCCGCGA CCAGGAGAGC 1620
GACCCGCTGC TGGGCGCAGA GCGGAGGAGG GAGGAGCGAGG AGGAGGAGGA GGAGGAGGAG 1680
GAGCTGTCTG TGGGCAACGA GAGCGGCGCC GAGTCCAGCT TCAGCATGGA CTCGGAGCTG 1740
AGCGCAACCC GCGGAGACGG CCGTCTGTGG GTGCGCGGGG TCCCGGCGCG GGGGGGCGGC 1800
GCGGCGAAGG CGCTGGCTGA CGAGAGGCG CTGGTGTCTG GCAAGGTCTG GGAGAACCTG 1860
GGCTTAGGCG CACTGCGCGA GTACGCGAG CTCCTGCGCG ACAGCAGAA GCGCGCGCGC 1920
TTCTGAAGC GTGCGGCGGG CCGGCGGAGC GCGGCGGAGC ACGACGAGCG GGGCGGCTGC 1980
GGGAGCGCGG GCGGCGGCGG CCGGCTCAAC GGGCGCGGCG GCGGCTTGGC GCCAGGCAAC 2040
GAGCCCTTCC CCGGCTCTT CCGCGCAGG CCGCGCGCGG TGCCAGGCGC CCGGCTCAAC 2100
AGCGCGGCGA AGCGCATCAA GGTGAGAAAG GACTTGGAGC TGCGCGCGCG CGGCTCATC 2160
CCGTGCGAGA ACGTGTACTC GCAGTGGCTG GTGGGCTAGC CCGGCTGCGG GCACTTCATG 2220
AAGGACCCCT TCTTGGGCTT CAGGAGCGCA CGACAGTCCG CCTTGGCCAC GTCTGCGAG 2280
CACTGTCTCG AGAAGCGCAG CCGGCGCTTC TCCAGCGCGC CCGGGGACCT GCTGGAGCGG 2340
GGCTCTCGG GCGGCGAGCG CAGGCGCAGC GGAGGCGAGCA CCGCGCACCT GGGCGGCGCG 2400
GGCGCGGCGC GCGGCGGCTC CAAGGAGGCG CCGCGCAGCG ACAAGTGGCA GTACTGCGGC 2460
AAGGTGTTCA AGAAGTGCAG CAACTTGAGC GTGACCGCGC GGAAGCCACG CCGGAGCGG 2520
CCTTACAGT GCGAGCTGT CACTACGCG TGCGCGCAGA CGACAGAGCT CAGCGCGCAC 2580
ATGAAGACCG ACGGCGAGAT CGGCAAGGAG GTGTACCGCT GCGACATCTG CCAGATGCC 2640
TTCAAGCTCT ACAGCACCTT GGAGAAACAC ATGAAGAAAGT GGCACGCGCA GCACTTGTG 2700
ACTAAGAGCG TCAAAATCGA CGAGGCGGAG AGGAGCTAAG CGCGCGGCGC CCGGCGCGCC 2760
GCACCTGTAC AGTGAACCG TTGCCAACCG AGAGAATGCT GACCTGACTT GCCTCGGTG 2820
CAGCGCCACC CCGCACCCCG CGTGTCCCGG GGGCGCGAGG GAGGCGCGAC TCCACCTAA 2880
CCTAGTCTG CGAAGTCTTA TGGAAACCGG AGGGTTGATT AAGGCGAGTAA AAATTGTGA 2940
GCCTTTTAA TGTGCAATAA TTCTGTATT TATTGGGTTT TGTAATTTT TTGGCATGTG 3000
CAGGTACTTT TTATTATTAT TTTTCTGTT TGAATTCCTT TAAGAGATT TGTGGGTAT 3060
CCATCCCTTC TTGTTTTTT TTTTAACCGG GTAGTAGCCT GAGCAATGAC TCGAAGCAA 3120
TGTAGAGGGA GAAGCATATC TTTTAAATTA TAATTGGGG GAGGCGGCGG TGCTGCTTTT 3180
TGAAATTTG CGAAGTATC GTGTAATTC TTGTGAAGAA GCCAACACTC AAATGACTTT 3240
TAAAGTTGTT TACTTTTCA TTCTTCTT TTTTGTGCC TGAATAAAA AGTGGCATGC 3300
AGTTTTTTTT TTAATTATT TTTTGTGTT TTTTGTGTT TTGTTTTGG GGTGGGGGGT 3360
GTGGATGTAC AGCGGATAAC AATCTTTCAA GTCGTAGCAC TTTGTTTCAG AACTGGAATG 3420
```

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70

GAGATGTAGC ACTCATGTGC TCCCGAGTCA AGCGGCCTTT TCTGTGTTGA TTTCCGGCTTT 3480  
CATATTACAT AAGGGAACC TTGAGTGGTG GTGCTGGGG AGGCACCCCA CAGACTCAGC 3540  
GCCGCCAGAG ATAGGGTTTT TGGAGGGGCTC CTCTGGGAAA TGGCCCGACA GCATTCTGAG 3600  
GTTGTGCATG ACCAGCAGAT ACTATCCTGT TGGTGTGCC TGGGGTGCCA TGGCTGCTAT 3660  
TCGCTGTAGA TTAGGCTACA TAAATGGGC TGAGGGTACC TTTTGGGGA GATGGGGTGG 3720  
CCTGCAGTGA CACAGAAAGG AAGAACTAG CGGTGTTCTT TTAGGCGTTT TCTGGCTTGA 3780  
CGGCTTCTCT CTTTTTTAA ATCACCCECA CCACATAAAT CTCAAATCCT ATGTTGCTAC 3840  
AAGGGGTCAAT CCATCATTTT CCAGCAGAG GAATGCCCTA ATTAATTGAA GTTAGTGTTC 3900  
TCTCATTTAA TGCACACTGA TGATATTGTA GGGATGGGTG GGGTGGGGAT CTGCAAAAT 3960  
TCTATTCTCT TTACTGAAA AAGCAGGGGA TGAGTTCCAT CAGAAGGTGC CCAGCGCTAC 4020  
TTCCAGGTT TTTATTTTTT TTTTCTATC TCATTAGTTT GGAAGGTACT AAATATTGAA 4080  
CTGTTAAGAT TAGACATTGG AATTCGTGTT ACCCGCACTT TAAAGCTTTT GTTTGCAATT 4140  
AAATTAATG GCTCTAAAC AAGAAATGTC AGCATATTCT TCTCTTTGGC CCAGAGGTGG 4200  
GTTAACTGT AAGGGACAGC TGAGATTGAG TGTCAAGTAT GCTAAGCGTG GCATTCACAA 4260  
TACTGGCACT ATAAAGACA AAATAAATA ATAATTTATA GGACAGTTT TCTACTGCCA 4320  
TTCAATTGA TGTGAGTGCC TTGAAAACG ATCTTCCTAT TTGAGTCTCT TGAGACAAAT 4380  
GCAAACTTT TTTTTGAAA TGAAAAGACT TTTTAAAAA GTAAAACAAG AAAAGTACAT 4440  
TCTTTAGAAA CTAACAAAGC CACATTTACT TTAAGTAAAA AAAAAAATA TTCTGGTTGA 4500  
AGATAGAGGA TATGAAATGC CATAAGACCC AATCAATGA AGAAATAAAC CCAGCACAAC 4560  
CTTGACATC CATTAGCTGA ATTACTCTCA GCCCTTTTG TTTTGGGAC AACGCTGCTT 4620  
AGATATGGAG TGGAGGTGAT TTACTGCTGA ATTAAACTC AAGTGACACA AGTTACAAGT 4680  
TGATATCGTT GAATGAAAAG CAAAACAAA ACAATTCAGG AACACCGCT AATTTTTCT 4740  
AAAGTTAAAT TTAGTGCACT CTGCTTAAA AATACGTTA CAGTATTGGG TACATACAAG 4800  
GGTAAAAAAA AAATGTGTG TATGTGTGT GGAGCGATCT TTTTTTTCA AAGTTTCTT 4860  
AATAGGTTAT ACAAAATGTC CACAGTGCC GCGTGTATAT TGTTTCTTT TGTGTACGGG 4920  
GTTTATGAT ATATTATATA TATTAATAAT TCTTGATTAC TGTAAAAGTG GACCAGTATT 4980  
TGTAATAATC GAGATGCTT GGGCATTTTA CAAAACAAGA AAAAAAATAC CCTTTCTTT 5040  
TCCCTGAAAA TGTGCACTA AAATTTAAAT GGTGGGTCTA TAAATTTGTT CTGTGTTGTT 5100  
TAACGTAAA GTCCGAGTTT TAGTAAATTT TTTCTGCTT TGGGTGTTGA ATTTTATT 5160  
CAAAAAAAT GTATAGAAC TTGTATTGG GATTCAAAG GGGATTGCTA CACCATGTAG 5220  
AAAAAGTATG TAGAAAAAAA GTGCTTAATA TTGTTATTGC TTGACAGAAA AAAAAAAT 5280  
CACATTCTG ACCGTGACTT ATTTTCTCT TCCCGCTCC CTCGGAATG GATATATTGG 5340  
TTGGTTCATA TGATGTAGGC ACTTGCTGTA TTTTACTGG AGCTCGAAT TTTTAACTG 5400  
TAAGCTGTG CTTTTAAAGG GATTAAATGT ACCTTTTGT TAGTGAATTT GGAATAAAAA 5460  
AGAAAAAATA AACAAAAACA AACAGGCTGC CATAATATAT TTTTAAAT TGGCAGGATA 5520  
AAATATTGCA AAAAAACAC ATTTGTATGT TAAGTCTAT TGTACAGGAG AAAAAGGTT 5580  
GTTTGACAACT CTTTGAGAAA AAGAAACAAA AGGAAGTAGT TAAATGCTT GTTTCACAAA 5640  
TCATTTAGTT GTATATATT TTTGTGCGAA TTGGCTTACA CAGAGAACC TCGTGTGTTG 5700  
GCTTCTCTCT GAACGCCCG AACCTTGCA CAAGGCTCCT TGGTGTGGCC ACAGCAGACC 5760  
AGATGGGAAA TTTATTGTGT TGAGTGGAAA AAAATCAGTT TTTGTAAGA TGTCAAGTAA 5820  
ATTCCACATC GTCTCTCTT TCTCTAAGAG GCCATCTCTA AGATGTGAGA TGTAGAGGAG 5880  
AGAGAGCGAG AGAACATCTT CCTTCTCTAC CATCACTCCT GTGGCGGTCA CCACCAACC 5940  
CTCTCCGCC CTTACCAGCA GAAAGCAATG CAACTGAGC TGCTTTAGTC CTTGAGAAAT 6000  
TGTGAACAAA ACACAAATAT CATAAAGGA GCTGGTGATT CAGCTGGGTC CAGGTGAAGT 6060  
GACCTGCTGT TGAGACCGGT ACAATTTGA TTTCAAGAA GAGACTCCAT CACAGCCAGG 6120  
ACCTTTCTGT CCATGGAGAG TGTGGGCTC TTGCTTTCT TCCCTGCTT GCTGCTTGC 6180  
TCTCTGAAC CTACATTCCG TCAGTTTCCG AATGCGAGGG CCTGGGATGA ATTTGGTGCC 6240  
TTTCCATATC TGTCTCTCT TCCCTCCCT GCGTTTCTCT TCCATCTTC ATCTCCCAT 6300  
GGTCTTTT TTTTCTTCA TTTTATTTT AATTTCTTT CTCTGTCTT GTTCTCTCC 6360  
TAATCTCTA TTTTATTTT ATTTTGTGA AAGCCAAGTA GCTTAAAGT AAGTGGTGG 6420  
TCTTTTGGAT GAGGGAATAA TGCATTTTTA AATAAAATAC CAATATCAGG AAGCCATTT 6480  
TTATTTGAGG AAATGTAGA AACCATTATT TCAGGTTATG AAGTATAAC CAGCATCCT 6540  
TTTGGGCAAT TCCTTACCAA ATGCAAGAGC TTTTCTGTT GATGCACITC TTCTCTCTG 6600  
CCACTTACCT TTGCAAGATT AAAAAAAGG GGGGAGGAAA TGGGAGAGAA AGCTGAGATT 6660  
TCAGTTTCTT ACTGCAGATT CTAAGTGA GATCCAGGGG CTGCTGTGTC CTTTGGATGC 6720  
CCCCTGAGG TCCTAGAGTG CCTCAGGGT GGTCTTCTG TAGTCATAAC AGCTAGCCAG 6780  
TGCTCACCAG CTTACCAGAT TGCCAGGACT AAGCCATCCC AAGCACAAG CATTGTGTGT 6840  
CTCTGTGACT GCAGAGAAGA GAGAATTTTG CTCTGTGTT GTGTTAAAA AACCAACAG 6900  
GAAGCAGATG ATCCCGAGAG AGAGGCTCT AGCATGGGTG ACCCAGCCGA CCTCAGGCG 6960  
GTTTCCGCAC TGCCCAACT TTGTTCAAAG TTGCCCCCAA TTGGAACCTG CCACTTGGCA 7020  
TTAGAGGGTC TTTCTATGGG AGAGAAGGAG ACTGAATTAC TCTAAGCAAA ATGTGAAAAG 7080  
TAAGGAAATC AGCTTTTCAT CCGGCTCTA AGTAACCGTC AGCCGAAGGT CTGTTGGAAC 7140  
ACAGGCAAC CCGTATTTT GGTGCTCCTT GTAACCTCAG CCTGCAAGC AAGTCCCAT 7200  
TGATTAAAGT TGTGTCATT TGTACTGGCA AGGCAAAATA TTTTATTAC CTTTCTATT 7260  
ACTTATTGTA TGAGCTTTTG TTGTTACTT GGAGGTTTGT TCTTTTACTA CAAGTTTGA 7320  
ACTATTTATT ATGCTTTGGT ATTGTGCTC TGTTAAGAA ACAGGCACTT TTTTATTA 7380  
TGGATAAAAT GTTGAGATGA CAGGAGTCA TTTCAATATG GCTTAGTAAA ATATTATTG 7440  
TTCTTTATT CTCTGTACAA GATTTTGGGC CTCTTTTTT CTTAATGTC ACAATGTTGA 7500  
GTTCAAGATG TGTCTGCCAT TTCATTGTA CGCTGTGTTA AAACCAAGTT TGTCTGTTT 7560  
TCAAGTTATA AAAATAAAT TGACATTAA CTGATCTCC AAA

Seq ID NO: B18 Protein sequence  
Protein Accession #: NP\_075049.1

75  
80

1 11 21 31 41 51  
MSRRKQGNPQ HLSQRELITP EADHVEAAIL EDEGLEIEE PSGLGLMVGG PDPDLLTCGQ 60  
QDMNFPGLDI LVFIEHKRQK CGSLGACYD KALDKSPPP SSRSELRRVS EPVEIGIQVT 120  
PDEDDHLLSP TKGICPKQEN IAGKDEPSSY ICTCKQFPN SANFLLQHAQ NTHGFRIYLE 180  
PGPASSSLTP RLTIPLPLGP EAVAQSLPMN FLGDSNPNFL LRMTGPILRD HPFGFEGRLP 240  
GTPPLFPSPV RHHLDPHRLS AEEMGLVAQH PSADFVRML NPMAIDSPAM DPSRRLRELA 300  
GNSSTPPFVS PGRGNPMHRL LNPFQSPKPS PFLSTPPLFP MPFGGTPPPQ PPAKSKSCEF 360  
CGKTFKQSN LIVHRRSHTG EKPVKQLCD HACSQASKLK RHMKTHMKA GSLAGRSSDDG 420  
LSAASSPEPG TSELAGEGLK AADGDFRHRB SDPSLGHEPR EDEEEEEEE EELLLENESR 480

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

PESSFSMDSE LSRNRENGGG GVPGVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPOYG 540  
ELLADKQKRG AFLKRAAGGG DAGDDDDAGG CGDAGAGGAV NGRGGGFAPG TEPFPLGFPR 600  
KPAPLPSPGL NSAAKRIKVE KDLELPPAAL IPSENVYSQW LVGYAASRHF MKDPFLGFTD 660  
ARQSPFATSS EHSSENGSLR FSTPPGDLDD GGLSGRSGTA SGGSTPHLGG PGPGRPSSKE 720  
GRSDDTCEYC GKVFKNCSNL TVHRRSHTGE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK 780  
EYVRCDICQM PFSVYSTLEK HMKKNHGEHL LTNDVKIEQA ERS

Seq ID NO: B19 DNA sequence  
Nucleic Acid Accession #: NM\_000399.2  
Coding sequence: 339..1769

1 11 21 31 41 51  
| | | | |  
TAACTGACGG AGGAGCAATT GATTAATAGC TCGGCGAGGG GACTCACTGA CTGTATAAT 60  
AACACTACAC CAGCAACTCC TGGCTTCCCA GCAGCCGGAA CACAGACAGG AGAGAGTCAG 120  
TGGCAATAG ACATTTTCTT TATTTCTTAA AAAACAGCAA CTGTGTGTCT ACTTTTATTT 180  
CTGTGTATTT TTTTTCCTTG GTGTGTGTGG TGGTGTGTTT TAAGTGTTGA GGGCAAAAGG 240  
AGATACCATC CCAGGCTCAG TCCAAACCCCT CTCCAAAACG GCTTTTCTGA CACTCCAGGT 300  
AGCGAGGGAG TTGGGTCTCC AGGTGTGTGG AGGAGCAAAAT GATGACCGCC AAGGCCGTAG 360  
ACAAAATCCC AGTAACTCTC AGTGGTTTTG TGACACAGCT GTCTGACAA ATCTACCCGG 420  
TGGAGGACCT CGCCGCCACG TCGGTGACCA TCTTTOCCAA TGCCGAACCT GAGGGCCCT 480  
TTGACCAGAT GAACGGAGTG GCCGGAGATG GCATGATCAA CATGACATG ACTGGAGAGA 540  
AGAGGTCTGT GGATCTCCCA TATCCACGCA GCTTTGCTCC CGTCTCTGCA CCTAGAAACC 600  
AGACCTTCAC TTACATGGGC AAGTTCTCCA TTGACCTCA GTACCTTGGT GCCAGCTGCT 660  
ACCCAGAGGG CATAATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGTC ACTTCCCGAG 720  
CTTCAACAC AGCCTCATCC AGCCTCACCT CTGCCCTCCC CAACCCACTG GCCACAGGAC 780  
CCCTGGGTGT GTGACCATG TCCAGACCC AGCCTGACCT GGACCACTG TACTCTCCGC 840  
CACGCTCTC TCCTCTTAT TCTGGCTGTG CAGGAGACCT CTACAGGAC CCTTCTGCGT 900  
TCTGTGACG AGCCACACCC TCCACCTCTT CCTCTCTGCG CTACCCACCA CCTCCTTCTT 960  
ATCCATCCCC CAAGCCAGCC ACGGACCCAG GTCTCTTCCC AATGATCCCA GACTATCCTG 1020  
GATTCTTTCC ATCTCAGTGC CAGAGAGACC TACATGGTAC AGCTGGCCCA GACCGTAAGC 1080  
CCTTTCCCTG CCACTGGAC ACCCTGCGGG TGCCCCCTCC ACTCACTCCA CTCTCTACAA 1140  
TCCGTAACCT TACCCTGGGG GGGCCAGTG CTGGGGTGAC CGGACCAGGG GCCAGTGGAG 1200  
GCAGCGAGGG ACCCCGGCTG CCTGGTAGCA GCTCAGCAGC AGCAGCAGCC GCCCGGCCG 1260  
CCGCTATATA CCAACACCA CTGCCACTGC GGGCCATTCT GAGGCTCGC AAGTACCCCA 1320  
ACAGACCCAG CAGAGCGCG GTGCACGAGA GGGCCCTACCC GTGCCAGCA GAAGGCTGG 1380  
ACCGGGGTT CTCCCGCTCT GACGAGCTGA CACGACCAT CCGAATCCAC ACTGGGCATA 1440  
AGCCCTTCCA GTGTGGATC TGCATGCGCA ACTTCAGCCG CAGTGACCAC CTCACCACCC 1500  
ATATCCGCAC CCACACCGGT GAGAAGCCCT TCGCTGTGA CTACTGTGGC CGAAAGTTTG 1560  
CCCGGAGTGA TGAGAGGAG CGCCACACCA AGATCCACCT GAGACAGAAA GAGCGGAAAA 1620  
GCAGTGCGA CTCTGATGCT GTGCCAGCCC CCTCTACAGC CTCTGCTCT GGGGGCGTGC 1680  
AGCCTGGGG TACCTGTGC AGCAGTACA GCAGCAGTCT TGGCGAGGG CCGCTCGCCC 1740  
CTTGCTCTC TCGGACCCGG ACACCTTGAG ATGAGACTCA GGCTGATACA CCAGCTCCCA 1800  
AAGGTCCCG AGGCCCTTG TCCACTGGAG CTCACACCA AACACTACCA CCTTTCTCTG 1860  
TCCCTCTCTC CTTTGTGTTG GCAAAGGGCT TTGTGGGAGC TAGCACTGCC CCTTTCCAC 1920  
CTAGAAGCAG CTTCTTCTTA AAACCTAGCC CATTCTAGTC TCTCTTAGT GAGTTGACTA 1980  
TCAACCCAG GCAAAGGGGA GGCTCAGAAG GAGGTGGTGT GGGGATCCCC TGGCCAAGAG 2040  
GGCTGAGGTC TGACCCCTGCT TTAAGGGGTT GTTTGACTAG GTTTTGCTAC CCACTTCCC 2100  
CTTATTTTGA CCAATCACAG GTTTTGACC CTGGATGTCA GAGTTGATCT AAGACGTTTT 2160  
CTACATAGG TTGGGAGAT CTGATCCCTT CAAGTGGGGA CAGCAAAAAG ACAAGCAAAA 2220  
CTGATGTGCA CTTTATGCTT TGGGACTGAT TTGGGGGACA TTGTACAGTG AGTGAAGTAT 2280  
AGCCTTTATG CCACTCTCTG TGGCCCTAAA ATGGTGAATC AGAGCATATC TAGTTGTCTC 2340  
AACCTTGAA GCAATATGTA TTATATATCT AGAGAACAGA AGTGCAATGT GATGGGAGGA 2400  
ACGTAGCAAT ATCTGCTCTT TTTCGAGTTG TTTGAGAAAT GTAGGCTATT TTTTCAGTGT 2460  
ATATCCATC AGATTTTGTG TATTTTGTAT GTACCCACAC TGTCTCTTAA ATTCTGAATC 2520  
TTTGGGAAA AATGTAAAGC ATTTATGATC TCAGAGGTTA ACTTATTTAA GGGGATGTA 2580  
CATATTCTCT GAAACTAGGA TGCATGCAAT TGTGTGGAA GTGCTCTTGG TCGCCTTGTG 2640  
TGATGTAGAC AAATGTTTCA AGGCTGCATG TAAATGGGTT GCCTTATTAT GGAGAAAAA 2700  
ATCACTCCCT GAGTTTAGTA TTTATGCCTA TTAATATTG GAATTTTTTT 2760  
TAGAAAGTAT ATTTTGTAT GCTTGTGTTT GTGACTTAAA AGTGTACCT TTGTAGTCAA 2820  
ATTTGAGATA AGAATGTACA TAATGTTAOC GGAGCTGATT TGTGTGTGTA TTAGCTCTTA 2880  
ATAGTTGTGA AAAATAAAT CTATTCTAAC GCAAAACCAC TAACTGAAGT TCAGATATAA 2940  
TGGATGGTTT GTGACTATAG TGTAAATAAA TACTTTTCAA CAAT

Seq ID NO: B20 Protein sequence  
Protein Accession #: NP\_000390.2

1 11 21 31 41 51  
| | | | |  
MMTAKAVDKI PVTLSGFVHQ LSDNIYFVED LAATSVTIFF NAELGGPFDD MNGVAGDGM 60  
NIDMTGKRS LDLPYPSSFA PVSAPRNQTF TYMGKFSIDP QYPGASCYPE GIINIVSAGI 120  
LQGVTSFAST TASSSVTSAS PNPLATPLGL VCTMSQTPD LDHLYSPPPP PPYPGSGCAGD 180  
LYQDPSAFLS AATTSTSSSL AYPPPPSYBS PKPATDPLGL PMIPDYGPFF PSQQRDLHG 240  
TAGPDRKPPF CPLDILRVPP PLTPLSTIRN PTLGGPSAGV TGPQASGGSB GPRLPSSSSA 300  
AAAAAAAY NPHELLPLRPI LRPRKYPNRP SKTPVHERPY PCPAEGCDRR FSRSEDLTRH 360  
IRIHTGKFP QCRICMNF SRSDDLTHIR THTGEKFPAC DYCGRKFPARS DERKRHTKIH 420  
LRQKERKSSA PSASVPAPST ASCSGGVQPG GTLCSSNSSS LGGGLAPCS SRTRTP

Seq ID NO: B21 DNA sequence  
Nucleic Acid Accession #: NM\_004962.2  
Coding sequence: 457..1893

1 11 21 31 41 51  
| | | | |

5	CACACACGGG	CGCACGCACA	CGGCAGCCGG	GCCAGGGACG	ACCCTGTCAG	CTGCAGCCCC	60
	AGAGGTCGGG	GGCGCGCAGC	CGGGTCCCCT	CGAGGGCGCA	GCCGGCCGCC	CCGCCCCGCC	120
	CCTCGAAGCA	GCCGGGCGGG	GCGCGCAGTG	GGCTACAAAC	TTTGCAGCG	CGAGTCCGCC	180
	AAGGCAGGCG	GCCGACTCGG	GCTCGGCTCG	GCTCTGCGCT	GCTCCGGACG	GCTGTGACCG	240
	CTGGCCGGGG	GCTCGGGCGG	CCGGTACCCA	CGGACCGCGC	GCCCGGGTGC	CTGCTCCGCT	300
	AAGCCCTCG	CCCCGCGCGG	ACCTCGGTAT	CCAGCGCCCT	GCTGCCCGGG	CTCTCCCGCG	360
	GCGCCCTACT	GCCGCGAGGT	CAGTCCGCAG	CCTCCGGTGC	GCCAGCGCTC	GCCTTCCTCC	420
	TCCTGGACTT	CGGCCCTTTG	CCGCCCTCAC	CACGCCATGG	TCATGTCTCC	CGCTCGGACC	480
10	AGCCCGGGAC	CGGGGCCCCA	GCTGCTGCTG	CTGCTGCTGC	CGTTGTTTCT	GCTGTTGCTC	540
	CGGATGTGG	CCGGCAGCCA	CAGGGCCCCC	GCCTGGTCCG	CACTGCCCGC	GGCCGCCGAC	600
	GGCCTGCAGG	GGGACAGGGA	TCTCCAGCGG	CACCTGGGG	ACGCGGCCGC	CACGTTGGGC	660
	CCAGGCGCCC	AGGACATGGT	CGCTGTCCAC	ATGCACAGGC	TCTATGAGAA	GTACAGCCGG	720
	CAGGGCGCCG	GGCGGGAGG	GGGCAACAG	GTCCGACGCT	TCAGGGCCAG	GCTGGAAGTG	780
	GTGACCCAGA	AGGCGGTGTA	TTTCTTCAAC	CTGACTTCCA	TGCAAGACTC	GGAAATGATC	840
15	CTTACGCCCA	CTTTCCACTT	CTACTCAGAG	CGGCTCGGT	GGCCTCGAGC	GCTCGAGGTG	900
	CTATGCAAGC	CGGCGGCCAA	GAAAGCTTCA	GGCGCCCGC	TGCCCTGGG	CCGCCCCACA	960
	GCCAGCACC	TGCTCTTCCG	CAGCCTCTCG	CAGAACACGG	CCACACAGGG	GCTACTCCGC	1020
	GGGCGCATGG	CCCTGGCGCC	CCCACCGCGC	GGCCTGTGGC	AGGCCAAGGA	CATCTCCCCC	1080
20	ATCGTCAAGC	CGGCGCGCCG	GGATGGCGAG	CTGCTCCTCT	CGGCCAGCT	GGATTCTGAG	1140
	GAGAGGAGCC	CGGGGGTGCC	CGGCGCCAGC	CCCTATGCGC	CCTACATCCT	AGTCTATGCC	1200
	AACGATCTGG	CCATCTCGGA	GCCCAACAGC	GTGGCAGTGA	CGCTGCAGAG	ATACGACCCC	1260
	TTCCCTGCGG	GAGACCCCGA	GCCCCGCGCA	GCCCCCAACA	ACTCAGCGGA	CCCCCGCGTG	1320
	CGCGAGCCG	CGCAGGCCAC	TGGGCCCCCTC	CAGGACAACG	AGCTGCCCGG	GCTGGATGAG	1380
25	AGGCCGCGCG	GGCCCCAAGC	ACAGCACTTC	CACAAGCACC	AGCTGTGGCC	CAGCCCCCTC	1440
	CGGCGCGCGC	AACCCCGGCC	AGGGCGCAAA	GACCGCAGGA	AGAAGGGCCA	GGAGGTGTTT	1500
	ATGGCCGCTT	CGCAGTGTCT	GGACTTTGAC	GAGAAGACGA	TGCAGAAAGC	CCGAGGAAAG	1560
	CAGTGGGATG	AGCCGAGGGT	GTGCTCCCGG	AGGTACCTGA	AGGTGGACTT	CGCAGACATC	1620
	GGCTGGAATG	AATGGATAAT	CTCACCGAAA	TCTTTTGATG	CCTACTACTG	CGCGGAGCA	1680
30	TGTGAGTTCC	CCATGCCCTAA	GATCGTTTGT	CCATCCAAAC	ATGCCACCAT	CCAGAGCATT	1740
	GTGAGGCTTG	TGGGATCAT	CCCTGGCATC	CCAGAGCCCT	GCTGTGTTC	CGATAAGATG	1800
	AACTCCCTTG	AGTGCTCTCT	CCTGGATGAG	AATCGGAATG	TGGTCTGAA	GGTGATCCCC	1860
	AACATGTCCG	TGGACACCTG	TGCTGCGCGG	TGAGACCACT	CCAGGGTGA	AAGAAGCCAC	1920
	GCCCAGCAGA	GCTGCTCTCT	CGGAGCCCTC	TGCAACCAGG	ACTTGTGGTG	CAGCTGCAGA	1980
35	CACAGAGCAC	AGCTCATGGG	CAACATCACT	GGGGCCCGA	GAGAGCTGTC	CGCCAGTGCA	2040
	TCATTAGGGG	GTCTTTTATT	GCTAGTACT	AGCCCCCTAA	ATGCCAGCCT	GAGTACCTGA	2100
	AGGAATCTGG	GAAATAGCCC	TGGCCTGAAA	TGGGCCCATC	ATTACATCCC	ACTGTTCTGA	2160
	AGGCTTGAAA	ACAAAACATA	TCCACAACAT	TGGCTTGATG	TGATCATCAT	CTCATAACTG	2220
	AGCAAGAAGA	CTATGCAAAAT	CTTAGGGGCG	TCGCTCCCTG	CACACGGA	GAACCTCTGT	2280
40	TAAATGCTCA	GTTCAGAAAC	CTTTGGGCCA	CATAGTGATT	TGGAAAAACA	GGATAATCGT	2340
	GGTGAATAG	AGTGTCTTCT	TTCAAGTCC	ACTGCAGAGC	TTTTATCCAT	ATGGTATGCA	2400
	CATGTAGCCA	ATATTGGTCT	CTTTTCTTA	ATATATATAT	TTTATTTTAA	AACAACAAAA	2460
	AGGGAGGGCG	TTGACACCAT	TCCCCACAGA	GATAGTCATG	CTGAGTGTGG	GTGTTTAA	2520
	CATGCATATT	GAATAACAC	ATATAGTAAC	GTGGGAATAC	TAAAAATAA	CCAAGATTCT	2580
45	ATATTTTGT	AAATTATACT	TTCTATACTG	TAGATTGTGT	ATGTTATGTG	TTTTTATGGA	2640
	AAGCTAATAA	ATTAAAGGTA	CAGTGGTATC	TTGA			

Seq ID NO: B22 Protein sequence  
Protein Accession #: NP\_004953.1

50	1	11	21	31	41	51	
	MAHVPARTSP	GPGPQLLLLL	LPLFLILLRD	VAGSHRAPAW	SALPAAADGL	QGDRLQRHP	60
	GDAATLGPS	AQDMVAVMHM	RLYEKYSRQG	ARPGGNTVR	SERARLEVD	QKAVYFNLIT	120
	SMQDSMILT	ATFHYSSEPP	RMPRALEVLC	KPRKNASGR	PLPLGPPTRG	HLLFRSLSQN	180
55	TATQGLLRCA	MALAPPPRGL	WQAKDISPIV	KAARDGELL	LSAQLDSEER	DPGVPRPSFY	240
	APYILVYND	LALSEPNVSA	VTLQRYDFPP	AGDPEPRAAP	NNSADPRVRR	AAQATGPLQD	300
	NELPGLDERP	PRAHAQHFKH	HQLWPSPPFA	LKPRPGRKDR	RKKGQEVFMA	ASQVLDPFDEK	360
	TMQKARRKQW	DEPRVCSRRY	LKVPADIGW	NEWIISPXS	DAYYCAGACE	FPMPIKVRPS	420
	NHATIQSIVR	AVGIIPGIPE	PCCVPDKMNS	LGVLFLENR	NVVLKVPYPM	SVDTACAR	

Seq ID NO: B23 DNA sequence  
Nucleic Acid Accession #: AK026322.1

65	1	11	21	31	41	51	
	ATTCTTTAAA	TACTTAAACA	TGGTTATAAC	AGCTGTGTTT	TAAGCTCCTT	GTCTGTTAAT	60
	TCCATCATCT	GTCAATTTTG	CACTGTGTTT	TATTGACTAA	CTTCTTCCT	CATCATGGTC	120
	ACATATCCCT	GCTTCTTCCC	ATATTAGTA	AAGTTAGTGT	GGATGCTGGA	TTGTTTAAAT	180
	TTAGCATTTT	GGAGTGACTG	CTTTTGCACT	TGCCCTTAAA	AGTATTGGAC	TTGTTTGA	240
70	TAGTTGAATT	ACTTGCAAA	CAGCTTGATC	ATTCTGAGAC	TTGTTTAA	CTTTTGTGCA	300
	AAAGGCTATG	CTATTCAAG	TATAATAAAA	CCTAGTTTAA	GTTTATCCT	ATAACTAAGG	360
	CATGTGTTC	ATTGTAATGT	CTCCAACCTT	GTGTGAACCT	TGAAATTTGT	TCAGCTCCCA	420
	ATTTGCGAGT	AAATTTTTTT	GTTCAGCCTT	GCAGTCTCAT	CCTACTCAAG	TGTGGCTCTG	480
	TATCCAACAA	CAGTCTTGGA	GATCTCATGA	AGATTCTGGA	AACTTTTGCT	CTGCAGGATA	540
75	CCTTCTTTTG	TGGTTATGTG	CCCTGAAAAC	TCCAGCCTCC	GTGCTCTCAA	TTCAAGTAAA	600
	CTACTACTCT	GCTTGGAATC	CCCTCTTATA	CAATGGTCTA	CCAAGTGACT	GCAACACAGAA	660
	ATCTAAGGGA	ATTTCAAGAG	TCACCTCAT	TATTTTCTT	TTTTTCAGG	ATTATAGTAG	720
	TACTATACCA	CTGTGAGCC	AATGTGTGAG	AATGTTGGTT	TCATACATT	TCTCAATTC	780
	TTTCTTGTTA	CAGGAGCCTC	CATTACTTTT	CAACAGTAA	TGCAGTTGCA	GTTCCTCTC	840
80	CTTTTCTTCA	TTATGTGTTT	ATCTCTGCA	GTTTGAGCCA	AGAGAGGGCA	CGGAGAAGTA	900
	CAATGAGTGC	AGAGCACTTC	TGTTGAGGCT	CAITCAATTGA	CCCTACCCC	AGTGCTTTAT	960
	GAATGRTGTC	TGCAGATGTC	ATACAGCATC	ACAGCTTCTT	CTCTAATTTA	TGAGCCATAA	1020
	TTTTTTTTTT	TGTAATTTTA	TTGTAATACC	TGCTTGGTTG	CAAGAGGATG	ATGAGGAGGA	1080
	CTACTATAGG	ATRAATTTGT	TTTTATAGAG	CAATTTCTCA	TGGGTACGA	GGGATAGTAC	1140

TCCATTTC TCACGTATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200  
TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCTGTTA CATGAAATAA AGCCAGAGTT 1260  
GATTGTGAAA AAAAAAAAAA AAAA

5 Seq ID NO: B24 DNA sequence  
Nucleic Acid Accession #: cat cluster

1 11 21 31 41 51  
10 TGTATACATT CCTTTCAAAT AAAGACCTTG AGAAAACAGC AGAGCCAAGT GAAGATCACC 60  
TAAAGAACTT TGTGGCTAAT TTATACCTCA TGATAGTACA GTGGGTACTG GGCAGGGTCT 120  
CTTTCCCACT CTGATGATTT GTGCTCTTAT TTTCTCTAGA TTTACCTCAT CTAGGGCATA 180  
TTCTTTTCCC TCTTCTCTT TACCTTTCTT GGTCTGATC CCTCTGTACT CAGTTCCTCC 240  
AAATTATTGG ACTACAAACT AATATACTAG AAAAGCATAC ACTTATTTTA TTTGAATGCA 300  
15 GAAATGCTAT CTATCAGTAT ATATACATAA GAATGTATAT TACAGTATAT CTATATATAC 360  
TTAACACTGT AACCTTCAGT ATTCCTCCAGT TAGCGTACCT AACTCTCCTG TGGGTTATGT 420  
TAATTTCTAT TAGACTACTA GAGAAAAACC AACTGGCAGT TTGCTAAGCA TATCTACTGG 480  
TGTGTCTTCT GCGCCTCTT TTGGCTAATT GATGTAATTA TACTGGCTCT AAAGATTTAC 540  
TGCCCCATAA GTAAATAGTA TAGCCACATT CTGAACATAT CAAAAGTACA AACTTAGGAG 600  
20 GAGTGTATGT ACAAATATGT AAAATTTTAT GAAAATGAAC ATGTTTTTAT GATGTTATTT 660  
CTAGTTTATA AGAATGTGAT GACTGCTTTG CTTCATTTAT GTACGTTCCC ATTATATTCT 720  
TGCTGTCAAT CAATCACAAA TTTATATCAG ATTAGGATAA ACTAAGCCAT TTTATGTAAT 780  
TTATTTTAAA CCTTATTTTG GCAGAGTAAT TCCTTAGAAT TGGAAAAGCT GTTACTTTGA 840  
AATTACCAAT TTATACAAA ACATAGAAAT GTATTGTAGC TACAAAGACA ACCAAGCATT 900  
25 TTCTGTGTTT TAATGAATAT CTAAAAAAT ACATTTAGTT TATTTTACTC AGTTTGTAAA 960  
TGATTTTTTT ACTGGCTCTA TTGCCCTTAA ATAACTAAGA GATTATGAT TCTTTGTATA 1020  
ATTTTCCTTT TCTTTGTTCT TTTTITIAA TTTCCGACAG TTATATCTAT AGTTTGTATA 1080  
ACAATTTCTT ATGATTTCTG GATAACTGAA AACAACATAA GGTGTGGGGC ATTAGAAAAT 1140  
AATTGTGAGC AGTAAGATTA CTGATGTAAT ATGATGTTG GACTGAAGTA TTTCTTTATA 1200  
30 AACATTCTAT TTGATTTTAA GCAAAATGTA TGTAAAGCA TGTTTTACA TCAGTAAAGT 1260  
CATTGTGCGA CCTTCGGAAT ATGAAAGGTT TTTACCTAGA TACTGTAAGT TACACCTCCT 1320  
TAACAATCAT ATTTGTGCTT GTTGTCTTCT GCAACACAAA ATGTTTATGG GCTTCATGTA 1380  
GGCTTAAGAT TGTAGGCAAA AATGGACTGA GTTCAGGACC CTTCAGCAGT TAGGCATTCA 1440  
GTTACAGAGC AGTTGGTACT TTGTAACCCA GACTTACAGT TTAATAATAT CAAGTTAGCT 1500  
35 GATGTTTCAT TATAATAAAA ATACTATTTT GCTTAAGAGT TGTATTACAA ATATTGTGTC 1560  
TTAACATTAG AAATAGCTGT TTTAAATTGT AGTTAACATA TTAACCTTTT CAGAAAAAAA 1620  
GCATGGTTTA TTTTAAATAA TGAAATAGAG AACATAATAC GTAATGTTCA GTATAACAGC 1680  
TGAGTTAAAA CATCTGCCAG GATTAAATAC AGTGGCTTTT TGCCAAATGCA TAGAGGCATT 1740  
40 TTTCTCTAAG TATGAGGCTT AATGATAACT ATTCCTTTGT ACACATTCAA GTCACTCCCA 1800  
TACAGTAAC TAGTGGGTGA TATGTTTAC TCCAAAGGGT GTATTAATTC TGAATGCTAA 1860  
TCATGAAGAC TTAAGTTAGG ACAACACTTC AAACAGGAA GTGTGAAGT ATTTA

45 Seq ID NO: B25 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1144

1 11 21 31 41 51  
50 ATGGAGCGCG GGTATGACCT CGGTGCAGCG GCGCGCGGCG AGGACGACCT CTTCTGCAC 60  
AAGAGCCTGA GGCCTCTCAC CTCCAAGCGC TTGGAAGCGG CTTTCCGCTC CACGCCCCCG 120  
GGCATGGACC TGTCCTCTGC GCGCGCGGCT CGGGAACGCC CGGCGTCTCT CTCCTGTCG 180  
CCCCTGGGCT GCTTCGAGCC GGCTGACCCC GAGGGGGCAG GGTCTGCTGT GCGCGCGGCT 240  
GGAGGAGGCG GCGCGCGGCG CGCGGGAAGT GCGCGCGGCG GCGCGCGGCG GGTGGGTGTC 300  
55 CCGGGCTGCG TAGTAGTTTC AGCGCGGCTT GGGGGCGACC CTAGCCTAAG CAGCCTGCGG 360  
GCGGGGCGCG CCTTTTGCTT CAAGTACGGC GAAAGCGCGA GCGGGGCTCT GGTGGCCGAG 420  
AGCAGCGGCG GCGAGCAGAG CCGGACGAC GACAGCGACG GTCGCTGCGA GCTCGTGTCT 480  
CGGGCGGAG TAGCGACCCC GCGGGCTCTC CCGGGAGCGG GAGGTGGTGG GCGGAAGGCA 540  
GCGAGGGCT GCTCCATGCT CCACCTCCAC GCGGGGCGCA GGTCTCCCCC GGGGGGCTCT 600  
60 GCGCGCGGCG GCGCGCGGCG TAGCAGCAGC GGTAGCAGTG GCGGCGGTGG CGGTAGCGGT 660  
AGCGGCGAGG GCGGCGGAGC CAGCAGCAGC AGCAGCAGCA GCAAGAAATC CAAAGAGCAA 720  
AAGGCGCTGC GCTTAAACAT CAATGCCGA GAGCGCGGCG GGTATGACGA CCGGAACGAC 780  
GCGCTGGACG AGCTGCGGCG GGTGATCCCC TACGCGCACA GCGCTCTGCT GCGGAAGCTC 840  
TCCAAGATGC CCACGCTGCT GCTGCGCAAG AACTACATCC TCATGTCAGC GCAGGCCCTG 900  
65 GAGGAGATGC GCGGCTAGT CGCTACCTC AACCAGGGCC AGGCCATCTC GGTGCTCTCC 960  
CTGCCAGCT GCGGGCTGC AGCGGCAGCA GCTGCTGCCC TGCAACCGGC GCTCGGCGCC 1020  
TACGAGCAGC CAGCGGCTGA CCGGTCAGC GCGGAGCTGC CCGCGGCTGC CTCCTGCGCG 1080  
GAGAAGTGCG CCTGTTTAA CAGCGCTCC TCCAGCTCT GCAACAGTG CACGAGAGG 1140  
CCTT

70 Seq ID NO: B26 Protein sequence  
Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
75 MERGMHLGAA AAGEDDLFLH KSLASASTSKR LEAAPRSTPP GMDLSLAPPP RERPASSSSS 60  
PLGCFEPADP EGAGLLLP PP GGGGGGSAGS GGGGGGGVGV PGLLVGSAGV GGDPSLSLPP 120  
AGAALCLIKY ESASRGSVAE SSGGEQSPDD DSDGRCELVL RAGVADPRAS PGAGGGGAKA 180  
AEGCSNAHLH GASVPPGGL GGGGGGGSSS GSSGGGGGSG SSSGGSSSSS SSSSKSKSEQ 240  
80 KALRLNINAR ERRRMHDLND ALDELRAVIP YAHSPSVKRL SKIATLLALK NYILMQAQL 300  
EEMRLVAVL NQQAISAAS LPSSAAAAA AAALHPALGA YQAAGYFFS AGLPPAASCP 360  
EKCALFNSVS SSLCKQCTEK P

Seq ID NO: B27 DNA sequence  
Nucleic Acid Accession #: cat cluster

```

1      11      21      31      41      51
|      |      |      |      |      |
5  TTTT TTTT TTTT TTTT TTTT TTTT 60
   TAGATACACA TACAAATGGT CGTACATAGC TGTATAGTC TGATTGACCT ATTTAATATA 120
   TATATCATTC TTTACACATC CAAAACCCGC CAACAGATCC ATCAGAGCTC CCAACTCACC 180
   ATCCAACCTG ACAAACCTGA TTTGTATTAT CTGCAAGGAG TGGAAAATAG CAGGACTCCA 240
   TTTTAAAAAA AGATTTTCTT GATTTTCATA GGGCGGAAAG GCAGTCAAAC AGCCATGCAA 300
10  AACTAAAACT GAAAGCTCAC TTTGGGTAAA TAGCTTCTTG TTTCTCCTTA GTTTTCTTTC 360
   TTTTAAATTT TTATTTTCTT AGAAAAATAA CAAAGGATTT CACACCATAG GCAAAATCAAA 420
   CCAGTCTTTT AACTTAAATA ATTCTCCACA GTTAAAAATA CATATATGTA CATATATATT 480
   AAAAGCAATT AAATTAGACC TTTTAAAAAT GCACAGCACA GCGTGGAAAA ATATTGCTT 540
   AGCATGTTCT TACGTATAGC AACTATTGCT GTGATGTTTT TCCCTTTTGG AATGTAAAGG 600
   AGTCCCTTTT CAAAAAGAG ATCAATTTCAT TCATCAATTA AGAATACACC TTTCCTGTAA 660
15  TTTTGGAGCT GAAACAATTT ATTAAGCTC AATTAAATA CAGGGATGAT GCAACTGAAA 720
   ATATCCAGGT GACCTTTCAT AAACCTAAGC AGCTCAGATA CATCAATATT TCTCTTCATA 780
   CTGTGGGCA AATAAACCTT TAAACACTTG GCACACAGCA TAAGTAATCT ATAAACAAT 840
   TTTAGAGGCA TTAATAAATAT CTGCACATAA GACCCATGAC TTTAACACAT GATAAATACT 900
   GTTGATGTGG AAGGCTCATT GAAGAATAAC AAATAAATAC CATGAATTGT TAATACATCA 960
20  TTGCAGAGTA GAAAGTAAAC AGGTGCACAT AAATATTTTT AAATGCAATT CTTTCAGCCA 1020
   CAGTCAGTTT TTTTATATCA CTCTCGCCAA AACTTTGAGC ATTTTTCAGG GATTAAAGTT 1080
   CAGAGACAAT AAAAAATACA AGTCTTTCAT AGTAACATGT TCTCTCTCTC TCGCTCTGGG 1140
   TTTTATTCCC CCTCACTTA AGTCAACATT TCAAGTTTTT CTCTGCGCTC AGAATCAAAA 1200
   TTTATTTTCA AGTGCCCTTT CTGATTGTGC TGAATGAATA TTCCATCTCT CATGCTACCG 1260
   ATCCGCT

```

Seq ID NO: B28 DNA sequence  
Nucleic Acid Accession #: NM\_002581.2  
Coding sequence: 368..5251

```

1      11      21      31      41      51
|      |      |      |      |      |
30  GGGGAGGGA ATTACGCGGA TCAGTCTTAA GAGGAGCTTT TTTTGGAGC GAGAAATCAT 60
   ATAAATAAAA ATGAATAAAA ACAAGGAGGA AGGCAACCAAG CTGTTAGGGG GAAAATAAGG 120
   CAGATAAAGG AGCGGGGAGA GAAATTAATT GCCAACCCAGG AGGAGTTGGG CTGTATTTTT 180
   CAAAGGTGGG GAGAGTGGAG CACACACCTT GAGGAGGAAA GCGAGAAAAG AAAGAAAAAA 240
   GCAAGTGAAG GGGGGCTCCG CCAAGAAAGG TGAAGAAAGC AAGAAAGTCG AGGCGCCGAG 300
   GCTCCCAAG CTGGCAGCTC CGGTGGGCGG TGCAGGGGCG AAGGGGGGGG CGGGGGGAAC 360
   GTGGGACATG CGGCTCTGGA GTTGGGTGCT GCACCTGGGG CTGCTGAGCG CCGCGCTGGG 420
   CTGCGGGCTG GCGGAGCGTC CCGCGCGGGC CCGGAGAGAC CCGCGGGCGG GCCGACCCCC 480
   GCGCGCGGCC GCGCGCGCGG CCACCTGCGC CACCGCGGCG CCGCGGGCGG CCGCGCTCGC 540
   CGCGCGCGCC GCGCGCGCGG GCGGTGCGTG GGAAGCGGTG CGGTCTCCCG GCGCGCGGCA 600
   GCAGCGGGAG GCGAGGGGCG CCACCGAGGA GCCGAGCCCG CGAGCGCGG CGCTCTATTT 660
   CAGCGGGCGA GCGAGGAGCG TGCGAGTCTT CCGGGCGGAC CTCGAGCTGC CCGGGAGCGC 720
   GTTCAGCTG CAAGTGTGGC TGCGAGCGGA GGGGGGCCAG AGGTCTCCGG CAGTGATCAC 780
   AGGCTGTAT GACAATGTT CTTATATCTC ACGTGAACGA GGATGGGTGG TGGGCATTCA 840
   CACCATCAGT GACCAAGACA ACAAGAGCCC AGCTACTTTT TTCTCTTGA AGACAGACCG 900
   AGCCCGGCAA GTGACCAACA TCAATGCCCA CGCAGCTTAC CTCCAGGCC AGTGGGTATA 960
   CCTAGCTGCC ACCTATGATG GGCAGTTTAT GAAGCTCTAT GTGAATGGTG CCCAGGTGGC 1020
   CACCTCTGGG GAAACAAGTG GTGGCATATT CAGCCCACTG ACCAGAAGT GCAAAAGTGT 1080
   CATGTTAGG CATCTGAGG TGAATCAAAA CTACCGGGGC TACATCGAGC ACTTCAGTCT 1140
   GTGGAAGGTG GCCAGSACTC AGCGGAGAT ACTGTCTGAC ATGGAACCCC ATGGGCGCCA 1200
   CACTGTCTTA CTCTAGCTCC TCTCTCAGGA GAATCTGGAC AATGTGAAGC ATGCTGTGCT 1260
   CCCCATGAAG GATGGCAGCA GCCCAAGT GGAATTCAGC AATGCCACG GCTTTCTGCT 1320
55  GGACACGAGT CTGAGGCTCT CTCTGTGCGG ACAGACATTG TGTGACACA CAGAGGTGAT 1380
   TGCAGCTAC AATCAGCTCT CAAGTTTCOG CCAGCCCAAG GTGGTGGCTG ACCGCTGGT 1440
   CAACCTCTAT GAAGATGATC ATAAGAACCC GACGGTGAGC CGGAGCAGG TGGACTTCCA 1500
   GCACCATCAG CTGGCTGAGG CCTTCAAGCA ATACAACATC TCTTGGGAGC TGGACGTGCT 1560
   GGAGGTGAGC AACTCTCCC TTGCGCGCGG CCTCATCTTG GCCAATGTG ACATCAGCAA 1620
   GATTGGGGAT GAGAACTGTG ACCCGAGTG CAACCAACAG CTGACGGGCC ACGACGCGCG 1680
   GGATTTGCGC CACTGTGCGC ACCCTGCTTT CGTGAAGAAG CAGCAACAAG GGGTGTGTGA 1740
   CATGAGTGC AACTATGAAC GTTCAACTT TGAATGTGA GAGTGTGTG ACCCTGAAAT 1800
   CACCAATGTC ACTCAGACTT GCTTTGACCC CGACTCTCCA CACAGAGCCT ACTTGATGT 1860
   TAATGAGCTG AAGAACATTC TTAATTTGA TGGATCAACA CATCTCAATA TTTTCTTTC 1920
65  AAAATCTTCA GAGGAGGAGT TGGCAGAGT AGCAACTTGG CCATGGGACA AGGAGGCCCT 1980
   GATGCACTTA GGTGGCAITG TCTTGAACCC ATCTTTCTAT GGCATGCTTG GGCACACCCA 2040
   CACCATGATC CATGAGATTG GTCAAGGCT GGGCTCTTAT CAGTCTTCC GAGGATCTC 2100
   AGAAATCCAG TCTGCAAGT ACCCTGTCAT GGAGACAGAG CCTCTCTTG AGACTGGAGA 2160
   CCTCTGCAAT GATACCAACC CAGCCCCATA ACACAAGTCC TGTGGTGACC CAGGGCCAGG 2220
   AAATGACACC TGTGGCTTTC ATAGCTTCTT CAACACTTCT TACAACAAC TCAATGAGTA 2280
70  TGCAGATGAC GACTGTACGG ACTCTTTCAC GCCCAATCAA GTGCGCAGAA TGCATGTTA 2340
   CCTGGACCTG GTCTACACAG GCTGGCAGCC CTCCAGGAAA CCAGCGCCTG TTGCCCTGCG 2400
   CCCCCAAGTT CTGGGCCACA CAACGAGTCT TGTGACACTG GAGTGGTTCC CACCTATAGA 2460
   TGGCCATTTC TTTGAAGAG AATTGGGATC AGCATGTCTT CTTTGCCTGG AAGGGAGAT 2520
   CCTGTGACG TATGCTTCCA ACGCTTCTCT CCCAATGCCC TGCAGCCCAT CAGGACACT 2580
75  GAGCCCTCGT GAAGCAGAAG GTCATCTGTA TGTGAACAG CCCTGTAAAT CCAGTGTCCG 2640
   CACCTGAGC CCAAAATTCAG CTGTCAACCC ACACAAGGTT CCTCCAGCT GCCCTGAGCC 2700
   TCAAGGCTGC TACCTCGAGC TGGAGTTCTT CTACCCCTTG GTCCCTGAGT CTCTGACCAT 2760
   TTGGGTGACC TTTGTCTCCA CTGACTGGGA CTCTAGTGGG GCTGTCAATG ACATCAAAT 2820
80  GTTGGCTGTC AGTGGGAAGA ACATCTCCCT GGGTCTCTAG AATGCTCTCT GTGATGTCCC 2880
   ACTGACATC AGCTCTGGG ACGTGGGCGA GGAGGTGTAT GGCATCCAAA TCTACACGCT 2940
   GGATGAGCAC CTGAGATCG ATGCTGCCAT GTTGACCTCC ACTGCAGACA CCCCACCTG 3000
   TCTACAGTGT AAGCCCTGA AGTATAAGGT GTTCCGGGAC CCTCTCTCC AGATGGATGT 3060
   GGCCTCCATC CTACATCTCA ATAGGAATTT CTTAGACATG GATCTAAATC TTGGCAGTGT 3120

```

5  
10  
15  
20  
25  
30  
35  
40

```

GTACCAGTAT TGGGTCATAA CTATTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT 3180
CACATACATC CATGGACGTG GGTACTGTGG CGATGGCATT ATACAAAAG ACCAAGGTGA 3240
ACAAATGGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTTCT GCCGACAAGA 3300
AGTCTCCTTC AATTGTATTG ATGAACCCAG CCGGTGCTAT TTCCATGATG GTGATGGGGT 3360
ATGTGAGGAG TTGAAACAAA AAACCCAGCAT TAAGGACTGT GGTGTCTACA CGCCCCAGGG 3420
ATTCTGGAT CAGTGGGCAT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCCAGG 3480
CTGGGTATC ATCGSACAGC CAGCAGCATC CCAGGTGTGT CGAACCAAGG TGATAGATCT 3540
CAGTGAAGGC ATTTCCAGC ATGCTGTGTA CCCTTGACCC ATCAGCTACC CATATTCCCA 3600
GCTGGCTCAG ACCACTTTT GGTCCGGGC GTATTTTCT CAACCAATGG TTGCGCAGC 3660
TGTCATTGTC CACCTGGTGA OGGATGGGAC ATATTATGGG GACCAAAAG AGGAGACCAT 3720
CAGOGTGCAG CTGCTTGATA CCAAGATCA GAGCCAGAT CTAGGCTCC ATGTCTTGAG 3780
CTGCAGAAC AATCCCTGA TTATCCCTGT GGTCCATGAC CTCAGCCAGC CCTTCTACCA 3840
CAGCCAGGCG GTACGTGTGA GCTTCAGTTC GCCCTGGTC GCCATCTCGG GGGTGGCCCT 3900
CCGTTCTTTC GACAACCTTG ACCCGTCAC CCTGAGCAGC TGCCAGAGAG GGGAGACCTA 3960
CAGCCCTGCC GAGCAGAGCT GOGTGCATT CGCATGTGAG AAAACTGACT GTCCAGAGCT 4020
GGCTGTGAG AATGCTTCT TCAATTGCTC CAGCAGGAC CGCTACCAG GTGCCAGTG 4080
TACTGTGAGC TGCCGACAG GCTACGTGCT CCAGATACGG CGGATGATG AGCTGATCAA 4140
GAGCCAGAGC GGACCCAGCG TCACAGTGAC CTGTACAGAG GGCAAGTGA ATAAGCAGGT 4200
GGCTGTGAG CACGTGACT GCAGCATCCC AGATCACCAT CAAGTCTATG CTGCTCCTT 4260
CTCCTGCCCT GAGGCGACCA CCTTTGGCAG TCAATGTTC TTCCAGTGCC GTACCCCTGC 4320
ACAAATGAAA GSCAACAAAC GCCTCTGAC CTGCATGGAG GATGGCTGT GGTCTTCCC 4380
AGAGGCCCTG TGTGAGCTCA TGTGCTCGC TCCACCCCT GTGCCAATG CAGACCTCCA 4440
GACCGCCCGG TGCCGAGAGA ATAGACAAA GGTGGGCTCC TTCTGCAAT ACAARTGCAA 4500
GCTGTGATC CATGCTGCT GATCCTCTG GAAGTCAAG AAAAGGCTC TCAAGACTCA 4560
GTGTACCCAG GATGGCAGCT GGCAGGAGG AGCTGTGTCT CCTGTGACT GTGACCCACC 4620
TCCACCAAAA TTCCATGGGC TCTACAGTG TACTAATGGC TTCCAGTTCA ACAGTGAGTG 4680
TAGGATCAAG TGTGAAGACA GTGATGCTC CCAGGCACTT GGGAGCAATG TCATTCAATG 4740
CCGAAAGAT GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGAGATGC AAGGCCAGTG 4800
CTCGTTTCCA ACAGTACTGA ACAGCAACT CAAACTGCAG TGCCCTGATG GCTATGCCAT 4860
AGGTCGGAG TGTGCCACT CGTGCTGGA CCACAAACAGC GAGTCCATCA TCCTGCCAAT 4920
GAACGTGACC GTGCGTGACA TCCCCACTG GCTGAACCCC ACACGGGTAG AGAGAGTTGT 4980
CTGCACCTGCT GGTCTCAAGT GGTATCTCA CCTGCTCTG ATTCACTGTG TCAAGGCTG 5040
TGAGCCCTTC ATGGAGAGACA ATTATTGTA TGCCATCAAC AACCGAGCCT TTTGCAACTA 5100
TGACGCTGGG GATTGCTGCA CTCCACAGT GAAGACCAAA AAGGTCAACC CATTCCTAT 5160
GTCTGTGAC CTACAGGTG ACTGTGCTT TCGGACCCCG CAGGCCCAAG AACACAGCCG 5220
GAAGACCTC CGGCGATACA GCCATGGCTA AGGAAGGACA AGAAGTTGTC AAGAATTC 5280
CAAGCCAGG ACCCAGATCC CTTTGGTATT GATTTCACAG TCAGTGTCTC AACGGAATGG 5340
CCTCTCCACA CCAGGGATCC TTAGCACCCA ACCGGTCTGC CTTTAATTTT ACCCAGGAAG 5400
GACTCAGATT CGGCGAATG AACCAAGTTT CGCCATGCTG GATGATGAAA TGGATTCCCA 5460
TCCCAAAGTC TGAGATGGAT TGATATACA GTGTGCAGTC CCAGAGCCTC CTAATAATTCT 5520
AGCCATTGT CACACAACCA CAGCAAAAA AAA

```

Seq ID NO: B29 Protein sequence

Protein Accession #: NP\_002572.1

45  
50  
55  
60  
65  
70  
75

```

1 11 21 31 41 51
| | | | |
MRLMSVHL GLLSALGCG LAERPRRRR DPRAGRPPRP AAGPATCATR GPRPPRLAAA 60
AAAAGRAWEA VRVPRRRQR EARGATEEPS PPSRALYFSG RGEQLRVLRA DLRLPRDAFT 120
LQVWLRAEGG QRSAPVITGL YDKCSYISRD RGWVVGIIHI SDQDNKDPRY FPSLKTDRAR 180
QVTTINAHRS YLPGQWVYLA ATYDQGFMLL YVNGAQVATS GEQVGGIFSP LTQKCKVLM 240
GGGALNNHYR GYIEHPSLWK VARTQREILS DMETHGAHTA LPQLLLQENW DNVKHAWSM 300
KDGSSPKVEP SNAHGFLDIT SLEPLLCGQT LCDNTEVIAS YNQLSSFRQP KVVRYRVVNL 360
YEDDHKNPTV TREQVDFQHH QLAERAFKQYN ISWELDVLEV SNSSLRRRLI LANCIDISKIG 420
DENCDPECNH TLTGDDGDC RHLRHPAFVK QHNGVCDMD CNYERFNFPG GECCDPEITN 480
VQTCTFDPDS PHRAYLDVNE LKNILKLDGS THLNIFFAKS SEELAGVAT WPDKEALMH 540
LGGIVLNPSE YGMPGHHTM IHEIGHSLGL YHVRGISEI QSCSDPCMET EPSFETGDL 600
NDTNPAKHK SCGDPGPGND TCGFHSFPNT PYNNFMSYAD DDCTDSFTPN QVARMHCYLD 660
LVYQWQPSR KPAFVALAPQ VLGHITDSVT LEWPPPIDGH FFERELGSAC HLCLEGRILV 720
QYASNASSEM PCSPSGHWSP REAEGHPDVE QPCKSSVTRW SPNSAVNPHT VPPACPEPQ 780
CYLELEFLYP LVPESLTIHV TFVSTDWDS GAVNDIKLLA VSGKNI SLGP QNVPCDVPLT 840
IRLWDVGEV YGIQIITLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVR DPPLQMDVAS 900
ILHLNRKFVD MDNLGSGVYQ YWVITISGTE ESEPSPAVTY IHGRGYCGDG IIQKDQGEQC 960
DDMNKINGDG CSLFCRQEV FNCIDEPSRC YFHDGCVCE EFEQKTSIKD CGVYTPQGFL 1020
DQWNASVSV HQDQCPGVV IIGQPAASQV CRTKVIDLSE GISQHWYPC TISYYPQSLA 1080
QTTFWLRAYF SQPMVAAYV VHLVTDGTY GDQKQETISV QLLDTKDQSH DLGLHVLSCR 1140
NNPLIIPVH DLSQPPYHSQ AVRVSFSSPL VAISGVALRS FNFDPVTL SQRGETYSP 1200
AEQSCVHFAC EKTDCPELAV ENASLNCSS DRYHGAQCTV SCRTGYVLQI RRDELKISQ 1260
TGPSVTVTCT EGKWNKQVAC EPVDCSIPDH HQVYAAAFSC PEGTTFGSQC SPQCRHPAQL 1320
KGNNSLLTMC EDGLWSFPEA LCELMCLAPP PVPNADLQTA RCRENKHKVG SPCKYKCKPG 1380
YHVPSSRSR KRAPKTQCT QDGSWQEGAC VPVTCPPPP KFHGLYQCTN GPQFNSECR 1440
KCEDSDASQ LGSNVHCRC DGTWNGSFHV CQENQGCQSV PHELNSNLKL QCPDGYAIGS 1500
ECATSCLDHN SESIILPMNV TVRDIPHWN PTRVERVCT AGLKWPHPA LIHCVKCEP 1560
PMGDNYCDAI NNRAFCNYDG GDCCTSTVKT KKVTPPPMSC DLQGDCACRD PQAQEHRSKD 1620
LRGYSHG

```

Seq ID NO: B30 DNA sequence

Nucleic Acid Accession #: NM\_032808.1

Coding sequence: 61..1008

80

```

1 11 21 31 41 51
| | | | |
CTAGTCTATC TCCGCTTCTT CAACCTCTCC TACAACCCCA TCAGCACCAT TGAGGGCTCC 60
ATGTTGCATG AGCTGCTCCG GCTGCAGGAG ATCCAGCTGG TGGGCGGGCA GCTGGCCGTG 120

```

5 GTGGAGCCCT ATGCTTCCG CGGCCTCAAC TACCTGCGCG TGCTCAATGT CTCTGGCAAC 180  
CAGCTGACCA CACTGGAGGA ATTAGTCTTC CACTCGGTGG GCAACCTGGA GACACTCATC 240  
CTGGACTCCA ACCCGCTGGC CTGCGACTGT CGGCTCCTGT GGGTGTTCG GCGCGCTGG 300  
CGGCTCAACT TCAACCGGCA GCAGCCACG TGCGCCACGC CCGAGTTTGT CCAGGGCAAG 360  
GAGTTCAAGG ACTTCCCTGA TGTGCTACTG CCCAACTACT TCACCTGCGG CCGCGCCCGC 420  
ATCCGGGACC GCAAGGCCCA GCAGGTGTTT GTGGACGAGG GCCACACGGT GCAGTTTGTG 480  
TGCCGGGCGG ATGGCGACCC GCGGCCCGCC ATCCTCTGGC TCTCACCCCG AAAGCACCTG 540  
GTCTCAGCCA AGAGCAATGG GCGGCTCACA GTCTTCCCTG ATGGCACGCT GGAGGTGCGC 600  
TACGCCCAGG TACAGGACAA CGGCACGTAC CTGTGCATCG CGGCCAACGC GGGCGGCAAC 660  
10 GACTCCATGC CCGCCACCT GCATGTGCGC AGTACTCGC CCGACTGGCC CCATCAGCCC 720  
AACAGACCT TCGCTTTTCT CTCCAACCAG CCGGGGAGG GAGAGGCCAA CAGCACCCGC 780  
GCCACTGTGC CTTTCCCTT CGACATCAAG ACCCTCATCA TCGCCACCAC CATGGGCTTC 840  
ATCTCTTCC TGGGCGTGT CTCTTCTGCG CTGGTGTGCG TGTTCCTCTG GAGCCGGGGC 900  
AAGGGCAACA CAAAGCAACA CATCGAGATC GAGTATGTGC CCGAAAGTGC GGACGCGAGC 960  
15 ATCAGCTCCG CCGAGCGGCC CCGCAAGTTC AACATGAAGA TGATATGAGG CCGGGGCGGG 1020  
GGGCGAGGAC CCGCGGGCGG CCGGGCAGGG GAAGGGGCGT GCGCGCCACC TGCTCACTCT 1080  
CCAGTCTTTC CCACCTCTTC CCTACCCTTC TACACAGGTT CTCTTCTCC CTCCCGCTTC 1140  
CGTCCCTTGC TGCCCGCCGC CAGCCCTCAC CAGCTGCCCT CCTTCTACCA GGACCTCAGA 1200  
20 AGCCGAGACT TGGGAGACCC ACCTACACAG GGCATTGAC AGACTGGAGT TGAAAGCCGA 1260  
CGAACCGACA CCGCGCAGAG TCAATAATTC AATAAAAAAG TTACGAACTT TCTCTGTAA 1320  
TTGGGTTTCA ATAATTATGG ATTTTATGA AAATTGAAA TAATAAAAAG AGAAAAAAC 1380  
TATTTCTTAT AGCTAGTCGG AATGCAAACT TTTGAGCTCC TGATTGCTCC AGGGCCCTCT 1440  
TCCAATCAG TTTCTGTGTT TTCTTCTCT CCTCTCTCT TTTCTCTCT TTTCTCTCT 1500  
25 CTTCCCAAGT GGGGAGGGAT CACTCAGGAA AACAGGAAAG GAGGTTCCAG CCCACCCAC 1560  
CTGCCACCC CCGCCGAGG ACCATCAGGA GCAGGCTAGG GGGCAGGCT GGGCCAGCT 1620  
CCGGGCTGGC TTTTGTGAGG GCGCAGGTGG AGGGGACAGG TCTGCCGATG GGGGTGGGG 1680  
CCTGTCTGCT GGGCTGCCAG GCGGCACCC TGAAGGGGT GGGAGCTGG CTTGGGTGTG 1740  
GCTGAGACTC TGGACAGAGG CTGGGGTCTT CCTGGGGGAC AGCAGCTCA GTGGAGAGAG 1800  
30 CCAGGGGCTG GAGGTGGGGC CCACCCAGC CTCTGGTCCC AGCTCTGCTG CTCACTTGCT 1860  
GTGTGGCTTC AAGCAGGTCA CTGGCCTCTC TGGGCTCAG TCTCCATC TGATCAAATG 1920  
GGAACATTAC CCCTGCCCT GCCTACCTCA CAGGCTGTT GTGAGGAATT GATGAGATGA 1980  
TGATGTGAA ACACCTTTGA ACCTGTAAAG CGCTGTGCAC AGTG

35 Seq ID NO: B31 Protein sequence  
Protein Accession #: NP\_116197.1

40 1 11 21 31 41 51  
MLHELLRLQE IQLVGGQLAV VEPYAFRGLN YLRVLNVSGN QLTITLEELVP HSVGNNLETLI 60  
LDSNPLACDC RLLNVFRRRW RLNFNRQOPT CATPEFVQK EFKDFPDVLL PNYFTCRRAR 120  
IRDRKAQVFE VDEGHTVQFV CRADGPPPA ILWLSPRKEL VSAKSNRLT VFPDGLTEVR 180  
YAQVQDNGTY LCIAANAGGN DSMPAHLHVR SYSPDWPHQP NKTFAFISNQ PGEGEANSTR 240  
ATVPFPFDIK TLIIATIMGF ISFLGVVLFPC LVLLFLWSRG KGMTKHNIEI EYVPRKSDAG 300  
ISSADAPRKF NKKMI

45 Seq ID NO: B32 DNA sequence  
Nucleic Acid Accession #: CAT cluster

50 1 11 21 31 41 51  
CAGCACATAC AAGAAACATA CAGTGTAACCT CAAAAGGGGC CCTTGAAATG TCATCAAAGG 60  
GTAATAACCT AGTGAGTGAG TTGTGATGTC ATCTGGAACA TAGGAAATGG GGCTCTTAGC 120  
GTATTCTGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAAATGATA ATCTTTGGGA 180  
55 AACCCAGACC CTGCTCTCCA GCCCAGAGGT GGAGGAGGGC GGTCAAGGCT GGGTCTACAG 240  
TGGCACAGCA CTGACAAAGG TAGAGGGGAAA TGTAATAGCA CATCTACGCT GCAGTCTGGT 300  
GAAAGTGCCG GGGGTGGTCC TTGGAAGAAC GTTGGGCTGT TCTTGGCAGG AATAGTAGAC 360  
AGCCTTTCCG TCACGGGCAG GGACGCTTG ATTTAAAAA AATAAATAA TAAAAAGTCT 420  
GGGTATAGAA A

60 Seq ID NO: B33 DNA sequence  
Nucleic Acid Accession #: NM\_006174.1  
Coding sequence: 71..1408

65 1 11 21 31 41 51  
GAAAGGCTAT CGGTAACAAC TGACCTGCCA CAAAGTTAGA AGAAAGGATT GATTCAAGAA 60  
AGACTATAAT ATGGATTAG AGCTCGACGA GTATTATAAC AAGACACTTG CCACAGAGAA 120  
TAATACTGCT GCCACTCGGA ATTCTGATT CCCAGTCTGG GATGACTATA AAAGCAGTGT 180  
70 AGATGACTTA CAGTATTTC TGATTGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT 240  
GGGGAACTCA CTTATTTTAA TGGCTCTCAT GAAAAGCGT AATCAGAAGA CTACGGTAAA 300  
CTTCTCATA GGCATCTGG CCTTTCTGA TATCTGGTT GTGCTGTTT GCTCACCTTT 360  
CACACTGAGC TCTGTCTTGC TGGATCAGTG GATGTTGGC AAAGTCAATG GGCATATTAT 420  
GCCTTTTCTT CAATGTGTGT CAGTTTGGT TTCACTTTA ATTTTAAAT CAATTGCCAT 480  
75 TGTCAAGTAT CATATGATA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540  
CTTCTGATA GCTACTGTCT GGACACTAGG TTTTGCCATC TGTTCCTCCC TTCAGTGTT 600  
TCACAGTCTT GTGGAACCTC AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATT 660  
ATGTGTTGAG TCATGGCCAT CTGATTCATA CAGAAATGCC TTTACTATCT CTTTATTGCT 720  
AGTTCAGTAT ATCTGCCCC TAGTTTGTCT TACTGTAAGT CATACAAGTG TCTGCAGAG 780  
80 TATAAGCTGT GGATTGTCCA ACAGAGAAAA CAGACTTGAA GAAAATGAGA TGATCAACTT 840  
AACTCTTCTT CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900  
GAGTATTACA TTCAACAAAA AACACAGAG AAGATATAGC AAGAAGACAG CATGTGTGTT 960  
ACCTGCTCCA GAAAGACCTT CTCAGAGAAA CCACTCCAGA ATACTTCCAG AAAACTTGG 1020  
CTCTGAAGA AGTCAGCTCT CTTCAATCCG TAAGTTCATA CCAGGGGTCC CCACTTGCTT 1080  
TGAGATAAAA CCTGAAGAAA ATTCAATGAT TCAATGAATT AGAGTAAAC GTTCTGTATC 1140



AAGAATAAAA AAGAGATCTC GAAGTGTITT CTACAGACTG ACCATACTGA TATTAGTATT 1200  
 TCGTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAACTCT 1260  
 TATTTCAAAT AGGCATTCTA AGTTGGTGTA TTGCATTGTG CATTGTGTGG GCATGATGTC 1320  
 CTGTGTCTT AATCCAAATC TATATGGGTT TCTTAATAAT GGGATTAAAG CTGATTTAGT 1380  
 GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence  
 Protein Accession #: NP\_006165.1

1 11 21 31 41 51  
 MDLELEDEYYN KTLATENNTA ATRNSDFPVW DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60  
 LILMALMKKR NQKTTVNFLI GNLAFFSDILV VLFCSPPFTLT SVLLDQNMFG KVMCHIMPFL 120  
 QCVSVLVSTL ILISIAIVRY HMIKHPISNN LTANHGYFLI ATVMTLGFAL CSPLPVFHSN 180  
 VELQETFGSA LLSSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240  
 GLSNKENRLE ENEMINLTLL PSKSGSPQVK LSGSHKWSYS FIKGHRRYS KKTACVLPAP 300  
 ERPSQENHSR ILPENFGSVR SQLSSSSKFI PGVPTCFEIK PEENSVDHEL RVKRSVTRIK 360  
 KRRSVFPYRL TILILVFAVS WMPLHLFHV TDFNDNLISN RHFKLVYVIC HLLGMMSCCL 420  
 NPILYGLNN GKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence  
 Nucleic Acid Accession #: NM\_014279.1  
 Coding sequence: 286..1689

1 11 21 31 41 51  
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCGCG CCAGCCCAGC 60  
 CCTGCCAGCG CCTGCCCGGA GCGAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120  
 CGGAGGCTTC GCGGACGAGA GCGCGGCGCG CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180  
 GGGACACGAG CCAGGCGCGG CCGCGGAGCG CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240  
 TCGCGCTCCA CGCAGCGCGG GCGCGGCGCG CACCCAGGGC CCGCATGCCC AGGTCGTGG 300  
 AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTCT 360  
 ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420  
 AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTGGCCCC ACAGCAGACC 480  
 ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCGAG TACTGGAGAA GTGCAGAAC 540  
 ATGTCTCAAT CCATAGAGGT CTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600  
 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660  
 AAGCAACACC TGGCCAGGCA GTTTAAGCGG ATAAAGCGA AAATGGATGA ACTTAGGCCT 720  
 TTGATACCTG TGTGGAAGA GTACAAGGCC GATGCCAAAT TGGTATTGCA GTTTAAAGAG 780  
 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATTTG CGCCTATGAC 840  
 TACGATGAAC TTCAGAGCAG AGTGTTCAAT CTGAAGAAA GGCTCCGTGC ATGCATGCAA 900  
 AAACTAGCTT GCGGGAAGTT GACGGGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC 960  
 TCGAGGTTTG GATCCTGGAT GACAGACCTT CTGCGCCCTG AAGGCGATAA CCGGTGTGG 1020  
 TACATGGAGC GCTATACAAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGACTTTC 1080  
 ATGAACACGG ACAATTTTCA CTCCCAACCG CTCCCAACCG CCTGTGCGGG CACGGGGCAG 1140  
 GTGGTCTACA ACGGTTCTAT CTACTTCAAC AAGTTCCAGA GCCACATCAT CATCAGGTTT 1200  
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCTGG ACTATGCCGG TTACAACAAC 1260  
 ATGTACCACT ACGCTCGGGG TGGCCACTCG GACATCGACC TCATGGTGGG CGAGAGCGGG 1320  
 CTGTGGGCGG TGTAGGCCAC CAACAGAAAC GCTGGCAACA TCGTGTGTCAG TAGGCTGGAC 1380  
 CCGGTGTCCC TGACAGCCCT GCAGACCTGG AACACGAGCT ACCCAAGCG CAGCGCGGGG 1440  
 GAGGCCCTCA TCGTGTGTCAG CACGCTGTAC GTACCAACCG GCTACTCAGG GGGTACCAAG 1500  
 GTCCACTATG CATACAGAC CAATGCCTCC ACCTATGAAT ACATGCACAT CCCATTCCAG 1560  
 AACAAATATC CCCACATCTC CATGTGAGAC TACAACCCCA AGGACCGGGC CCTGTATGCC 1620  
 TGGAAACAAG GCCACACAGT CCTCTACAAC GTGACCTCTT TCCACGTCTT CCGCTCCGAC 1680  
 GAGTTGTAGC TCCTCTCTCC TGGAGGCCAA GGGCCCAAGT CCTCACCACA AAGGGACTCC 1740  
 TGTGAAACTG CTGCCAAAAG GATACCAATA AACTAAACAA TACCGATCTT GAAAAATCAT 1800  
 CAGCAGTGCG GATTCTGACA TCGAGGGATG GCATTACCTC CGTGTCTTC CTTTCTGAGC 1860  
 CGCGGGGGCA CAGAGTTCGG AAGAAATCC CGTATTTGCA GCTGGAAGTC CAGCCCAAGG 1920  
 CGCCCGGCTT TTCTCCCGCG CCTGTCCCTT CTCTGTGCAA ACAACATACT AAGAGGGCGA 1980  
 GGCATGACT GTTGCCAGT TCTCACCGGG GAAAAACCCA CTGTAGGAT GGCATGAACA 2040  
 TTTCTTAGA TCGTGTGTCAG CTCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100  
 CTRGCACCCG GCGTAGGCT AGTGTAACTC GCATCCCAT CAGTGTCCGT TCTTGTACTG 2160  
 TGTGTCTGTC TCTTAGATTA ACGTGTCTGA GGTCCACAT AGCTCCTGGA CCTGTGTCTA 2220  
 GTACATACTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACATTGTTT 2280  
 AACTCGCTGA CCCCGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCTT TGAGGTGGTA 2340  
 ACTTCGTATG TTCAGTTTAT GCGATGATTG TTGTAATATG AATGCCGTAG TTTGGATTAA 2400  
 TAAGTGGATG GTTTTTGTTT CTAAGAAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460  
 CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTTCTTGT TAAATTAGCT 2520  
 AAATCATGTA ACCGACGATA GGAAGGGCTC ACCTGGGGAA ACTCTGGTTT CCGATGGGAC 2580  
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAGTAA AAAACAAAGG 2640  
 CAACTTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAGG 2700  
 AAAAAAAGG AAAAAAAGG AAAAAAAGG AAAAAAAGG A

Seq ID NO: B36 Protein sequence  
 Protein Accession #: NP\_055094.1

1 11 21 31 41 51  
 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPPE SQVYSSAQD SEGRICITVV 60  
 APQQTMCSDR ARTKQLRLQLL EKVQNMSSSI EVLDRRTQRD LQYVEKMENQ MKGLESKFKQ 120  
 VESBKHQHLA RQFKAIKAKM DELRPLIPVL EYKADAKLV LQFKEEVQNL TSVLNEHQEE 180  
 IGAYDYDELO SRVSNLEERL RACMQKLACG KLTGISDPVT VKTSGSRFSG WMTDPLAPEG 240  
 DNRVWYMDGY HNNRFVREYK SMVDFMNTDN FTSRLPLPHW SGTGQVVYNG SIYFNKQFSH 300  
 IIRFPLKTE TILKTRSLDY AGYNNMYHYA NGGHSIDILM VDESGLVAVY ATNQNAGNIV 360

VSRLDPVSLQ TLQWNTSYSP KRSAGEAFII CGTLYVTNGY SGGTKVHYAY QTNASTYEYI 420  
DIPFQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLFH VIRSDEL

Seq ID NO: B37 DNA sequence  
Nucleic Acid Accession #: NM\_006334.1  
Coding sequence: 286..693

```

1      11      21      31      41      51
|      |      |      |      |      |
10  GCGCGGGGA GCCATTAGGA GCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
    CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
    CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTAA TCCAGGCGTG 180
    GGGACACGAG CCAGGCGCGC CCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
    TCCGCTCCA CCGACCGGCC GCGCGGCCAG CACCCAGGCC CCTGCATGCC AGGTCGTTGG 300
15  AGGTGGCAGC GAGACATGCA CCGCGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
    ATGGGCACTG AACTCACTCA AGTGTCTCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
    AGCTCTGCCC AGGACAGCGA GGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480
    ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
    ATGTCTCAAT CCATAGAGGT CTTGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
20  AAGATGGAGA ACCAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
    AAGCAACACC TGGCCAGGCA GTTAAAGGCG TAACCTAAAA GAGTTTTTTC AATGCTGCAG 720
    TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTGTCA 780
    CCATGCATT TTAATATTAT TTTCCAATAC TTAGCACCAT TTCCTAAGG AACCTTGAAT 840
    ACAACACAGA TCCTCCTTTG CATCGCACTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900
25  TGTCAATGCA TTTTGTGAAA AAGAAAGAAA AAAAAAACTT CGTGTATGTG ACTCAAAGCA 960
    TGTAACTTA AGATGTTGCA TTCTAAACTG ACAATAAAGA CCTTTCCTCC

```

Seq ID NO: B38 Protein sequence  
Protein Accession #: NP\_006325.1

```

1      11      21      31      41      51
|      |      |      |      |      |
30  MPGRWRWORD MHPARKLLSL LFLILMGTEL TQVLPNPEE SQVYSSAQD SEGRICITVV 60
    APQQTMCSDR ARTKQLRQLL EKVNMSQSI EVLDRRTQRD LQYVEKMENQ MKGLESKFQK 120
35  VEESHQHLA RQPKG

```

Seq ID NO: B39 DNA sequence  
Nucleic Acid Accession #: NM\_058199.1  
Coding sequence: 286..795

```

1      11      21      31      41      51
|      |      |      |      |      |
40  GCGCGGGGA GCCATTAGGA GCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
    CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
    CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTAA TCCAGGCGTG 180
    GGGACACGAG CCAGGCGCGC CCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
    TCCGCTCCA CCGACCGGCC GCGCGGCCAG CACCCAGGCC CCTGCATGCC AGGTCGTTGG 300
    AGGTGGCAGC GAGACATGCA CCGCGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
    ATGGGCACTG AACTCACTCA AAATAAAAGA GAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
    GAGAGCGAGA GGAAGACCAC AGGAGAGAAG AACTGAAAG AGCTTCCCTT GTTTTGCTG 480
    GAAGCCACAG CTGGCTCCTT GGCTCTGCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
    GTGGGGTTAT GTGCTCCCGC TTACCTCAG AGCCCTTCTC CTGGTGTGTC CCAGACGATC 600
    AGCCAGTCCC TCTTGGAGAG GTTCTGCATG GCCTCTAGGA GAGAAGTTT CTGGCCCCA 660
    GGAAGGCTCT GTGGAGGCTG GTGGTTGTGC ACTGTTGCTG GACAGATGCA TTCATTGATG 720
    TGACACACAC CACACACACA TGACACACA GGGAGCAGA TACTGCAGA GAAGAGCCAA 780
    CAGGTCTCTG ATTATGGCA AGCTGCCCA CAAAGGCTA TGCTGTGTC TTATTGAGAC 840
    ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTGGAC ATGGCCGAC CCAAGGCCCC 900
    TCAAGCCTT AATGGCACCC TGAAGCCTCC ATGCCCAGGC CAAAGATGTC TTTTCTCC 960
    TAAAAAATA AAAAAAATA

```

Seq ID NO: B40 Protein sequence  
Protein Accession #: NP\_478106.1

```

1      11      21      31      41      51
|      |      |      |      |      |
65  MPGRWRWORD MHPARKLLSL LFLILMGTEL TQNKRENAE RMGGPESERK TTGEKTLNEL 60
    PLFCLAHAG SLALPRMCSF NPNFAVGLCR PAYQSPSPG AAQTISQSL ERFMASRRE 120
    VFLAPGRPGG GNLCTVAGQ MHPMCTHTH TBAHTGEQIP AEKSQPGPD

```

Seq ID NO: B41 DNA sequence  
Nucleic Acid Accession #: AY038071.1  
Coding sequence: 1..1686

```

1      11      21      31      41      51
|      |      |      |      |      |
75  ATGACGAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60
    CCAACTTTGC TCTCTCTTA CTGCATCGAC AGCATCCTGG GCGGAGGAG CCGTGCAAA 120
    ATGCGGTTGC TGGGAGCGCG GCAGAGCTTG CTGTCTCCGC TGACCAAGCG CGCCGACCCG 180
    GAAAAGGCGG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTCGAGGC CGAGCTGCAC 240
    CTGCGGCCCA AGCTGCGCGC CTGTATCGGC CCGGCGGGGG GCGCCTCCT TCAGGCTGG 300
    GCAGCGCGCG CCGCGCGCGC GCGGCGCGCG GCGGCAAGCG CGCCACAGGC CACGCGGGT 360
    CCACGCGGGG AGGCCCTTCC GCGGCCACCG CCAACCGCGC GGGCCGGGGA ACGGCGGAC 420
    GCGCGAGGGG CCGCGCGCGC AGCCGCGGCC GCGGCGCGCG CGGCTGGGA CAGCTCAAG 480
    ATCAGCCAGG CGCCGAGGT GAGCATCAGC CGCAGCAAGT CGTACCGGGA GAACGGGGCG 540

```

5  
 10  
 15  
 20

```

CCCTTCGTGC CGCCGCGCCG CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCACGCAC 600
CCGGAGGAGC GCCTCGGCGT GGCCGCGCGC CCGGGCAGCG CCCCGGCTGC GGGTGGTGGC 660
ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA 720
GAGGAACTGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGACGCCCG CGCGCTGCTC 780
AAGGAGCCCC GCGCTGTGCT TGTGGCCGCG ACTGGCGCCG TGGCCGCGAG AGCTGCGGCT 840
GCAGTGGCCA CAGAGGGGCG GGAGCTGTCA CCAAGGAGG AGCTGCTGCT GCACCGGAA 900
GACGCTGAGG GCAAGGACCG CGAGGACAGC GTGTGCCTCT CTGCGGCGAG CGACTCGGAG 960
GAGGGGCTGC TGAACGCAAC ACAGAGGCGC TACCGCACC CGTTCACCAG CTACCAGCTG 1020
GAGGAACTGG AGCGGGCCTT CCAAGAGAGC CACTACCCCG ACGTCTTCAC CAGGGAGGAA 1080
CTGGCCATGA GGTGGACTT GACCGAGGCC CGAGTCCAGG TCTGTTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGACAGC GCGCAGACCC ACCCCCTGG GCTGCCCTTC 1200
CGGGGCGCGC TCTCCGCCAC CCACCCGCTC AGCCCTACC TGGACGCCAG CCCCTTCCTT 1260
CGCACCAACC CGCGCTCGA CTCGCTTGG ACTGCCGCTG CCGCCGCGCG CGCCGCGCGC 1320
TTCCCGAGCC TACCTCCGCC TCOCGGCTCG GCCAGCCTGC CGCCAGCGG GCGCGCGCTG 1380
GGCTGAGCA CTTCCTCGG AGCGGCAGT TTCCGACACC CAGCTTTCAT CAGCCCGGCA 1440
TTCCGAGGC TCTTTTCCAC AATGGCCCC CTGACCGAG CGTCGACCGG GCGCGCGCTC 1500
CTGAGACAGC CCACCCCGC CGTGGAGGCG GCAGTGGCAT CCGGCGCCCT GCGCGACCCG 1560
GCCACGCGCG CCGCAGACAG ACGCGCTCT AGCATAGCCG CGCTGAGGCT CAAGGCCAAG 1620
GAGCAGCGCG CGCAGCTCAC GCAGCTCAAC ATCTGCGCG GCACGACGAC GGGCAAGGAG 1680
GTGTGC
  
```

Seq ID NO: B42 Protein sequence  
Protein Accession #: AAK93901.1

25  
 30  
 35

```

1 11 21 31 41 51
MSNQYQEEGC SERPECKSKS FTLLSSYCID SILGRRSPCK MRLLGAAQSL PAPLTSRADP 60
EKAVQGSFSPK SSAPFEAEHL LPPKLRLRYG PGGGRLLQGA AAAAAAAAAA AAAAATATAG 120
PRGEAPPPPP PTARPERPDP GAGAAAAAAA AAAAANDTLK ISQAPQVSIS RSKSYRENGA 180
PFVPPPPALD ELGGPGGVTH PEERLGVAGG PGSAPAAAGG TGTEDEDEEL LEDEDEDEEE 240
EELLEDEDEE LLEDDARALL KEPRRCPVAA TGAVAAAAAA AVATERGELS PKEELLHPE 300
DAEGKDGEDS VCLSGSDSE EGLLKRKQRR YRTFTSYQL BELEAFQKT HYPDVFTRFE 360
LAMRLDLTEA RVQVWFQNRK AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASFPF 420
PHHPALDSAW TAAAAAATAA FPLPPPPPGS ASLPPSGAPL GLSTFLGAUV FRHPAFISPA 480
FGRLESTMAP LTSASTAAAL LRQPTFAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAAQLTQLN ILPGTSTGKE VC
  
```

Seq ID NO: B43 DNA sequence  
Nucleic Acid Accession #: CAT cluster

40  
 45  
 50  
 55

```

1 11 21 31 41 51
CGCTGCCCC CCGTTGCTT CTCTCTCTTC CTTCTGCGCT GCGTGTCTCG CCGTCTTTGG 60
TTCCGCGCGT TCGGTGCGCC CTCTCTGGGC TTCGGCTTCA CCTCCGCTG GGTGTGTGCT 120
CTGCTCTCCT CCGCTCTCAT GCCCTTTCA GCTCCTACTC TGGTGTGCTC CCCCTCCCTC 180
GCTCGTTTCT CTGTTCCTTC TCCTCCCGG TTGTTGTTCT GCTTCTTCTG GTTCCCTCTC 240
GTCTGTGTTT TGGGTGCTG CTCTGCGTCC TGCCCTTTTC TCTTGGCTTT CCGCGCGCTT 300
CCTGTTTGGG TCCCTCTGCT TCTGCGCGGG TTCTGTGTGC GCGGCGCGCC CCGTCTTTTC 360
TTGGTGTCTT GCTCTGCTG TCTGTCTGGT GTTCTCGGCC GTCTGTGCTC TTCTCCTTTT 420
ATCTCTGTTT TTCTCTTTT CTGTCTCTT CTGTTTATT TTGTCTTTG TTTTCTCTTA 480
GCTGAGGTGG GGGAGAGATA ACGCTGTAAA CTTTATTATT TCAGGAAATC TGAAGAACTA 540
CAGTCTCCAT GCGTCTCTAG CCAAGAAGGA GCTCACTGTG GGCACCAGAG ACAGGAGACC 600
AATGTGGAGA CCTGTGAGCC TGTGTCCGGC CCTGAATCTT CAAGCAGAG GCAGGCTTCC 660
TGAGCATTTA AGAGAAATAT TGGGAGAAAC AAACAGAAAC TGAAAGAAAT TGCAAGGTGT 720
CTTCTTTGGA TGTATTTCCT TAGATAGTAG TAGGGGAGG AGTGAGAGAG GCTGACTAGG 780
TCTGACATAT GAGCTCGGAA GAGTCAGGCT GTGATTCCGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGCTGGAAAT CTGAGGCTCA GTGTCCAG TCACTCAGAG ACAGAAATCAC 900
AGCATAGCCC TTGCTGATGG CAA
  
```

Seq ID NO: B44 DNA sequence  
Nucleic Acid Accession #: NM\_014421.1  
Coding sequence: 718..1497

65  
 70  
 75  
 80

```

1 11 21 31 41 51
CCACGCGTCC GCGGGGAGCC CGCGGCGAGC GTAGCGCAAG TCCGCTCCCT AGGCATCGCT 60
GGCTGCGCAG CGATTGCTG TCTCTGTGTA GTCAGGGGAC AACGCTTCGG GGCACACTGTG 120
AGTGGCGGTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCGTC CGGGGACGTC 180
TCTGATCCC CTACTAAAGC GCCTGCTAAC TTTGAAAAGG AGCACTGTGT CCTGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAGGGA 300
GCTGATGCGG GCCTCTCTAT CAATTAAGAG GAGAGTTAAA CCGCCGAGAT CCGCGCGGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGOGA TCCACAGGCG TGGGTTTCT 420
TGCACTTGG GTACAGCTTC CTGCGGAGA AAGCGCTCG CATTTGATTG CTTCCAGTTA 480
TTGAGAACT TCCTGTCTGT GTGGAGAAGC GGGTCTCGCT TGGTTCGCG TAATTTCTGT 540
CCTGAGCGCT GAGACTGAGT TCATAGGGTC CTGGTCCCG GAACACAGGA GGGTGTAGGG 600
AACACATCT CCAAGCCCC GCGACCCAAG TGAGGGGCGC CGTGTGGGG TCCTCCCTCC 660
CTTGTGATTC CCACCCCTCC GGGCTTTGCG TCTTCTTGG GACCCCTCG CCGGAGATG 720
GCGCGTTGA TGGGAGCAA GGATTCGTCC TGCTGCTGCG TCCTACTGGC CGCGGTGCTG 780
ATGGTGGAGA GCTCAGAGAT CGGCAGTTCG CGGGCCAAAC TCAACTCCAT CAAGTCTCT 840
CTGGGCGGGG AGACGCTCG TCAGGCGGCC AATCGATCTG CCGGCATGTA CCAAGGACTG 900
GCATTGCGG CCAAGGCCCC GGGCAAAAAC CTGGGCGAGG CTAACCTCTG TAGCAGTGAT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCAACC AAGGATCATC GGCCTGCATG 1020
GTGTGTCGGA GAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCC CAGTACCGCG 1080
TGCAATAATG GCATCTGTAT CCCAGTACT GAAAGCATCT TAACCCCTCA CATCCCGGCT 1140
  
```

CTGGATGGTA CTCGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200  
 TGGCAGAATC TAGGAAGACC ACACACTAAG ATGTACATA TAAAGGGCA TGAAGGAGAC 1260  
 CCCTGCTAC GATCATCAGA CTGCATTGAA GGGTTTGTCT GTGCTCGTCA TTTCTGGACC 1320  
 AAAATCTGCA AACCAGTGCT CCATCAGGGG GAAGTCTGTA CCAACAACG CAAGAAGGGT 1380  
 TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAGTA 1440  
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTTCAGAA AATTGTATCA 1500  
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560  
 GGTGAAAAAT AAGGTTTCAA TGCAGAAGAA TGGCTAAAA TGAAGAACTG ATAAGAATAT 1620  
 AGATGATCAC AAAAGGGAG AAAGAAAACA TGAAGTGAAT AGATTAGAAT GGGTGACAAA 1680  
 TGCAGTCGAG CCAGTGTTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTTGT 1740  
 GGAAATGTCT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTACTGATGA GTAGCATGTG 1800  
 ACTTTCCAAG AGTTTAGGTT GTGCTGGAGG AGAGGTTTCC TTCAGATTGC TGATTGCTTA 1860  
 TACAAATAAC CTACATGCCA GATTCTATT CAACGTTAGA GTTTAACAAA ATACTCCTAG 1920  
 AATAACTTGT TATACATAG GTTCTAAAA TAAATTGCT AAACAAGAAA TGAACATG 1980  
 GAGCATTTGT AATTACAAC AGAAAATTAC CTTTGTGATT GTAACACTAC TTCTGCTGTT 2040  
 CAATCAAGAG TCTTGTAGA TAAGAAAAAA ATCAGTCAAT ATTTCCAAT AATTGCAAAA 2100  
 TAATGGCCAG TTGTTTAGGA AGGCCCTTAG GAAGACAAAT AATAACAAA CAAACAGCCA 2160  
 CAAATACTTT TTTTCAAAA TTTTAGTTT ACCTGTAAT AATAAGAACT GATACAAGAC 2220  
 AAAACAGATT CCTTCAGATT CTACGGAATG ACAGTATATC TCTCTTATC CTATGTGATT 2280  
 CCTGCTCTGA ATGCATTATA TTTTCCAAG TATACCCATA AATTGTGACT AGTAAAAATAC 2340  
 TTACACAGAG CAGAAATTTT ACAGATGGCA AAAAATTTA AAGATGTCCA ATATATGTGG 2400  
 GAAAAGAGCT AACAGAGAGA TCATTATTTT TTAAGATTG GCCATAACT GTATTTTGAT 2460  
 AGAATTAGAT TGGTAAATAC ATGATTTTCT ACATCTCTG TGGTAATAGA GACTTGAGCT 2520  
 GGATCTGTAC TGCACATGAG TAAGCAAGAA AATTGGGAAA ACTTTTCGT TTGTTGAGT 2580  
 TTTGGCAACA CATAGATCAT ATGCTGAGG CACAAGTTGG CTGTTTCTCT TTGAAACCA 2640  
 GGGATGCACA GTCTAAATGA ATATCTGCAT GGGATTGCT ATCATAATNT TTCCTATGCT 2700  
 GNTGAATTCT GTGTGAGGCT CTGTGCTCGT CCTATCTCA AATTATTAT TTTATAGTGC 2760  
 TGAGATCTCT AAATAATCTC AATTTCGGAG GTTTCACAAA ATGAGCTCCT GAAGTAGACA 2820  
 GAGTAGTGAG GTTTCTATGC CCTCTATAAG CTTCTGACTA GCCAATGGCA TCATCCAATT 2880  
 TTCTTCCCAA ACCTCTGCAG CATCTGCTTT ATTGCCAAG GGCTAGTTTC GGTTTCTGCT 2940  
 CAGCCATTGC GGTAAAAAATA TATAAGTAGG ATAACCTGTA AAACCTGCAT ATTGCTAATC 3000  
 TATAGACACC ACAGTTTCTA AATCTTTTGA AACCACTTTA CTACTTTT TAAACTTAAC 3060  
 TCAGTTCTAA ATACTTTGTC TGGAGCACAA AACAAATAAA GGTATCTTA TAGTTGTGAC 3120  
 TTTAACTTT TGTAGCCAC AATTCACCTT TTAGTTTCT TTTACTTAA TCCCATCTGC 3180  
 AGTCTCAAT TTAAGTTCTC CCAGTAGAGA TTGAGTTTGA GCCTGTATAT CTATTAAAA 3240  
 TTTCACTTC CCACATATAT TACTAAGAT GATTAAAGCT TACATTITCT GCACAGGTCT 3300  
 GCAAAAACAA AAATTATATA CTAGTCCATC CAAGAACCAA AGTTTGTATA AACAGGTTC 3360  
 TATAAGCTTG GTGAATGAA AATGGAACAT TTCAATCAA CATTTCTAT ATAACAATTA 3420  
 TTAATTTAC AATTGTTTCT CTGCAATATT TTTCTTATGT CCACCTTTT AAAAATTATT 3480  
 ATTTGAAGTA ATTTATTAC AGGAAATGTT AATGAGATGT ATTTCTTAT AGAGATATT 3540  
 CTTACAGAA GCTTTGTAGC AGAATATATT TGCAGCTATT GACTTTGTAA TTAGGAAAA 3600  
 ATGTATAATA AGATAAAATC TATTAAATTT TTCTCTCTA AAAACTGAAA AAAAAAATA 3660  
 AAAAAAATA A

45 Seq ID NO: B45 Protein sequence  
 Protein Accession #: NP\_055236.1

50 1 11 21 31 41 51  
 MAALMRKSDS SCCLLLLAIV LMVSSQIGS SRALNSIKS SLGGETPGQA ANRSAGMYQG 60  
 LAFGSSKKGK NLGQAYPCSS DKECEVGRYC HSPHQSSSAC MVRKRKKRRC HRDGMCCPST 120  
 RCNNGICIPV TESILTPHIP ALDGTNRHRR NHGHYSNHD L GWQNLGRPHT KMSHIKHEG 180  
 DPCLRSSDCI EGFCCARHFV TRICKPVLHQ GEVCTKQRKQ GSHGLEIPQR CDCAKGLSCK 240  
 VWKDATYSSK ARLHVCQKI

55 Seq ID NO: 46 DNA sequence  
 Nucleic Acid Accession #: NM\_019885.1  
 Coding sequence: 1..1539

60 1 11 21 31 41 51  
 ATGCTCTTTG AGGGCTTGA TCTGTGTCTG GCGCTGGCCA CCCTCGCCGC GTGCTGGTG 60  
 TCGTGAGCGC TGCTGTGCGC CGTGTGCGAG CAGCTGTGGC AGCTGCGCTG GCGCGCCACT 120  
 CGCGACAAGA GCTGCAAGCT GCCCATCCCC AAGGGATCCA TGGGCTTCCC GCTCATCGGA 180  
 GAGACCGGCC ACTGGCTGCT GCAGGGTTCT GGCTTCCAGT CGTGGCGGAG GGAGAAGTAT 240  
 GGCACAGTGT TCAAGACGCA TTGTGTTGGG CGGCGGCTGA TACGCTGAC CGGCGCGGAG 300  
 AACGTGCGCA AGATCTCTAT GGGCGAGCAC CACTCTGTGA GCACCGAGTG GCCTCGCAGC 360  
 ACCCGCATGT TGCTGGGCCC CAACACGGTG TCCAATTCCA TTGCGACAT CCACCGCAAC 420  
 AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CACGAGGCC TGGAGAGTTA CCTGCCCAAG 480  
 ATCCAGCTGG TGATCCAGGA CACACTGCGC GCCTGGAGCA GCCACCCGGA GGCCATCAAC 540  
 GTGTACAGG AGGCGCAGAA GCTGACCTTC CGCATGGCCA TCCGGGTGCT GCTGGGCTTC 600  
 AGCATCCCTG AGGAGGACCT TGGGCACCTC TTGAGGTCT ACCAGCAGTT TGTGGACAAT 660  
 GTCTTCTCCC TGCTGTGCGA CCTGCCCTTC AGTGGCTACC GCGCGGCAT TCAGGCTCGG 720  
 CAGATCCTGC AGAAGGGGCT GGAGAAGGCC ATCCGGGAGA AGCTGCACTG CACACAGGGC 780  
 AAGGACTACT TGGACGCCCT GGACCTCCTC ATTGAGAGCA GCAAGGAGCA CGGGAAGGAG 840  
 ATGACCATGC AGGAGCTGAA GGACGGGACC CTGGAGCTGA TCTTTGGGCT CTATGCCACC 900  
 ACGGCCAGCG CCAGCACCTC ACTCATCATG CAGCTGTGTA AGCAACCCAC TGTGTGGAG 960  
 AAGCTGCGGG ATGAGCTGCG GGCTCATGGC ATCTGTGACA GTGGCGGCTG CCCCTGCGAG 1020  
 GGCACACTGC GCCTGGACAC GCTCAGTGGG CTGGCTTACC TGGACTCGGT CATCAAGGAG 1080  
 GTCATGCGCC TGTTCACGCC CATTTCCGGC GGCTACCGCA CTGTGCTGCA GACCTTCGAG 1140  
 TCTGATGTTT TCCGATCCCC CAAAGGCTGG AGTGTATGT ATAGCATCG GGACACCCAT 1200  
 GACACAGCGC CGGTGTTCAA AGACGTGAAC GTGTGCGACC CGATCGCTT CAGCCAGGCG 1260  
 CGGAGCGAGG ACAAGGATGG CGCTTCCAT TACCTCCCGT TCGGTGGCGG TGTCCGAGC 1320  
 TGCTGGGCA AGCACCTGGC CAAGCTGTTT CTGAAGGTGC TGGCGGTGGA GCTGGCTAGC 1380

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

ACCAGCCGCT TTGAGCTGGC TACAAGGACC TTCCCCCGCA TCACCTTGST CCCCCTCCTG 1440  
 CACCCCGTGG ATGGGCTCAG CGTCAAGTTC TTTGGGCTGG ACTCCAACCA GAACGAGATC 1500  
 CTGCGGAGAGA CGAGAGCCAT GCTGAGGCGC ACAGTCTAAC CCAAGACCCA CCGCGCTCAG 1560  
 CCCAGCCGAG CGAGCGGGGT GGTGGTGTGT GGAGGTAGAA ACCTGTGTGT GGGAGGGGGC 1620  
 CGGAACGGGG AGGGCGAGTG GCCCCATAC TTGCCCTCCC TTGCTCCCC TCCTTGGCAA 1680  
 ACCCTACCCA AAGCCAGTGG GCCCATTCCT TAGGGCTGGG CTCCCCTTCT GGCTCCAGCT 1740  
 TCCCTCCAGC CACTCCCAT TTACCATCAG CTCAGCCCTT GGAAGGGGG TGGCAGGGGC 1800  
 TCTGCATGCC CGTGACAGTG TTAGSTGTCA GCGCGTGCTA CAGTGTITTT GTGATGTCT 1860  
 GAACTGCTCC CTTCCTCCG TTCTTTTTCG ACCCTTTTAG CTGGGTTTGG GGGACGGGAA 1920  
 GAGCGGTGCC CCGTGGGGG CACTCTTCAG CGTCTCTCC TCCTGCGCCC CCACTGGGTC 1980  
 TGCCAGAGAA CAGCCAGCTG GGTAGCAGAA CAGGAGTCAA CCTTGGCGGG GCGGGGGCTG 2040  
 CGTCAACCT GGAGATTGCC CTTCCTATG CCAAGTITCC CACCTCCCT CACCAAGTTG 2100  
 GACAATTGA AATTACCTAT TGCTGCTACT TGTCTGTCC TCTGACCTT GGGCAAAGGA 2160  
 GCGCCAGGCC CTGTCTCCC AGCATCCTCC CTGGTGGCCC TGGGCAGGT CACTGACACC 2220  
 CCCACCTTCC CATCCCTGCG TGAACAGGC CCTGTTACAC ACAGCCGCTT AAGGCCGCGC 2280  
 GCTCATGTGT CAGCCGCCC CATATTTATT CACTGATAGA GAATCTTGGG GATGCTGGGG 2340  
 TCTGGAGTGA ACATCTCTCT CCGTTCATGC CCGTACCTGT GTTCTAGCTG TCCTGGCGAG 2400  
 ACTTCTGTGA GTGAAGAGGA AGGGGTCTCT GGTCAAACCC AGCCCCCAGG GCCTAGGGTT 2460  
 GAAAGCCTTC CCGGCTCCG GGCATTATTT GGGTTTAACT TCGGAGCCTC ACTCCTGGAC 2520  
 TGAAGTCGGG TGCTCTGCC TTATCCCTGG TGGAGATGGA ATGTGGCCCA TTGCTCCTC 2580  
 CCTCTCTCTG CAAAAACCTG GATCAGGTAG ATTTGGAGGC GGCCACGATT TCCTGTTTGG 2640  
 CCCCTGTTCA CCGCAGTGCA CTGGCCCTGA CTCAGGCGGT GAGTATGGGG AAGGATACGG 2700  
 GTTCTCTGA CCGGGAGCAA GGGCCTCCGT CTCCTCTCC TTAACCTCTC CCCTTTGCC 2760  
 TCGCCCTGA AAAAGGTGTC CTGGAAGTCC CTCCACCTC TATGCCACTG TCTGCTTAGC 2820  
 CCAGCTCAGG GGTGGGGAAG AGGCGAAAGC GTGGGGGAGG TGAGCGCAGC GGCAGTTCTG 2880  
 CCTCGAGCT TGCTGAGGG CCGTGTGTGG TCTCGGACA GCTGCGGGA GGCTGCCGCA 2940  
 GCTGAAGCTG AAGAGGCGGC TACGTGCGGT TTGTCAGGGG GATTGGGTTG AAACTGGCC 3000  
 AGTCGGGATG ACTGGGTGAA AGAGGAGTAG CTCCTGCCAC TGGCGTTTGG AGTGTGGCA 3060  
 ATTTGGGATG CCTCTGGGG AAGGTTCCG GCGTGTGGT GAGTCTCTAG ATTTTCTCTT 3120  
 GCTTCTGTG TTTATTGGTT TTTGATGTTG TAAAAGCAAT GAATCCCTT TACAAGAAAA 3180  
 TCGAAAACAC AGAAGAATGA AGGACATGCC AGTCCCGAT CGCTGCTGTG AGCACTCAG 3240  
 TGGCTCCCTC AGACAGATC CCGTAGGCAG CCCCACAGC CGACCTGAC CCCACTCACA 3300  
 GCCACCTGA AGATAGACTA TAGGAACGGG CCCATACCAC ACAGACTGCT TCCCAATCCC 3360  
 TGAGTCTCAG ATGTTTCATT TATTTCTTAC TTTTCCACTA CTAAAAACA GTGTGGAATA 3420  
 GACATTATTG GCAAAATGTC TCATCCCTAA TCCTGAAAAA CAGGCCAGAA TGGGTAAAGA 3480  
 CTGTGCAAG CTGTCAACAT AGCTACATGG TGACCCCGGA CCTGTACCCC CTCCCCCAA 3540  
 CACAAAACCA GTGTCTGGGA GGTTCATTTT CCTTTAAACT GATCCAGCTG GCCCTGAACC 3600  
 AATTGTTTTT GACTGAGTAT CTAGGAGAGC AGTAAGTGA ACITCAGACA AGCCCACTGG 3660  
 GTCTGTTCCA GGTGAGGGGC AGGGGGCATG GGGCTGGGAG GTCTCAGGG CCTTCCTCG 3720  
 GGGTGGCCAG CCGTGATGGG GGCAGAGAAG GAAAGCTGA GGGGGGTCCT TGTGAGGGAG 3780  
 GAAAGAAGAT TCATTTGCCG CGCTGGGTCT CAAAGGCAGT GAGAAGAGAG CTGAAGAAAG 3840  
 CTCTGGCTGG CTGACAGGAT CCGTGTGTG TAATTGGTCC CTCTTTTCAG CTCTCTAGTG 3900  
 AGATGCCCGT GTCTGTGCGT GTGCGTGTGT GTTTCATACA GCTAGCATTG GATGGGTGAT 3960  
 GTTCTTACT TATCATCCCT AACTATTGCA ACTTGACCTT AAAAGACAA AACCCACAA 4020  
 AACTCTTCTT GCCACGGGCT TGCAGATTGA AGCACTTTCG ATGTTGGGCG CTGGCGTTTG 4080  
 TGTTCTGGGC ACCACCGTGA CCGTGCCAG ATGGCTATAA TATTATTTA TACACAAACC 4140  
 TTTTITTTCA TAAATGTTAT AATTTTGTGT CTGTCTTTAT AAACATTAT AAGTACTATT 4200  
 TTTGTTATAA TTCAAATAG ATATTAGTA TAAAGTTTTT GCTGTTAAAT ATTTGTTATT 4260  
 TAGTAAATA TGAATTTGTC TCTATTGTAA ACATGGTTCA AAATATTAA ATGTTTITAT 4320  
 CACAGTCGTT TTAATATTGA AAAAGCACTT GTGTGTTTGT TTTTGATATG AAACCTGTAC 4380  
 CGTGTGAGTG TTTTCTCTGT CGTGTTTGA ATCTGTATAT AATATTCCAT GTTGCATATT 4440  
 AAAAA

Seq ID NO: B47 Protein sequence  
 Protein Accession #: NP\_063938.1

55  
60  
65

1 11 21 31 41 51  
 MLFEGLDLVS ALATLAACLV SVTLILLAVSQ QLWQLRWAAT RDKSCQLPIP KSGMGFPLIG 60  
 ETGHWLLQGS GFQSSRRREKY GNVFKTHLGG RPLIRVTGAE NVRKILMGEH HLVSTEWFRS 120  
 TRMLLGENTV SNSIGDIHRN KRKVPFKIFS HEALESYLPK IQLVIQDTLR ANSSHPRAIN 180  
 VYQEAQKLTP RMAIRVLVGF SIPEEDLGHF FEVYQQFVDN VFSLPVDLPF SGYRRGIQAR 240  
 QILQKGLKA IREKLQCTQG KDYLDALELL IESSKEHGKE MTMQLKDGTT LELIFAAYAT 300  
 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRDLDTLSG LRYLDCVIKE 360  
 VMRLFTPISG GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPVFKDVN VFPDPRFSQA 420  
 RSEDKGRFPH YLPFGGTVRT CLGKHLAKLF LKVLAVELAS TSRFELATRT FPRITLVFVL 480  
 HFPVDGLSVKF PGLDSNQNEI LPETEAMLSA TV

70  
75

Seq ID NO: B48 DNA sequence  
 Nucleic Acid Accession #: AB040527.1; AL136582.1  
 Coding sequence: 94..2319

80

1 11 21 31 41 51  
 GCGGCTGCGG GGTTCCTGGT GCTGAGGACG GAGGCCATTG GAGTTCCCGA GAAGCATGGC 60  
 TGAGGGAAGC TTCAGCGTGC AATCGGAAGG CTACAGTGTG GAAGACATGG ATGAGGGTAG 120  
 CGACCAAGTC GGGGAGGAAG AGATGGTTGA AGGCAACGAC TATGAAGAA TCGGTGCGTT 180  
 TGGTGGCTAT GGCACCTCA CCAGCTTTGA CATCCATATC CTCAGAGCCT TCGGAAGCTT 240  
 GGGTCCAGGC CTTCGCATCT TATCGAATGA GCCCTGGGAA CTGGAAGACC CTGTGCTGGC 300  
 CCAGACCCCT GTGGAGGCAT TGCAGCTGGA TCGGAAACA CTTGCAATG AGACGCGCGC 360  
 CGTGTGCTCC AACGTAGCCC GCGCCGCGCG CTCCAACCGT GCGGCTGCGG CGCTGCGCGC 420  
 CGCTGCGCGT ACCGCTTCA GTCAAGTGGT CGCTAGCCAC CGGCTGGCCA CGCGCAGGT 480  
 CTCAGGAGAG GATACCCAGC CCACGACCTA CGCCGCGGAG GCTCAGGGGC CCACCCCTGA 540  
 GCCACCCCTT GCTTCTCCGC AGACCTCCCA GATGTTAGTC ACCAGTAAGA TGGCTGCCCC 600

5  
10  
15  
20  
25  
30

CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CGGCCCCAGG AGGCTGCTAC 660  
 TGAGGGGCTT AGTAGCGCTT GTGCTTTCTC TCAGGCTCCG TGTGCCAGGG AGGTGGACGC 720  
 CAACCGGCTT AGCAGGCTT TCCTGGGCTT GAATGATGTC TTCGATTTC AATCAGCCGC 780  
 AGGTGTCTAGT GGCATGGCTT TCCCGGCTT CAAGAGACTT GCCCAGCTT AAGAGGCTGC 840  
 CACAGAGGCTT CCCAGTGGCTT CCTCTGGTGT GCGCCAGCTT GGACCTGGCA GGGAGGTGGC 900  
 AGCCACCGCTT CCAAGAGCTT CCAAGTGGCTT GAAGGCGCTT GCCAAGACTT GGTGGGTGGA 960  
 GCCTCAGAAAT GTTGTGGCAG CAGCTGTCTG CAAGGCCAAG ATGGCCACGA GCATCCCTGA 1020  
 GCGGAGGGT GCAGCTGCTT CCACTGCTCA GCACAGTGTG GAGCCCTGGG CCAGGATGGG 1080  
 AGGCAAGAGG ACCAAGAAAT CCAAGCACTT GGATGATGAG TATGAGAGCA GCGAGGAGGA 1140  
 GAGAGAGACTT CCGCGGCTT CACCCACCTT GAGAGCATCA CAGCCCTCAT TGACGGTGGG 1200  
 GGCTCAGTTG GCGCTGGGCTT CCGGATGGT CCGAGGCTT CAGATACCTT CAAGGCAGCT 1260  
 ACTGTGCTGT CCGCCCGCTT AGTGACCTT TCTGACGAG AGGGCAAAAT AGTTGGTGAA 1320  
 ATACCTGATG ATTAAGGACT ACAAGAAGT CCGCATCAAG CGCGCAGACA TGCTGAAGGA 1380  
 TGTCTATCAGA GAATATGATG AACATTTCCC TGAGATCATT GAACGAGCAA CGTACACCTT 1440  
 GGAAAGAAGG TTTGGGATCTT ACCTGAAGGA GATGACAAAG GAAGAACACC TGTATATTCT 1500  
 TGTCTGCACA CCGGACTCTT CAGCTCGCTT CCTTGGAAA ACCAAGGACA CTCCAGGCTT 1560  
 GAGTCTCTCT TTTGGTATTC TGGGCGTCTT CTTCATGAAT GGCAACCGTG CCAGCGAGGC 1620  
 TGTCTCTCTG GAGGCACTAC GCAAGATGGG ACTGCGCTT GGGGTGAGGC ACCATTCTCT 1680  
 CCGCGATCTG AGGAAGCTCA TCACAGATGA CTTTGTGAAG CAGAATGACC TGAATAACAA 1740  
 GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTT TGGGCGCTGC GAGCCCGCCA 1800  
 TGAGACGAGC AGAGTGAAGG TCCTGAGATT CATCGCCAG AATCAGAAAC GAGACCCCGG 1860  
 GGAATGGGAG GCTCATTTCT TGGAGGCTGT GGATGATGCT TTCAAGACAA TGGATGTGGA 1920  
 TATGGCCGAG GAACATGCCA GCGCCAGAT GAGGCGCCAG ATGAATATCG GGGATGAAGC 1980  
 GCTGATTGGA CGGTGGAGCT GGGATGACAT ACAAGTCGAG CTCCTGACCT GGGATGAGGA 2040  
 CGGAGATTTT GCGGATGCTT GGGCCAGGAT CCGCTTTGCT TTCTGGGCCA GATACCATCA 2100  
 GTACATTTCT AATAGCAACC GTGCCAACAG GAGGCGCCAG TGGAGAGCTG GCGTCAGCAG 2160  
 TGGCACCATG GAGGCGGCCA GCACGAGCTT CCTAGATGCT CCCAGCACA GCTCCACCAT 2220  
 CCGGACCGAG AATGCTGCCA GAGCTGGCGC CAGCTTCTTC TCCTGGATCC AGCACCCTTG 2280  
 ACGAACTGCA CGGATCTTAC TGGCCAAAGC AGAGCGCTTC CTCTCAGATT CCTTCTCGAC 2340  
 ACAGACCTCT AGGCGGCTTC TTCCTGTCTG TCGGAGGTGG CATGCAAGAT GAAGCTCTCT 2400  
 TTGCTCTTCC TGCTTTCTAT TTGTGCTTTT CCTTGTGTTT TCATGTTTGG GGTATCAGTG 2460  
 TTACATTAAT GTTGCAAAAT TAAAT

35 Seq ID NO: B49 Protein sequence  
 Protein Accession #: BAB33378.1; CAB66517.1

40  
45  
50

1 11 21 31 41 51  
 MAEGSPSVQS ESYSVEDMDE GSDEVGEEM VEGNDYEEFG AFGGYGLTS FDIHILRAFG 60  
 SLGPGRLRLS NEPNELENPV LAQTLVEALQ LDPETLANET AARAANVARA AASNRAARA 120  
 AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQGP PEPPLASPT SMLVTSKMA 180  
 APEAPATSAQ SQTGSPAQEA ATEGPSSACA FSQAPCAREV DANRPSTAF LQNDVDFDTQ 240  
 PAGVSGMAFP RKPRPAPAQE AATEGSPAAS GVPQTGPGR VAAATRPKTK SGKALAKTRW 300  
 VEPQNVVAAA AAKAKMATSI PEPEGAAAT AQSASPEWAR MGGKRTKSK HLDDEYESS 360  
 EERETPAVPP TWASQPSLT VRAQLAPRPP MAPRSQIPSR HVLCLFPRNV TLLQERANKL 420  
 VKYLMKDYK KIPKIRADML KDVIREDYEH FPEIIRATY TLEKKEFGIHL KEIDKEEHL 480  
 ILVCTRSSA RLLGKTIDTP RLKLLLVILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540  
 FLGDLRLKIT DDFVQKYLE YKKIPNSNPP EYEFWGLRL RHETS KMRLV RFLAQONQRD 600  
 PREWKAHFLE AVDDAFKTM DVMAREHARA QMRAQMNIGD EALIGRWSWD DIQVELLTD 660  
 EDGDFGDAWA RIPFAPWARY HQYILNSNRA NRRATWRAGV SSGTNGGAST SVLDGPSTSS 720  
 TIRTRNAARA GASFFSWIQH R

55 Seq ID NO: B50 DNA sequence  
 Nucleic Acid Accession #: XM\_084965.1  
 Coding sequence: 356..2014

60  
65  
70  
75  
80

1 11 21 31 41 51  
 GACCTAGCGT GTGCTCAGCT CTGGACAAGA CATGGATGTA GGCAGACATG CTCTCTGCTT 60  
 GCTGGGCTTA GTGCACCAAT GCTAAGGACA GACATGAAGG GCTTGGGAAA GGCATGAAGA 120  
 TGCAGGAGGT CTAGGAGAGA GGATAAGAAA AACAAAGCATT TTGTGGTGGG TGAATTTGCG 180  
 TTGTCTTTT TAGAGGCAAT TCGTGTATCA TGGTTGCGCT CCGCTGAAGA GCGAGCTAG 240  
 AGAAGGAATC CSAAGCGGCG GCGGCGAGCG CCGCTCAGGT TGATTAGAA TACGGGTGAC 300  
 AGTGGCCTGG GCGAGCCCA CTGCTGACGA AAGCGGCTTA TCCCGCGCGG TTCCATGGA 360  
 GACGAGCCGG AGCGCGGCG GCGGCGGGGCT TGTGAGCGAG CGCGCGCGAG CTGCGCGCTC 420  
 CGTGGGGGTC TGCAAGAGGA AGCGGAGGC CGGGCGCGG ACCCGGACCC TCGCGGAGA 480  
 CATGGAATTC CATTTGTGCT GTGCGCGGCA AACCGCGGCC GCGGAGCCCG CCGCGGGGAA 540  
 GATTAATAAA GCTGCTTCA AATTATTCAA GAAGAGGAAA TCGGTGGCA CCATGCCAG 600  
 CATTTTGGG GTCAAAAACA AAGGGGACCG GAAAGCTCG GGTCCGAGCG GGTGGTGGG 660  
 GAGCAGGACC CAGCAGGAC TTGCGGAGGT GCTGGTGTG GAGAGCGGCA GGAAGGAGGA 720  
 GCGCGCGGCT GCGGCGGACA GCGGCGGGG CCGCGGAGC CCGCGGAGC CCGCGGAGC 780  
 CAGAGCGGCA GGGCGGCGG GGGGCTCTCT CGCCAGCAGC TCGGTGGCCA AGTCGACAG 840  
 CTTCTTCTCG CTGCTGAAGA AGAACGGCG CTGGAAGAAC GGCAGGAGG AGCCTGTGGA 900  
 CGCGAGCAAG GCGGCGGCA AACAAAAGCG GGGCTGCGG GGGCTGTCA GCGGCATGGG 960  
 CTGGCAGG AAAGACAAGC GGGCCAGGCG GAGGCGCGG GAGGCGCGG CCGCGGCGG 1020  
 CCGCTGTGAT CTACCGGCT CAGCTCAGCG CAGCTGAGG TCGCTCAGG AGGAGACGCC 1080  
 CAGAGCCGCG CCGAGCGCG AGGAGCCGAG CCAGGAGGCC CCGGAGACC CAGCAGGCTG 1140  
 TGGAGATATT ATTGCAGACC AAGAGGAAGA GCGAGGTCCC AGCTGTGACA AGCATGTCCC 1200  
 CCGGCGAGGC AAGCGGCTC TGTCTAAAAA GAACCCCGGC GTGGTGGCTT ACCAAGGAGG 1260  
 CCGGGAAGAG ATGGCCAGGC CGGACGAGGT GGACGACACC TATCTACAGG AGTTCTGGTG 1320  
 CATGCTCTCC CAGACCGAGG AGCAGGAGCC CGAGCCCGAG GAGGCGCGG CTAAGGTGGC 1380  
 AGCTGCGCTG GAAACCAAGG TGGTGCCCGA GACCCCGCAA GACACCAAGT GTGTGGAAGC 1440  
 GGCCAGGAG GCGTCTCTCG TCAAGCGCAG GAGGCTCAAC CGGATTCCCA TCGAGCCCCA 1500  
 TCCTAAGGAG GAGCCCAAGC ACCCGGAGAA GGAGCAGCAG GAAGGCGTCC CCAAGCAGCA 1560

5  
10  
15

```

CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620
GAAGCGGGG ATCCCCCGGG ATAGCTACAG CGGGGAGCGG CTCTATGATC TCTATGCTGA 1680
CCCGGACGGA AGTCCAGCAA CCCTTCCTGG AGGGAAGGAC AACGAGGAGA CGTCTCCCT 1740
GTCCCGGTTA AAGCCCGTAT CTCCAGGCAC CATCACCTGT CCACGCGAA CACGAGGCG 1800
CTTGCTGAAG GACTCTAAGA TCCTATTAG CATCAAGCAC CTGACCAACC TTCCATCTAG 1860
CCATCCCGTG GTGCACCAGC AACCTCCAG GAGTGAGATG CCCAGAACAA AAATCCCGGT 1920
TTCCAAAGTG CTGCTCCGCA GAGTCAGCAA CCGGGGCTTG GCTGGGACCA CCATCAGAGC 1980
AACGCGCTGC CAGCAGAGTG CCAAAAAGTT GTGAGGTCTT CCAGGCCAAG GTGGATGGGC 2040
CCCATGCCAA GGAATACAAC TTTTCCCTGG AAACCACTAA AGTAAGTTTT GCTTTTCTTA 2100
AAGAAAGTCT TTTAGGACAC CAOCCTGCC CCGCCCTGCT CCAGAGCGTG GACCGAGGAG 2160
GTCTTTGTGC CCTGAGCAGG GACCGGATAA CACCAGAAAG AGGGATGCTA CACGGGGGTT 2220
TCTCCTCTCA AGATAAGTCC CTGAGAATTA TTTTCAAGCA CTTTTTCTT TTTTACCTT 2280
AAGTTTTTCT TCCTTTTGTCT TTAATATACT GAACACTTGG AAGTCACCTT TACTTGCCTT 2340
TGCAGAAAC AGAAGTCTAG CAAACCTAAG TAAGAGTCAT GCCTGGATAT TGGGATAAGC 2400
CAGTGTCTAG AGGCCTGAAG GAACCGCTGA AGAACAGAG GAGATCTCCT CTTCCAAGAC 2460
ACGTTTCCTT CTTTCCCTTC TTTCTCTTT CTTTCCAGT T

```

Seq ID NO: B51 Protein sequence  
Protein Accession #: XP\_084965.1

20  
25  
30

```

1      11      21      31      41      51
|      |      |      |      |      |
METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
EPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKKN GRSENGKGEP 180
VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE 240
TPRAAREPEE PSQDAPRDPFA GCGDIADQEE EAGPSCDKH VPGPGKPAIS KINPGVVAYQ 300
GGGEEMASPD EVDNLYLQEF WDMLSQTEEQ GPPEQEGAAK VAAALETKVV PETPKDTRCV 360
EAKDASSVK RRLNRIPIE PHPKEEPKHP EKEQEGEVNP SDEGYWDSST PGPEEDSSSS 420
GKAGIPRDS YSGDALYDLY ADPDGSPATL PGKDNNEETS SLRLKPVSP GTITCPLRTP 480
GSLKDSKIP ISIKHLINLP SSHPVVHQRP SRSEMPRTKI FVSKVLVRRV SNRGLAGTTI 540
RATACHDSAK KL

```

Seq ID NO: B52 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2016

35  
40  
45  
50  
55  
60  
65  
70  
75

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGACGA GCCCGAGCCG CGCGCGGCGC GGGGCTGTCA GCGAGCGCGG CCGAGCTGGC 60
GGTCCCTGG GGGTCTCAG GAGGAAGGCG GAGGCGGGG CCGGACCGG GACCTCGCG 120
GCAGACATGG ACTTGCATTG TGAATGTGCC GCCGAAACGC CGGCCGCGGA GCCCGCGTG 180
GGGAAGATTA ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAATCCGG TGGCACCATG 240
CCAGCATTT TTGGGGTCAA AAACAAGGG GACGGGAAA GCTCGGGTCC GACGGGGCTG 300
GTGAGGAGCA GGACCCACGA CGGACTTGCC GAGGTGCTGG TGCTGGAGAG CCGCAGGAAG 360
GAGGAGCGCG CGCGCGGGGG CGACAGCGGC GGGGCGGGG GGGGGCGGCC GAACCCGGGG 420
CCCCCAGAG CGCAGGGGCC CGCGCGGGGC TCCCTCGCCA GCAGCTCGGT GGCCAAGTCG 480
CACAGCTTCT TCTCGTGTCT GAAGAAGAAC GGGCGCTCG AAAACCGCAA GGGAGAGCCT 540
GTGGACGCGA GCAAGGGCGG CGGCAACAA AAGCGGGGG TGCGGGGGCT GTTCAGCGGC 600
ATGCGCTGGC ACAGAAAAGA CAAGCGGGCC AAGCGGAGG CCGCGGAGGG GCGCGCGCCC 660
GGGGCGGCTG TGATCTTACC CGGCTGCTC ACGCCAGCC TGAGTGTGCT CAAGGAGGAG 720
ACGCCAGAG CGCGCGCGGA GCGGAGGAG CCCAGCCAG AGCCCGCGCG AGACCCAGCA 780
GGTAGGCGCG CAGGGGGAGA GGAGGTGCC GCGCCGCGCG ACGCGCGCCC AGCGCGGAGC 840
TGCGAGAGAG CAGAGGGGCT CGCGCACCCC GCGGACACCG CGCGCGGGG AGAGGACGCG 900
GGCGGGCATC GCGCGCGCGA GCGCGGGGCC GGGGAGGTCC GCACGCGAGA GGACGCTTCC 960
AGGACGGGG CGTTCCTCGT AAAGACGGTC CCCCTTGTGC ACTCCGAGG CGGCAGCGCG 1020
CGGGCGCCCG CGGCCCCAGA CCTTGCCTCT GTGATCCAC CCTCAGACC GTCGGCAGAT 1080
CGTATTGTGT TGATGTTTTT TGACGTGACT TCACTGAAA GCTTTGACTC TCCTACAGGC 1140
TGTGAGATA TTATTGCGA CCAAGAGGAA GAGGAGGTC CCAGCTGTGA CAAGCATGTC 1200
CCCGGCCAG GCAAGCCCGG TCTGTCTAAA AAGAACCCCG CGGTGTGTGC CTACCAAGGA 1260
GGCGGGGAAG AGATGGCCAG CCGGACGAG GTGGACGACA CCTATCTACA GGAGTTCTGG 1320
GACATGCTCT CCCAGACGGA GGAGCAGGGA CCGGAGCCCC AGGAGGGGCG GGCTAAGGTG 1380
GCAGCTGGCG TGGAAACCAA GGTGGTGCCC GAGACCCCA AAGACACCAG GTGTGTGGA 1440
GCGGCCAAGG ACGCGTCTC GTCAAGCGC AGGAGGCTCA ACCGATTCC CATCGAGCCC 1500
CATCTTAAGG AGGAGCCCAA GCACCGGAG AAGGAGCAG AGGAAGCGT CCCCAACAGC 1560
GACGAGGCTC ACTGGGACTC CACCAAGCCA GGCACAGAG AAGACAGCTC GAGCAGCGGG 1620
AAGAAGCGCG GCATCCCCCG GGATAGCTAC AGCGGGGAG CGCTCTATGA TCTCTATGCT 1680
GACCCGAGCG GAAGTCCAG AACCTTCTCT GGAGGGAAG ACAACGAGGA GACGTCTCTC 1740
CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACAGGC 1800
AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAG ACCTGACCAA CCTTCCATCT 1860
AGCCATCCCG TGGTGACACA GCAACCTCC AGGAGTGAGA TGCCCAAGAA AAAAATCCCG 1920
GTTTCCAAAG TGCTGTGTCG CAGAGTCAGC AACCGGGGCT TGGCTGGGAC CACCATCAGA 1980
GCAACGGCCT GCCACGACAG TGCCAAAAAG TTGTGA

```

Seq ID NO: B53 Protein sequence  
Protein Accession #: FGENESH predicted

80

```

1      11      21      31      41      51
|      |      |      |      |      |
METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
EPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKKN GRSENGKGEP 180
VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE 240
TPRAAREPEE PSQDAPRDPFA GEPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA 300

```

5 AGHRRAPGPG GEVRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPSPDPSAD 360  
 RICLMFSDVT SLKSFDSLGT CGDIIADQEE EAGPSCDKHV PGPGKPAISK KNPGVVAYQG 420  
 GGEEMASPE VDDTYLQEPW DMLSQTEBQG PEPQEGAAKV AAALETKVVP ETPKDTRCVE 480  
 AAKDASSVKR RRLNRIPIEP HPKEEPKHPE KEQQEGVENS DEGYWDSTTP GPEEDSSSSG 540  
 KKAGIPRDSY SGDALYDLVA DFDGSPATLP GGDNEETSS LSRLKPVSPG TITCPLRTPG 600  
 SLLKDSKIPI SIKHLTNLPS SHPVVHQQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660  
 ATACHDSAKK L

10 Seq ID NO: B54 DNA sequence  
 Nucleic Acid Accession #: NM\_014138.1  
 Coding sequence: 60..854

15 1 11 21 31 41 51  
 CTGCAGAGAC TTCCAGGAA GGTCCAGGCG CCTCTCAGCC TTCGTACTCA GAACAGCCGA 60  
 TGATGGGCTC CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCCAG 120  
 AGGGGCTGCT CCGCCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA 180  
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTCGCGCA TGTGAGGAGG AGACACCGCG 240  
 ATCAGATGGC CCCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCGCCATTA GGTGACAGAA 300  
 20 GTCAAGATGC ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360  
 GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGCAGG 420  
 GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAGCC CGGGCCTCTG CCTGAAGCGG 480  
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540  
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCCATG 600  
 25 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC 660  
 CCATTTTGGG GACCAACACG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720  
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCCG AGGAAGGTCC TCATGTTTCG 780  
 TGCTGTCTAT TCTCGGATGG CTGTGAGGCA TTCCTTGCCA AGGCAAGCTG CGTACCGAG 840  
 GTCTCAACCG CATCTCACAT GGCTCCTGTG ATGCATGTTG TCGCTTCCG ACCCGGGATC 900  
 30 TCCATCTCTC TCTCCTCTCT GCTGTCACTA AGAGATCACA TGTCTGTGTA GTGTGAATGC 960  
 CTGTGCGTGG TCTGTGCTTT TTGCACCATT GAGTTGACTG CCTCTGAGAA CGACGACTAG 1020  
 GCCCTGTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGATGGGC AGGTAACCGC 1080  
 AGTGTGGGAA AGGAATGTGG AATGAGAACT TGGTGGTTCA CCGCTGTACT ATTTGTGTAA 1140  
 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCCAG 1200  
 35 TAGTAGTCTC CCTTACAGGA ATTTTTCAGC GGGTTCCTCA TCATCAATAC CAAATAAATA 1260  
 TATGTAGGAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

40 Seq ID NO: B55 Protein sequence  
 Protein Accession #: NP\_054857.1

45 1 11 21 31 41 51  
 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA FLRHVRRRHR 60  
 DIMAPYAVGR EARISPLGDR SQNRFRCECR YCQSHRPNLS GIPGESNRAP HPSSWETLVQ 120  
 GLSGILTSLG TNQPGPLPEA ALQPOETEEK RQRERQESK IMFQRLKQW LEEN

50 Seq ID NO: B56 DNA sequence  
 Nucleic Acid Accession #: NM\_000025.1  
 Coding sequence: 198..1424

55 1 11 21 31 41 51  
 GCTACTCCTC CCCAAGAGC GGTGGCACCG AGGGAGTTGG GGTGGGGGGA GGCTGAGCGC 60  
 TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTGGCTCTC ATGCCCTGCT 120  
 GTCCCTCCCC CTGAGCCAGG TGATTGGGA GACCCCTCC TCTCTCTCT CCCTACCGCC 180  
 CCAAGCGGGA CCGGGGATG GCTCCGTGGC CTCACGAGAA CAGCTCTCTT GCCCATGGC 240  
 CGGACCTCCC CACCCTGGCG CCCAATACCG CCAACACCAG TGGGCTGCCA GGGTTCCGT 300  
 60 GGGAGGCGCG CCTAGCCGGG GCCCTGCTGG CCGTGGCGGT GCTGGCCACC GTGGGAGGCA 360  
 ACCGTCTGGT CATGCTGGCC ATCCCTGGA CTCGAGACT CCAGACCATG ACCAACGTGT 420  
 TCGTACTTC GCTGGCCGCA GCGGACCTGG TGATGGGACT CCTGGTGGT CCGCCGGCGG 480  
 CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGGAG CTGTGGACCT 540  
 CGGTGGAGCT GCTGTGTGTG ACCGCCAGCA TGGAAACCT GTCCGCCCTG GCCGTGGACC 600  
 65 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTCAACAG CGCTGGCCCC 660  
 GGACAGCTGT GGTCTGTTG TGGGTCTGT CCGCGCGGT GTCGTTTGG CCCATCATGA 720  
 GCCAGTGGTG GCGGTAGGG GCGGACGCG AGGCGCAGCG CTGCCACTCC AACCGCGCT 780  
 GCTGTGCTCT CGCCTCAAC ATGCCCTACG TGTGCTGTC CTCTCGCTC TCCTTCTACC 840  
 TTCTCTCTCT CGTGATGCTC TTGCTTACG CGCGGTTTT CTGTGTGGCT ACGCGCCAGC 900  
 70 TCGCTTGTCT GCGCGGGGAG CTGGGCCGCT TTCCGCCCGA GGAGTCTCCG CCGGCGCGCT 960  
 CGCGCTCTCT GACCCCGGCC CCGGTGGGGA CGTGCGCTCC GCCCGAAGGG GTGCCCGCT 1020  
 GCGGCGCGCG GCGCGCGCGC CTCCTGCTC TCAGGGAACA CCGGCGCGCT TGCACTTGG 1080  
 GTCTCATCAT GGGACCTTC ACTCTCTGCT GGTGCGCTT CTCTGCGCC AACGTGCTGC 1140  
 GCGCCCTGGG GGGCCCTCT CTAGTCCCGG GCCCGGCTTT CCTTGGCTG AACTGGCTAG 1200  
 75 GTTATGCCAA TTCTGCTTC AACCCGCTCA TCTACTGCG CAGCCCGAGC TTTCGAGCG 1260  
 CCTTCCGCGT GGTCTGTGCG CGCTGCGGCC GTGCGCTGCC TCCGAGAGCC TGCGCGCGCG 1320  
 CCGGCGCGCG CCTCTTCCCG TCGGCGGCTC CTGGGCGCG GAGCAGCCCA GCGCAGCCCA 1380  
 GGCTTTGCCA ACGGCTCGAC GGGGCTTCTT GGGAGTTTC TTAGGCTGA AGGACAAGAA 1440  
 80 GCAACAACCT TGTGTATGAC AACCTGTGGA AAACCTCTGG CCTCTGTTC GAATGAGTCC 1500  
 CATGGGATTC CCGCGCTGTG ACACCTTACC CTCCAGAAC TGACGACTGG GCCATGTGAC 1560  
 CCAAGGAGG ATCTTACCA AGTGGGTTTT CACCATCTC TTGCTCTCTG TCTGAGAGAT 1620  
 GTTTTCTAAA CCGGACCTT GAACCTTACT CCTCCCTCAG TGGTAGTGT CAGGTGCCGT 1680  
 GGAGCAGCAG GCTGGCTTTG ATAGGGGCAC CCATCACCG GCTTGCCTGT GCAGTCAGTG 1740  
 AGTGCTTAGG GCAAGAGAG CTCCCTGGT TCCATTCCTT CTGCCACCCA AACCTGATG 1800



5  
10  
15

```

AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGCT AGAAAAGACC 1860
AAGATTGGGG GTTTTATCTC TGGTTCCTTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTCGCCAGGG 1980
TTTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATTAG AACAGATCCC TTCTTTCTCT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTCGGCCCA CTTCCTCTCC 2100
GTTTGTITTC TTTTCATAAT CCACTTACTC CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCGAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAAAACAAA 2220
AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCTTCTCTG AAATCTCTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGCAGGTTT AGGGCAGGGG 2400
GCATTTGTCC CCTCCATGCT ATAATCCAGT GGTGCCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGGTGTGTG TGTGTGTGTG TGTGTGTGGA GGCACAGGCA CAAAGCATTG CTGGGGTTGG 2520
TCAAATGTCT TGTGTGATAA ATATATTCTG ATGTTTCCCA GCCTTTCCAC AACCTCTACC 2580
TTCCCACTCA CCTTCCCCAG CTACAAAAAT TGTATTATC CTCTAAAGT AAAACTGGAG 2640
TTAC

```

Seq ID NO: B57 Protein sequence  
Protein Accession #: NP\_000016.1

20  
25  
30

```

1 11 21 31 41 51
MAPWPHENSS LAPWPDLPFL APNTANTSGI PGVPWEAALA GALLALAVLA TVGNNLLVIV 60
AIAMTPRLQT MTNVFVTSIA AADLVMLGLV VPPAATLALT GHWELGATGC ELWTSVDVLC 120
VTASIELTCA LAVDRYLAVT NPLRYGALVT KRCARTAVLV VVVVSAAVSF APIMSQWNRV 180
GADAEARQCH SNPRCCAFAS NMPYVLLSSS VSFYPLLLVM LFVYARVFVV ATROLRLLRG 240
ELGRFPPEES PPAPSRSLAP APVGTCAPE GVPACGRPPA RLLPLREHRA LCTGLIMGT 300
FTLCWLPFFL ANVLRALGGP SLVPGPAFLA LNWLYGANSR FNPLIYCRSP DFRSAFRRL 360
CRGRRLPPE PCAARPALF PSQVPAARSS PAQPRLCQRL DGASHGVS

```

Seq ID NO: B58 DNA sequence  
Nucleic Acid Accession #: NM\_032553.1  
Coding sequence: 37..1038

35  
40  
45  
50  
55

```

1 11 21 31 41 51
CACCATTAGG CAAAGATAGT TTCTCTAGAG AGAATCATGC CTGCTAATTA CACGTGTACC 60
AGGCCAGATG GAGACAATAC AGATTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC 120
ATTCTGTGTC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTATATG 180
AAAGAAACAA AACGAGCTGT GATATTTATG ATAAACTTAG CCATTGCTGA CTTACTACAA 240
GTTCTTCTCT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300
GGTCTCTGCA TGTCTCTGTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGGTCTGCA TCAGTGTGCG ACGATTTTGG TTCTCATGT ACCCTTTTCC CTTCATGAC 420
TGCAACAGAA AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCCTTGC 480
TGTGTACTCT TTCCACTCCT CAGAACCAGT GATGATACCT CTGGCAATAG GACCAATGTC 540
TTTGTGGATC TTCCCTACCG GAATGTCAAC CTGGCCCACT CGGTGTTTAT GATGACCAT 600
GGGAGATGTA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660
GTTTTATCAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TTGAAGATGA TTCTAACCTG TGCAGGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780
AGTTTTCTCT TAGATTCTCT GGTGAAGTCC AATGAAATTA AAAGCTGCCT AGCCAGAAGG 840
GTGATTCTAA TATTTTCTTC TGTGGCATG TGTCTTGCTA GTCTGAATTC ATGCTCTGAC 900
CCAGTCATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAAG ACAAGATTG 960
CATGACAGCA TCCAACCTCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
ACACCTGAAT TATGCTAAAA CAAAAACCA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080
CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAC ACAGCTTTTC 1140
AGTTCTGCTC TATCTTACTG CTATGGGGAA TTCACTTCTT CAAAGCAGGA CCTATTGGGA 1200
GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTT CTTCAGAT

```

Seq ID NO: B59 Protein sequence  
Protein Accession #: NP\_115942.1

60  
65  
70

```

1 11 21 31 41 51
MPANYTCTRP DGDNTDFRYF IYAVTYTVIL VPGLIGNILA LNVFYGYMKE TKRAVIFMIN 60
LAIADLLQVL SLPLRIFYFL NHDWPFPGPL CMFCFYLYKV NMYASIFYLV CISVRRFNFL 120
MYPFRPHDCK QKYDLYISIA GWLIICLACV LPPLRLTSDS TSGNRTKCFV DLPTRNVNLA 180
QSVVMTIGE LIGFVTEPLI VLYCTWKTIV SLQDKYPMQA DLGEKQKALK MLTTCAGVFL 240
ICFAPYHFSF PLDFLVKSNE IKSLARRVI LIFHSVALCL ASLNSCLDPV IYFSTNEFR 300
RRLSRQDLHD SIQLHAKSFV SNHASTMTTP ELC

```

Seq ID NO: B60 DNA sequence  
Nucleic Acid Accession #: CAT cluster

75  
80

```

1 11 21 31 41 51
GATTCGGATT TTAATCCGAC TCACTATAGG GAATTTTGGC CTCGAGGCC AAGAATTCCG 60
CCCGAGGGTT AGACATTAA CTTGAGTCTT TTCATATCAC GGTATGCTTT TATTTTACCC 120
TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTCTTTTCA 180
TACATTTTAA GGAATTTATA CATTGTCATC TGAATTTGTA TTCAATATCT TCTAGAAACC 240
AAGAGTGGAC TTGGTATCCG TCTGATTATA TTTTCTTTGT TGGTAAAGAG CCTCTTTT 300
CCCTTTTAT TTTTCTCTC TCTTCTCTTA GTGTTTATA TCTTATTTT ATGAATGTAG 360
TCTAATATT TAGAACACTG TCTCCGAGTA TGTGTTTATT TGGGTTTGTG TTTTGAACAT 420
TGCCCTCAGG TCGAGTTTAA TGTGTGTTTA TGTTCCTAT TTGAGGTGG ACACCTAGAA 480
AATTTTCTCA ATTCGAAAC TATTTTCTT CAGCACTCAG AAATTTTAT CAAAGATTAT 540
TTCCAGGATT ATTTCTGTGCT CTGTTTCTT CGTGTCTTCA ACCTAGAATT CAATTGTTTA 600

```

ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATTGTC 660  
 ATATCTTTTG GACTATTGTG TGAAGCAAT AAATGTATAT TACTTTAAAA AAAAAAAAAA 720  
 AAAACTHCAT TTTCAAATTT AATACACACA AATTGTGCAT ACCACACAC ATATACCACA 780  
 GATATATTCA TTTCAGGAT TTCTTTAAGT GTTATTTTAA AAATAATCAT ATTCTTATTT 840  
 TGTGAACCTG GGGATTTCCT GAAACTTTTT GAAAACTCTC ATTAGTCTGT GTTGTGTGG 900  
 TTTCTTTAAA TTATCTCTTC CTTCAGAAAT ACTTTTGTGT TTTGAATTG AGTCTTTGCC 960  
 ATTCATAAGG CGGCTTTCC TTGAATACCA GATAACTCTG AGTTTCTGT TCATATTTAA 1020  
 GAATAATAA CCTAATTGA AAAAAAAAAA AAAAA

10 Seq ID NO: B61 DNA sequence  
 Nucleic Acid Accession #: NM\_014522.1  
 Coding sequence: 846..3911

1 11 21 31 41 51  
 15 CTGGTGGTCC AGTACCTCCA AAGATATGGA ATACACTCCT GAAATATCCT GAAAACTTTT 60  
 TTTTTCAGA ATCCCTTAAT AAGCAGTTAT GTCAATCTGA AAGTTGCTTA CTGTACTTTT 120  
 ATATTAATAG CTATTCTTGT TTTTCTTATC CAAAGAAAAA TCCTCTAATC CCCTTTTCAC 180  
 20 ATGATAGTTG TTACCATGTT TAGGCATTAG TCACATCAAC CCCTCTCCTC TCCCAAACCTT 240  
 CTCCTCTTCA AATCAAATCT TATTAGTCCC TCCTTTATAA TGATTCCTTG CCTCGTTTAA 300  
 TCCGATCAA TTTTTTTCCA CTTTGATGCC CAGAGCTGAA GAAATGGACT ACTGTATAAA 360  
 TTATTCATTG CCAAGAGAAAT AATTGCATT TAAACCCATA TTATAACAA GAATAATGAT 420  
 TATATTTTGT GATTGTGAAC AAATACCCCT TATTTTCCCT TAACATTGA ATTAATATTT 480  
 25 TTAATTATTT GTATTCTCTT TAACTATCTT GGTATATTAA AGTATTATCT TTTATATATT 540  
 TATCAATGGT GGACACTTTT ATAGGTACTC TGTGTCAATT TGTACTGTGT AGGTATCTTA 600  
 TTTCAATTAT CTTTATTCTT AATGTACGAA TTCATAATAT TGTATTGAGA ACAAATTTAT 660  
 CACTAATTAA CAGAGTGTC AATTATGCTAA CATCTCAATT ACTGATTTTA ATTTAAACAA 720  
 GTTTTGTGTA ACATGCACTG TTAGGGTTGG CTCTTAATA ATTTCTTCTT CCTCTCTCTT 780  
 30 CTCTCTCTT CTTTGGTCA GTGTGTGCG GGTTAATACA ACAAACCTGA ACAAGTGTAC 840  
 CTGGTATGGA CTGTGTGTC GGGACGTACA TTTTCCGGT CCTGCTAGCA TGCGTGGTGT 900  
 TCCACTCTGG CGCCAGGAG AAAAACTACA CCATCCGAGA AGAAATGCCA GAAAACGTCC 960  
 TGATAGGCGA CTGTGTGAAA GACCTTAAT TGTGCTGAT TCCAAACAG TCCTTGACAA 1020  
 CTGCTATGCA GTTCAAGCTA GTGTACAAGA CCGGAGATGT GCCACTGATT CGAATTGAAG 1080  
 35 AGGATACTGG TGAGATCTTC ACTACTGGCG CTGCAATTGA TCGTGAGAAA TTATGTGCTG 1140  
 GTATCCCAAG GGATGAGCAT TGCTTTTATG AAGTGGAGGT TGCCATTTTG CCGGATGAAA 1200  
 TATTTAGACT GGTTAAGATA CGTTTTCTGA TAGAAGATAT AAATGATAAT GCACCATTTG 1260  
 TCCAGCAAC AGTTATCAAC ATATCAATTC CAGAGAATCT GGCTATAAAC TCTAAATATA 1320  
 CTCTCCACGC GGCTGTGTAT CCTGACGTAG GAATAAACCG AGTTCAAAC TACGAACATA 1380  
 40 TTAAGAGTCA AAACATTTT GGCCTCGATG TCATTGAAAC ACCAGAAGGA GACRAGATGC 1440  
 CACACTGAT TGTTCAAAAG GAGTTAGATA GGGAAAGAAA GGATACCTAC GTGATGAAA 1500  
 TAAAGGTTGA AGATGTTGAC TTCTCTCAA GATCCAGTAC TGCTATTTTG CAAGTGAGTG 1560  
 TTACTGATAC AAATGACAAC CACCCAGTCT TTAAGGAGAC AGAGATTGAA GTCACTATAC 1620  
 CAGAAAATGC TCCGTGATGG ACTTCAGTGA CACAGCTCCA TGCCACAGAT CTGACATAG 1680  
 GTGAAAATGC CAAGATCCAC TTCTCTTCA GCAATCTAGT CTCCACATT GCCAGGAGAT 1740  
 45 TATTTCACTT CAATGCCACC ACTGGACTTA TCACAAATCA AGAACCACTG GATAGGGAAG 1800  
 AAACACCAA CCAAGTTA CTGGTTTGG CAAGTGTGAG TGGATTGATG CCAGCAAGAG 1860  
 CAATGGTGTG GGTAAATGTT ACAGATGTCA ATGATAATGT CCCATCCATT GACATAAGAT 1920  
 ACATCGTCAA TCCTGTCAAT GACACAGTTG TTCTTTCAGA AAATATTCCA CTCAACACCA 1980  
 50 AAATTGCTCT CATAACTGTG ACGGATAAGG ATGOGGACCA TAATGGCAGG GTGACATGCT 2040  
 TCACAGATCA TGAATCCCTT TCAAGTTAA GGCAGTATT CAGTAATCAG TTCTCTCTGG 2100  
 AGACTGCAGC ATATCTTGAC TATGAGTCCA CAAAGAATA TGCCATTAAA TTACTGGCTG 2160  
 CAGATGCTGG AAAAACTCTT TTGAATCAGT CAGCAATGCT CTTCATCAA GTGAAAGATG 2220  
 AAAATGACAA TGCTCCAGTT TTCAACCCAGT CTTTCTTAAC TGTTCCTATT CCTGAGAATA 2280  
 55 ACTCTCTCTG CATCCAGTTG ACGAAGTAA GTGCAATGGA TGCAGACAGT GGCCTTAATG 2340  
 CTAAGATCAA TTACTGTCTA GGCCCTGATG CTCCACCTGA ATTCAGCCTG GATTGTCTGA 2400  
 CAGGCATGCT GACTGTAGTG AAGAACTAG ATAGAGAAAA AGAGGATAAA TATTATTCCA 2460  
 CAATTCTGGC AAAAGATAAC GGGGTACCAC CCTTAACCAAG CAATGTCAAC GTCTTTGTAA 2520  
 GCATTATTGA TCAAGATGAC AATAGCCAG TTTTCACTCA CAATGAATAC AACTTCTATG 2580  
 60 TCCAGAAAAA CCTTCCAAGG CATGGTACAG TAGGACTAAT CACTGTAACT GATCCTGATT 2640  
 ATGGAGACAA TTCTGCAGTT ACGCTCTCCA TTTTAGATGA GAATGATGAC TTCACCATG 2700  
 ATTCAACAA TGGTGTCTC CGACCAAATA TTTCAATTGA TAGAGAAAAA CAAGAATCTT 2760  
 TACCATTTCTA TGTAAAGGCT GAGGATGGTG GTAGAGTATC ACGTTCTTCA AGTGCCAAAG 2820  
 TAACCATAAA TGTGGTGTAT GTCAATGACA ACAACCACT TTTCAATTGTC CCTCCTTCCA 2880  
 65 ACTGTTCTTA TGAATTGGTT CTACOGTCCA CTAATCCAGG CACAGTGGTC TTTCAAGTAA 2940  
 TTGCTGTGTA CAATGACACT GGCATGAATG CAGAGGTTGG TTACAGCATT GTAGGAGGAA 3000  
 ACACAAGAGA TCTGTTTGCA ATOGACCAAG AAACAGGCAA CATAACATTG ATGGAGAAAT 3060  
 GTGATGTTAC AGACCTTGGT TTACACAGAG TGTGGTCAA AGCTAATGAC TTAGGACAGC 3120  
 CTGATTCTCT CTTCAGTGTG GTAATTGTCA ATCTGTTCTG GAATGAGTGG GTGACCAATG 3180  
 CTACACTGAT TAATGAACCT GTGCGCAAAA GCACCTGAAGC ACCAGTGACC CCAAACTCTG 3240  
 70 AGATAGCTGA TGTATCTCTA CCAACTAGTG ACTATGTCAA GATCTCTGTT GCAGCTGTTG 3300  
 CTGGACCACT AACTGTGTTT GTAGTTATTT TCATCACTGC TGTAGTAAAG TGTGCGCAGG 3360  
 CACCACACCT TAAGGCTGCT CAGAAAAACA AGCAGAAATC TGAATGGGCT ACCCCAAACC 3420  
 CAGAAAACAG GCAGATGATA ATGATGAAGA AAAAGAAAAA GAAGAAGAAG CATTCCCCTA 3480  
 75 AGAACTTGCT GCTTAATTTT GTCACATTG AAGAACTAA GGCAGATGAT GTTGACAGTG 3540  
 ATGGAAACAG AGTCACACTA GACCTTCTTA TTGATCTAGA AGAGCAAAACA ATGGGAAAGT 3600  
 ACAATTGGGT AACTACACCT ACTACTTTCA AGCCGACAG CCCTGATTGG GCCCGACACT 3660  
 ACAAATCTGC CTCTCCACAG CCGCTCTTCC AAATTCAGCC TGAATCTCCC CTGAATTCTG 3720  
 AGCACCATAT CATCAAGAAA CTGCTCTCTG ATAACACCTT TGTGGCTGTG GACTCTATCT 3780  
 80 CCAAGTGTTC CTCAAGCAGT TCAGATCCCT ACAGCGTTTC TGACTGTGGC TATCCAGTGA 3840  
 CGACCTCTGA GGTACCTGTT TCCGTACACA CCAGACCGGT AGGTATCCAA GTTCTTAACA 3900  
 CACTTTCTTA ACTATTGTTT TATTATTATT TTCAGTTGAT GTAGAACTTT ACAAATCTTA 3960  
 TTGACTTCAA AGAGGGATCA AAACATCAT ATTCTACAGA TGTACCAAT AGATATATGG 4020  
 ATTCATTTAA GTTGGTGA GAATGAGAAC AAAATAACTA CTGATTAGG AAATTTGGAT 4080  
 GCAGAATAAT AATTATAGTA GGGGCAATTT TGTCTGTAGA TGGCAGTATG ACAATTCTTG 4140

5 CTAGAGAATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCACTGTC CTCAGTACCA 4200  
 TTGTGTGCAT GAGGATCAGA ATAGTCTGGG CTAGATACAT CACATTAAG CTTTTCAGAA 4260  
 TCTGATAAAT AGCTCTAAAT ACTAATGATA TTGAGAAGCC TAGCTTCACT TGGGAAAAATC 4320  
 TGTGGCTGTT CACAGAAATT CAGCACCAAG TTATTCCCC CATACTCTAC CAGGCCCTTCA 4380  
 GGTCCTCATA AAGAAAAAGT TCGTTTTT CAG ATTAGGAAC CAAATATT TTGGTGCATC 4440  
 AAATCTACAG TCACACAATA TAACAAGAT GGGATTAGAA AAATGAAAGC CTACTCATT 4500  
 TCATCTTTAA GCCAGAGAAT GAAATATATA TGAGGTCTCT GGATAGCTAT TTAAATATT 4560  
 GCATATTAT GCAAGGTATT TTGAGCCCTT CAGAAGACAT TCT

10 Seq ID NO: B62 Protein sequence  
 Protein Accession #: NP\_055337.1

15 1 11 21 31 41 51  
 MDLLSGTYIF AVLLACVVFH SGAQEKNTYI REEMPENVLI GDLLKDLNLS LIPNKSLLTA 60  
 MQFKLVYKTG DVPLIRIEED TGEIPTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF 120  
 RLVKIRFLIE DINDNAPLEP ATVINISIEP NSAINSKYTL PAAVDPDVGI NGVQNYELIK 180  
 SQNIFGLDVI ETEPGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQSVT 240  
 DTNDNHPVPE ETEIEVSIPE NAPVGTSTVQ LHATDADIGE NAKIHPSFSN LVSNIRRLRF 300  
 20 HLNATTGLIT IKEPLDREET FNHKLVLAS DGLMPARAM VLVNVTVDND NVPSIDIRYI 360  
 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCT DHEIPFRLRP VFSNQFLLET 420  
 AAYLDYESTK EYAIKLLAAD AGKPLNQSA MLFIKVKDEN DNAPVFTQSF VTSIPENNNS 480  
 PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKLLDR EKEDKYLFTI 540  
 LAKDNGVPEL TSNVTVFVSI IDQNDNSPVP THNEYNFYVP ENLPRHGTG LITVTDPDYG 600  
 25 DNSAVTSLIL DEENDPTIDS QTGVIRPNIS PDREKQESYT FYVKAEDGGR VSRSSSAKVT 660  
 INVVDVNDNK PVFIVPPSPK SYELVLPSTN PGTVVVFQVIA VDNDTGMNAE VRSIVGGNT 720  
 RDLFAIDQET GNITLMEKCD VTDLGLHRLV VKANDLGQPD SLFSVVIINL FVNESVTNAT 780  
 LINELVKST EAPVTPNTEI ADVSSPSTSY VKILVAAVAG TITVVVVIFI TAVVRCRQAP 840  
 30 HLKAAQKNQK NSEWATNPPE NRQMIMMKKK KKKKXHSPPN LLLNFVTIEE TKADDVDSOG 900  
 NRVTLDLPID LEEQTMGKYN WVTPTTFKP DSPDLARHYK SASQPAFQI QPETPLNSKH 960  
 HIQELPLDN TFVACDSISK CSSSSSDPYS VSDCGYPVTT FEVPVSVTR PVGIQVSNNT 1020  
 F

35 Seq ID NO: B63 DNA sequence  
 Nucleic Acid Accession #: XM\_059180.2  
 Coding sequence: 276..3740

40 1 11 21 31 41 51  
 GCGGCGGCCG CGGAGTATCC TGGAGCTGCA GACAGTGCGG GCCTGCGCCC AGTCCCGGCT 60  
 GTCTCGCGCG CGACCCCTCC TCAGCCCTGG GCGCGCGCAC GCTGGGGCCC CGCGGGGCTG 120  
 GCGCGCTAGC GAGCCTCGCG GTCCGACCCA GCCAGCGCAG CGACGGGGCG CTGCTTGGCC 180  
 CAGGCGCACA CGGAAGTGCG CTCTCTGAA GTAGCTTTGG AAGTAGAGA AGAAATCCA 240  
 45 GTTTGCTTCT TGGAGAACAC TGGACAGCTG AATAAATGCA GTATCTAAAT ATAAAGAGG 300  
 ACTGCAATGC CATGGCTTTC TGTGCTAAAA TGAGGAGCTC CAAGAGACT GAGGTGAACC 360  
 TGAGGCGCCC TGAGCCAGGG GTGGAAGTGA TCTTCTATCT GTCGACAGG GAGGCCCTCC 420  
 GGCTGGCGAG TGGACAGTAC ACAGCAGAGG AACTGTGCTC CAGGGCTGCA CAGGCATGCC 480  
 GTATCTCTCC TCTTTGTGAC AACCTCTTTG CCCTGTATGA CGAGAACACC AAGCTCTGGT 540  
 50 ATGCTCCAAA TCGCACCATC ACOGTTGATG ACAAGATGTC CCTCGGCTC CACTACCGGA 600  
 TGAGGTTCTA TTTACCAAT TGGCATGGAA CCAACGACAA TGAGCAGTCA GTGTGGCGTC 660  
 ATTCTCCAAA GAAGCAGAAA AATGGCTACG AGAAAAAATA GATTCCAGAT GCAACCCCTC 720  
 TCCTTGATGC CAGCTCACTG GAGTATCTGT TTGCTCAGGG ACAGTATGAT TTGGTGAAAT 780  
 GCCTGGCTCC TATTCGAGAC CCCAAGACCG AGCAGGATGG ACATGATATT GAGAACGAGT 840  
 55 GTCTAGGGAT GGCTGTCTGT GCCATCTCAT ACTATGCCAT GATGAAGAAG ATGCAGTTGC 900  
 CAGAACTGCC CAGAGCATCT AGCTACAAGC GATATATTCG AGAAACATTG AATAAGTCCA 960  
 TCAGACGAGC GAACCTTCTC ACCAGGATGC GGATAAATAA TGTTTTCAAG GATTCTCTAA 1020  
 AGGAATTTAA CACACAGACC ATTGTGACA GCAGCGTGTG CAGCGATGAC CTGAAGGTGA 1080  
 AATACTTGGC TACCTTGGAA ACTTTGACAA AACATTACGG TGCTGAAATA TTTGAGACTT 1140  
 60 CCATGTTACT GATTTCATCA GAAAATGAGA TGAATTGGTT TCATTGCAAT GACCGTGGAA 1200  
 ACCTTCTCTA CTACGAAGTG ATGTGACTG GGAATCTTGG AATCCAGTGG AGGCATAAAC 1260  
 CAAATGTTGT TCTGTGTGAA AAGGAAAAAA ATAAACTGAA GCGGAAAAAA CTGGAATAA 1320  
 AACACAGAAA GGATGAGGAG AAAACAAGA TCCGGGAAGA GTGGAACAAT TTTCTTACT 1380  
 TCCTGAAAT CACTCACATT GTAATAAAG AGTCTGTGGT CAGCATTAA CAGCAGGACA 1440  
 65 ACAAGAAAAAT GGAACCTGAAG CTCTCTTCCC ACGAGGAGGC CTGTCTCTTT GTGTCCCTGG 1500  
 TAGATGGCTA CTTCGGGCTC ACAGCAGATG CCCATCATTA CCTCTGCACC GACGTGGCCC 1560  
 CCGGTTGAT CGTCCACAAC ATACAGAATG GCTGTCTATG TCCAATCTGT ACAGAATAAG 1620  
 CCATCAATAA ATTGCGGCAA GAAGGAAGCG AGGAGGGGAT GTACGTGCTG AGGTGGAGCT 1680  
 GCACCGACTT TGACAACATC CTCATGACCG TCACTGTCTT TGAGAAGTCT GAGCAGGTGC 1740  
 70 AGGGTGCCCA GAAGCAGTTC AAGAACTTTC AGATCGAGGT GCAGAAGGCG CGCTACAGTC 1800  
 TGCAACGGTTC GGACCGCAGC TTCCCCAGCT TGGGAGACCT CATGAGCCAC CTCAGAAGC 1860  
 AGATCTCTGG CACGGATAAC ATCAGCTTCA TGCTAAAAAG CTGTCTGCCAG CCAAGCCCC 1920  
 GAGAAATCTC CAACCTGCTG GTGGCTACTA AGAAGGCCA GAGATGGCAG CCGGTCTACC 1980  
 CCATGAGCCA GCTGAGTTTC GATCGGATCC TCAAGAAGGA TCTGGTGCAG GCGAGCACC 2040  
 75 TTGGGAGAGG CACGAGAACA CACATCTATT CTGGGACCTT GATGGATTAC AAGGATGACG 2100  
 AAGGAACCTC TGAAGAGAAG AAGATAAAG TGATCCTCAA AGTCTTAGAC CCCAGCCACA 2160  
 GGGATATTTC CTGCGCTTTC TTGAGGCGAG CCAGCATGAT GAGACAGGTC TCCACAAAC 2220  
 ACATCGTGTA CCTCTATGGC GTCTGTGTCC GCGACGTGGA GAATATCATG GTGGAAGAGT 2280  
 TTGTGGAAGG GGGTCTCTCT GATCTCTTCA TGCACGGAA AAGCGATGTC CTTACCAAC 2340  
 80 CATGGAAATT CAAAGTTGCC AAACAGCTGG CCAAGTCCCT GAGCTACTTG GAGGATAAAG 2400  
 ACCTGGTCCA TGGAAATGTG TGTAATAAAA ACCTCTCTCT GGCCCGTGAG GGCATCGACA 2460  
 GTGAGTGTGG CCCATTACAT AAGCTCAGTG ACCCGGCAT CCCCATTACG GTGCTGTCTA 2520  
 GGCAGGAATG CATTGAACGA ATCCCATGGA TTGCTCTGTA GTGTGTTGAG GACTCCAAGA 2580  
 ACCTGAGTGT GGCTGCTGAC AAGTGGAGCT TTGGAACAC GCTCTGGGAA ATCTGCTACA 2640  
 ATGGCGAGAT CCCCTTGAAA GACAAGACGC TGATTGAGAA AGAGAGATTG TATGAAGCC 2700

5  
10  
15  
20  
25  
30  
35  
40

```

GGTGCAGGCC AGTGACACCA TCATGTAAGG AGCTGGCTGA CCTCATGACC CGCTGCATGA 2760
ACTATGACCC CAATCAGAGG CCTTCTCTCC GAGCCATCAT GAGAGACATT AATAAGCTTG 2820
AAGAGCAGAA TCCAGATATT GTTTCAGAAA AAAAACCAGC AACTGAAGTG GACCCACAC 2880
ATTTTGA AAA GCGCTTCTTA AAGAGGATCC GTGACTTGGG AGAGGGCCAC TTGGGAAGG 2940
TTGAGCTCTG CAGGTATGAC CCCGAAGGGG ACAATACAGG GGAGCAGGTG GCTGTTAAAT 3000
CTCTGAAGCC TGAGAGTGGG GGTAACCACA TAGCTGATCT GAAAAAGGAA ATCGAGATCT 3060
TAAGGAACCT CTATCATGAG AACATTGTGA AGTACAAAGG AATCTGCACA GAAGACGGAG 3120
GAAATGGTAT TAAGCTCATC ATGGAATTTC TGCTTTCGGG AAGCCTTAAG GAATATCTTC 3180
CAAGAATAA GAACAAAATA AACCTCAAAC AGCAGCTAAA ATATGCGGTT CAGATTGTGA 3240
AGGGGATGGA CTATTGGGT TCTCGGCAAT ACGTTACCGG GGAATTGGCA GCAAGAAATG 3300
TCCTTGTGGA GAGTGAACAC CAAGTGA AAA TTGAGAGACT CGGTTTAACC AAAGCAATTG 3360
AAACCGATAA GGAGTATTAC ACGTCAAAG ATGACCGGGA CAGCCCTGTG TTTTGGTATG 3420
CTCCAGAATG TTTAATGCAA TCTAAATTTT ATATTGCTC TGACGCTGG TCITTTGGAG 3480
TCACTCTGCA TGAGCTGCTG ACTTACTGTG ATTGAGATTC TAGTCCCATG GCTTTGTTC 3540
TGAAAAGTAA AGGCCCAACC CATGCCAGA TGACAGTCAC AAGACTTGTG AATACGTTAA 3600
AAGAAGGAAA AGCGCTGCGG TGCCCACTTA ACTGTCCAGA TGAGGTTTAT CAACCTATGA 3660
GGAAATGCTG GGAATTCCAA CCATCCAATC GGACAAGCTT TCAGAACCTT ATTGAAGGAT 3720
TTGAAGCACT TTTAAATAA GAAGCATGAA TAACATTATA ATTCCACAGA TTATCAAGTC 3780
CTTCTCCTCG AACAAATGCC CAAGTCATTT TTTAAAAAT TCTAATGAAA GAAGTTTGTG 3840
TTCTGTCCAA AAGTCACTG AACTCATACT TCAGTACATA TACATGTATA AGGCACACTG 3900
TAGTGTCTGA TAGTGTGAAG GACTTCTCT TTAATTTGG TACCAGTAAC TTAGTGACAC 3960
ATAATGACAA CCAAAATATT TGAAAGCACT TAAGCACTCC TCCTTGTGGA AAGAATATAC 4020
CACCATTCA TCYGGCTAGT TCACCATCAC AACTGCATTA CCAAAAGGGG ATTTTGA 4080
ACGAGGAGTT GACCAAAATA ATATCTGAAG ATGATTGCTT TTCCTGCTG CCAGCTGATC 4140
TGAAATGTTT TGCTGGCACA TTAATCATAG ATAAAGAAAG ATTGATGGAC TTAGCCCTCA 4200
AATTTCAGTA TCTATACAGT ACTAGACCAT GCATTCTTAA AATATTAGAT ACCAGGTAGT 4260
ATATATTGTT TCTGTACAAA AATGACTGTA TTCTCTCACC AGTAGGACTT AAACCTTTGT 4320
TCCTCAGTGG CTTAGCTCTT GTTCTTGG GTGATCACTA GCACCATTT TTGAGAAAGC 4380
TGGTTCTACA TGGGGGGATA GCTGTGGAAT AGATAATTG CTGCATGTTA ATTCTCAAGA 4440
ACTAAGCCTG TGCCAGTCTT TTCCTAAGCA GTATACCTTT AATCAGAACT CATTCCCA 4500
ACCTGGATGC TATTACACAT GCTTTAAGA AACGTCAATG TATATCCTTT TATAACTCTA 4560
CCACTTTGGG GCAAGCTATT CCAGCACTGG TTTTGAATGC TGTATGCAAC CAGTCTGAAT 4620
ACCATATAG CTGCACTGTT CTTAGAGGGT TTCATACCT ACCACCGATC TACAGGGTT 4680
GATCCCTGTT TTTACCATCA ATCATCAGCC TGTGGTGCAA CACTTGAAAG ACCCGGCTAG 4740
AGGCACATG GACTTCAGGA TCCACTAGAC AGTTTTCAGT TTGCTGGAG GTAGCTGGGT 4800
AATCAAAAT GTTTAGTCTAT TGATTCAATG TGAACGATTA CGGTCTTAT GACCAAGAGT 4860
CTGAAAATCT TTTTGTATG CTGTTTAGTA TCTGTTTGTG ATTGTTACTT TTCACCTGTT 4920
GAGCCCAAT TCAGGATGTT TTCAGTGGCA GCAATGAAGT TGCCATTATA ATTGTTTCAT 4980
AGCCTACATC ACCAAGGTCT CTGTGTCAAA CCTGTGGCCA CTCTATATGC ACTTTGTTTA 5040
CTCTTATAC AATAAATAT ACTAAAGACT TT

```

Seq ID NO: B64 Protein sequence  
Protein Accession #: A39577

45  
50  
55  
60  
65

```

1 11 21 31 41 51
| | | | |
MQYLNIEDC NAMAFCAKMR SSKKTEVNLE APEPGVEVIF YLSDREPLRL GSGEYTAEEEL 60
CIRAAQACRI SPLCHNLPAL YDENTKLWYA PNRTITVDDK MSLRLHYMR FYFTNWHGTN 120
DNEQSVWRHS PKQKQNGYEK KKIIPDAPLL DASSLEYLFA QQQYDLVKCL APIRDPKTEQ 180
DGHDIENECL GMAVLAIASHY AMMKQMQLPE LPKDISYKRY IPETLNKSIR QRNLLTRMRI 240
NNVFDFLKE PNKLTICDSS VSTHDLKVYK LATLETLTGH YGAEIPETSM LLISSENNM 300
WHSNDGNGV LLYEYMTGNG LGIQWRHKPN VVSVEKEKNK LKRRKLEND KKDEEKNKIR 360
BEWNFSFPP EITHIVIKES VVSINKQDNK KMELKLSHE EALSFVSLVD GYFRLTADAH 420
HYLCTDVAPP LIVHNIQNGC HGPICTEYAI NKLRQEGSEE GMYVLWVSC DFDNIMLVT 480
CFEKSEQVQG AQRQKFNQI EVQKGRYSIH GSDRSFPLG DLMHLKKQI LRTDNISFML 540
KRCCQPKLE ISNLLVATKK AQEWQPVYPM SQLSPDRILK KDLVQGEHLG RGRTRHIYSG 600
TLADYKDEB TSEEKKIKVI LKVLDPSHRD ISLAPFEAAS MMRQVSHKHI VYLYGVCVRD 660
VENIMVEEFV EGGPLDLFMI RKSDVLTTPW KFKVAKQLAS ALSYLEDKDL VHGNVCTKNL 720
LLAREGIDSE CGPFIKLSDP GIPITVLSRQ ECIERIPWIA PECVEDSKNL SVAADKWSFG 780
TTLWEICYNQ EIPLKDKTLI EKERFYESRC RPTVPSCKEL ADLMTRCMY DPNQRPFFRA 840
IMRDINKLEE QNPDIIVSRKK NQPTVEDPTH FEKRFLKRIR DLGEGHFGK ELCRYDPEDN 900
TGEQVAVKSL KPESGGNHIA DLKKEIEILR NLYHENIVKY KGICTEDGDN GIKLIMEFLP 960
SGSLKEYLPK NKOKINLKQO LKYAVQICKG MDYLSRQYV HRDLAARNVL VESEHQVKIG 1020
DFGLTKALET DKEYYTVKDD RDSFVFWYAP ECLMQSKFYI ASDVWSFGVT LHELLTYCDS 1080
DSSPMALFLK MIGPTHGQMT VTRLVNTLKE GKRLPCFPNC PDEYVQIMRK CWEPQPSNRT 1140
SFQNLIEGFE ALLK

```

Seq ID NO: B65 DNA sequence  
Nucleic Acid Accession #: NM\_004867.1  
Coding sequence: 140..931

75  
80

```

1 11 21 31 41 51
| | | | |
GATCCAGAC CTCGGCTTGC AGTAGTGTTA GACTGAAGAT AAAGTAAGTG CTGTTTGGGC 60
TAACAGGATC TCCTCTTGCA GTCTGCAGCC CAGGACGCTG ATTCCAGCAG CGCCTTACCG 120
CGAGCCCGA AGATTCACTA TGGTGAAAAT CGCCTTCAAT ACCCTACCG CGGTGCAAAA 180
GGAGGAGGG CGGCAAGACG TGGAGGCCCT CCTGAGCCGC ACGGTCAAG CTCAGATACT 240
GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGAAGAGAG GGCTCCTCTG GGAGATGTAT 300
GCTTACTCTC TTAGGCCCTT CATTTCATCT GGCAGGACTT ATTGTTGGTG GAGCCTGCAT 360
TTACAAGTAT TTCAATGCCA AGAGCACCAT TTACCGTGGG GAGATGTGCT TTTTGTATTC 420
TGAGGATCCT CCAAAATCCC TTGCTGGAGG AGAGCCTAAC TTCTGCTCTG TGACTGAGGA 480
GGCTGACATT CGTGAGGATG ACAACATGTC AATCATTGAT GTGCCCTGCC CCAGTTTCTC 540
TGATAGTGAC CCGTGCAGCA TTATTCATGA CTTTGAAAAG GGAATGACTG CTTACCTGGA 600
CTTGTGTGCT GGGAACTGCT ATCTGATGCC CCTCAACTACT TCTATTGTGA TGCCCTCAAA 660

```

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

AAATCTGGTA GAGCTCTTTG GCAAACTGGC GAGTGGCAGA TATCTGCCTC AAACCTATGT 720  
GGTTGAGAAA GACCTAGTTG CTGTGGAGGA AATTCGTGAT GTTAGTAACC TTGGCATCTT 780  
TATTTACCAA CTTTGCAATA ACAGAAAGTC CTTCGCCTT CGTCGCAGAG ACCTCTTGCT 840  
GGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAACGAATT 900  
TATTGTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAAT 960  
AAGAAGTCAG AGATTTACAA TATGACTTTA ACATTAAGGT TTATGGGATA CTCAAGATAT 1020  
TTACTCATGC ATTTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080  
AA

Seq ID NO: B66 Protein sequence  
Protein Accession #: NP\_004858.1

1 11 21 31 41 51  
MVKIAFNTPT AVQKEEARQD VEALLSRTVR TQILTGKELR VATQEKEGSS GRCLMTLLGL 60  
SFILAGLIVG GACIYKYFMP KSTIYRGEMC PFDSEDPANS LRGGEPNPLP VTEEDADIRE 120  
DNIAIIDVPV PSFSDSDPAA ITHDFEKGMT AYLDLLLGNC YLMLPLNTSIV MPPKMLVELF 180  
GKLASGRYLP QTYVVRDELV AVEBIRDVS N LGIPYQLCN NRKSPRLRRR DLLLGFNKRA 240  
IDKCWKIRHF PNEFIVETKI CQE

Seq ID NO: B67 DNA sequence  
Nucleic Acid Accession #: XM\_083862.1  
Coding sequence: 121..813

1 11 21 31 41 51  
ACGCGGGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGCGATG 60  
CCTTGAACCT GGGAAACTAT GTGAAGCAAC ACTCTGGATT TTGAAGACA TCCTTTCATC 120  
ATGGGACAGC AAATTTCCGA TCAGACACAG TTGGTTATTA ACAAGTTACC AGAAAAAGTA 180  
GCAAAACATG TTACTGTTGT TCGAGAGAGT GGCTCCTTAA CTTATGAAGA ATTTCTCGGG 240  
AGAGTAGCTG AGCTTAATGA TGTAAACGGCT AAAGTGGCTT CTGGCCAGGA AAAACATCTT 300  
CTCTTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTT GGAAGTGGT TGTACGGGTG 360  
GTCTGTACCA AGATTAACAA AAGCAGTGGC ATTGTGGAGG CATCACGGAT CATGAATTTA 420  
TACCACTTTA TTCAACTTTA TAAAGATATC ACAAGTCAAG CAGCAGGAGT ATCGGCACAG 480  
AGCTCCACCT CTGAAGAACC TGATGAAAC TCATCTCTG TAACATCTTG TCAGGCTAGT 540  
CTTTGGATGG GAAGGTGAA GCAGCTGACC GATGAGGAGG AGTGTGTAT CTGTATGGAT 600  
GGGCGGGCTG ACCTCATCTT GCCTTGTGCT CACAGCTTTT GTGCAAGTG TATTGATAAA 660  
TGGAGTGATC GACACAGGAA TTGCCCTATT TGTCGCTAC AGATGACTGG AGCAATGAA 720  
TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACATAT TCTTAACATG 780  
CTGTATGAGG CAGGCCAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTGTCTA 840  
TTGTGGGCTC AATATTTTGG TCATGGGGGA AGAATGTAGG GTTGTGGCAC TGGCACAGAC 900  
ACAGGAAAT CCAATTTCCC CACTCTTTA TTTTGTCTAT TCTGATCAT TGTCCCCCTT 960  
TTAAAAATAA ACTTCCCATG TCTTCCAAA AAAAAAAAAA AAAAA

Seq ID NO: B68 Protein sequence  
Protein Accession #: XP\_083862.1

1 11 21 31 41 51  
MGQQLSDQIQ IVINKLPEKV AKHVLVRES GSLTYEEFLG RVARLNDVTA KVASGQEKHL 60  
LFEVQPGSDS SAFKVVVVRV VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120  
SSTSEEPDEN SSSVTSQAS LWMGRVKQLT DEEECCICMD GRADLILPCA HSFCQKCIDK 180  
WSDRHRNCPI CRLQMTGANE SWVVSADPTE DDMANYILNM ADEAGQPHRP

Seq ID NO: B69 DNA sequence  
Nucleic Acid Accession #: NM\_002975.1  
Coding sequence: 180..1151

1 11 21 31 41 51  
CGACCAACGG ACCGGACAGA GACGAGGAGA GGAACAGGAA GAGAGAAGCT GGGAGAATCG 60  
GGAACCTGGG GGCTAGTGAC CTGCACACAG GGCAGGGGCA CTGGCAGTT CCCAGAGGCC 120  
ACCCCTCCCA CCCAGACAT CCAGACATCT GGAACCTTGG GTGCCAAGAG TCCAGCTTAA 180  
TGCAAGCAGC CTGGCTTTTG GGGGCTTTGG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG 240  
GGGCTCGGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCAG GAGGAGGAGC 300  
GGGAGAGGGA GGCCCTGATG CTGAAGCATC TGCAGGAAGC CCTAGGACTG CTTGCTGGGA 360  
GGGGGGATGA GAATCTTGCC GGAACCTGTT AGGGAAAAGA GGAAGTGGAG ATGGAGGAGG 420  
ACCAGGGGGA GGAAGAGGAG GAGGAAGCAA CSCCAACCCC ATCCTCGGC CCCAGCCCTT 480  
CTCCACCCCT TGAGGACATC GTCACTTACA TCCTGGGCGG CCTGGCCGGC CTGGACGCAG 540  
GCCTGCACCA GCTGCACGTC CGTCTGCAG CGTTGGACAC CGCGTGGTTC GAGCTGACCC 600  
AGGGGCTGGG GCAGCTGGGG AACGGGGCAG GCGACACCCG CGATGCCGTG CAGCCCTGCG 660  
AGGAGGGCCA GGGTGGCGCC GAGGCGGAGC ACGGCGGCTT GGAGGGCTGC CTGAAGGGGC 720  
TGCGCTCTGG CCACAAGTGC TTCTGCTCT CGCGGACCT GGAAGCTCAG GCGGCGGCGC 780  
AGGCGCGGTG CAGGCTGGGG GCGGGGAGCC TGGCGCAGCC GGCAGACCGC CAGCAGATGG 840  
AGGCGCTCAC TCGGTACCTG CGCGCGGCGC TCGCTCCCTA CAACCTGGCC GTGTGGCTGG 900  
GGTGCACGTA TCGGGCGGCC GAGGGCCCTT ACCTCTTGA AAAACGCCAG CGCGTGTCTT 960  
TCTTCCGCTG GCATCGCTCA CCCGCGCCCG AGCTGGGCGC CCAGCCCGAG CCCTCGCGCG 1020  
ATCCGCTCAG CCCGAGCCAG CCCAACGGTG GCAAGCTCGA GAACTGCGTG GCGCAGGCTT 1080  
CTGACGACGG CTCTGGTGG GACCACGACT GCCAGCGGCG TCTCTACTAC GTCTGCGAGT 1140  
TCCCTCTCTA GCGGGGCGCG TACCCGCGCT CCTTGCCCAT CCCACCAACC GGCCCTTTCC 1200  
TGCGGCGTGC CACCCCTCTC CCGGAATGCG CCTTCCCTTC CTGGCCACGA ATGGCAGCGT 1260  
CCTCCCGGAC CCCAGTCTG GCGCTTCTG GAGGGGCTCT TGCGGTGCGC GCATCTCTCC 1320  
TTGTTAGTGT CTTTCTTTGA AGGGGCGGGC ACCAGGCTAG GTCCGGTGGC AATAAATCCT 1380  
TGTGAATCT GAAAAAATAA AAAAAA

Seq ID NO: B70 Protein sequence  
Protein Accession #: NP\_002966.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MQAANLLGAL VVPQLLGFGH GARGAEREWE GGWGGAEQEE REREALMLKH LQEALGLPAG 60
RGDENPAGTV EGKEDWEMEE DQGEDEEEEA TPTPSSGPSP SPTPEDIVTY ILGRLAGLDA 120
GLHQLHVRHL ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGLCKG 180
10    LRLGHKCFLL SRDFAQAAA QARCTARGGS LAQPADRQOM EALTRYLRAA LAPYNWFWVL 240
GVHDDRRAEGL YLFENGQKRS FFAWHRSPRP ELGAQPSASP HPLSPDQPNG GTLENCVAQA 300
SDDGSWWDHD CQRRLYYVCE PPF

```

Seq ID NO: B71 DNA sequence  
Nucleic Acid Accession #: BC000839.1

```

15      1      11      21      31      41      51
      |      |      |      |      |      |
CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG 60
20    TGGGGCTTTG TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGSTCCCCC TTCCTATGAT 120
GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AAGTAACCTC GAGGAGATGG 180
GCCCTGCAAG CCTCTCTCTT AGCGTCTGTG TCAGAAAATA GCGTTTTCGA AATGCCCTGA 240
GTTGACCTAA TGCTCTATTG GGCCTCTGTC TGCAGGATTI ACGGCAAGT TGGAAACGAA 300
25    GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA 360
GACCCATCTT TATGCAAAAG CAGCGTTACA GTAATGTTC AGCATCTCAT AATCTATCCT 420
GGGGAATCCA GCTGCCTCCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCCTCTAT 480
CTTACAGAGC AGCTTGTGTC TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC 540
TAACCAATAA CCTGCTTGCC TCAAGGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
30    TTGAGGAAAA CTAGGTGTCT GTGTTCACTC CAGGCTGAAG TTACAGGTCT GAGCAATAAA 660
GGTGATATAA AATGGAATC TGTCTGGAG GACATCAGAA GGTGAATTTT CCAAGTCTCT 720
GGACAACCTA GCTGTTGAAA AGCTTCTGCG GTTTGGGGGG TATTTCAGAT GTACCTTAAA 780
GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGTTTGCT 840
GTGTATCACA TTCTGTATT TTATCACCCC CTTCCTGCAA CATTATTAT CTGGAATCTA 900
35    CCTGCCCTTT TGTTTTITAG ATACAAGGGC TTGGTTTTGT TACCCAGGCT GGTTTCAAGG 960
CCATAGCTTT AAGAGATCCT CTCACCACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
TTCATGSCAC CCAGACTTTG CTGCCTTTCT TACATGATCC AGGCCAGAA CCCAACTCA 1080
GGCACTGTAT AGATGACCAC TTCTGTAAAC TACTGACCTA GCTTGTGCC AATTGTTGAT 1140
TGAATCTCCC ATAACCTCAC TTCGTGCTG TTCTCTGTA TACAGCCACC TTCTGTTCCC 1200
40    GTCATGAGCC TTAGGTCTC CATTGTCATA TTGCAATAC TATGTTCCAT GTAGGTAGCT 1260
CAITCAGGGC CTGCTCTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCATTTG 1320
TGTGCTGTG TTGTTGTTG ATGAAAAATA TAAATGATT GATTACATA AAAAAAATAA 1380
AAAAAAA

```

Seq ID NO: B72 DNA sequence  
Nucleic Acid Accession #: CAT cluster

```

45      1      11      21      31      41      51
      |      |      |      |      |      |
TGCTAGTAGG GCCTGGGTTA ATGCGCCGAG GGTGGCTTGG TGGTCTTTAT AGCTGTACT 60
50    CTTTGTACTT GTCTTTTCT TTTATTTCT TTTGAGCGAT TGTGGGAACA TAGCATAGCA 120
CGCACTATGG CACGAGGCTC GTGCTGCTG GCCAGGGGGA CTGGCGGATA AGGTCTTGTG 180
CGTGGCCTCG AGGCTTAAAA GTAGCAGTGG GGCCTTTGTA AGGACAAAAT GGCAGTGGCG 240
GGCCGTGTAG GTCCCCCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG 300
55    TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTCTC 360
GAAAATAGCG TTTTGAATAT GCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC 420
AGGATTTAGC CGCAGCTTGG AACCGAAGAG AGCTCTGTTG TTGCAATGTT CAGCCCAACA 480
GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCAAGCCAG CGTTACAGTA 540
ATGTTCCAGC ATCTCATAAT CTATCTGCGG GAATTCAGCT GCCTCCAGG GTGAATACAG 600
GTATTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGCTGTG TTCACTCCAG 660
60    AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC 720
ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGCTGTG TTCACTCCAG 780
GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAAATCTG CTGGAAGGAC 840
ATCAGAAGGT GAATTTTCCA AGTCTTGGG CAACCTAGCT GTTGAAAGC TTTCTGGGTT 900
65    TGGGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAAAG CACTGGGAGC 960
CAATGAAACA GCAGTTGAGG GTTGTCTGTG TATCACATTT CTGTATTTTA TCACCCCTTT 1020
CCTGCAACAT TATTATCTG GAATCTACCT GGCCTTTTGT TTTTATAGATA CAAGGGCTTG 1080
GTTTGTGTAC CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
TCCAAAGTGC TGGGATTGCA GGTGTGATTG ATGGCACCCT GACTTGTCTG CCTTCTTAC 1200
70    ATGATCCAGG CCCAGAACCC AAAGTCAGGC ACTGTATAGA TGACCACTTT CGTAAACTAC 1260
TGACCTAGCT TGTGTCGAAT TGTGATGTA ACTTCCATA ACTCCACTTC GTGTCTGTTC 1320
CTCTGTATAC AGCCACCTTC TGTTCCTGTC ATGAGCCTTT AGGTCTCCAT TTGCATATTG 1380
CAATATCTAT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG 1440
TTCCCTTGAG GACTGSGCTG CAATTTGTGT TGCTGTGTG GTGTGTGATG AAAATAATAA 1500
75    AATGATTGAT TACATAAAAA AAAAAAATAA AAAAAAATAA CAAAAAATAA 1560
CGCGCGCTT TTCCCGGGC GCACAAAGTT ATAAACGCC GTCCATC

```

Seq ID NO: B73 sequence  
Nucleic Acid Accession #: NM\_000222.1  
Coding sequence: 22..2952

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGGGGCG CTTGGGATTT TCTCTGCGTT 60
CTGCTCTTAC TGCTTCGCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120

```

	CCGTCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGCACCTGA	TCCGGGCTTT	GTCAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACACGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCCAAGC	TTTTCTTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCACAGA	CCCAGAAAGT	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGGCAT	CATGATCAAA	540
	AGTGTGAAC	GCGCTACCA	TGGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGCTGT	CGGAAAAATT	CATCTGAAA	GTGAGGCCAG	CCTTCAAAGC	TGTGCTCTGT	660
	GTGTCTGTGT	CCAAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTAC	AGTGACGTGC	720
	ACAATAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAAAGTGGG	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTACAGGA	840
	ACGTGACTA	TCAGTTCAGC	GAGAGTTAAT	GATTCTGGAG	TGTTTATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACAACA	ACCTTGAAG	TAGTAGATAA	AGGATTCAAT	960
	AAATATCTCC	CCATGATAAA	CACATACAGT	TTTGTAAACG	ATGGAGAAAA	TGTAGATTGG	1020
	ATTGTTGAAT	CAATGATGAT	CCCCAAACCT	GAACACCAGC	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAGTAA	TATCAGATAC	1140
	GTAAGTGAAC	TTTATCTAAC	GAGATTAAAA	GGCACCAGAG	GAGCACTTAA	CACATTCTTA	1200
20	GTGTCCAATT	CTGACGTCAG	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAATCTCTGA	CTTACGACAG	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTC	1320
	CCAGAGCCCA	CAATGATGAT	GTATTTTGT	CCAGGAACCT	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGATGTGCA	GACACTAAAC	TCACTGCGGC	CACCGTTTGG	AAAGCTAGTG	1440
	GTTCAGAGTT	CTATAGATTC	TAGTGCATT	AAGCACAATG	GCACGGTTGA	ATGTAAGGCT	1500
25	TACAACGATG	TGGGCAAGAG	TTCTGCCTAT	TTTAACTTTG	CATTTAAAGG	TAACACACAA	1560
	GAGCAATCC	ATCCCCACAC	CCTGTTCACT	CCTTTGCTGA	TGTGTTTCTG	AATCGTAGCT	1620
	GGCATGATGT	GCATTTATTG	GATGATTCTG	ACCTACAAAT	ATTTACAGAA	ACCCATGTAT	1680
	GAAGTACAGT	GGAGGTTTGT	TGAGGAGATA	AATGGAAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAACCTC	CTTATGATCA	CAAATGGGAG	TTTCCCAGAA	ACAGGCTGAG	TTTGGGAAAA	1800
30	ACCTGGGTG	CTGGAGCTTT	CGGGAAGGTT	GTTGAGGCAA	CTGCTTATGG	CTTAATTAAG	1860
	TCAGATGCGG	CCATGACTGT	CGCTGTAAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGGAAGCCG	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TTGGAATATCA	CATGAATATT	1980
	GTGAATCTAC	TTGAGGCGTG	CACCATTTGA	GGGCCACCCC	TGGTCATTAC	AGAATATTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTGAGA	AGAAAACGTG	ATTCAATTAT	TGTGTCAAAG	2100
35	CAGGAAGATC	ATGCAGAAGC	TGCACCTTAT	AAGAATCTTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCCG	ACAAAGGAGG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCCGCCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAGGTGG	CAAAGGGCAT	GGCTTTCCTC	GCCTCCAAGA	ATTGTATTCA	CAGAGACTTG	2400
40	GCAGCCAGAA	ATATCCTCCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTTGGTCTA	2460
	GCCAGAGACA	TCAAGAATGA	TTCTAATTAT	GTGGTTAAAG	GAAACGCTCG	ACTACCTGTG	2520
	AAGTGACATG	CGGCTGAAAG	CATTTTCAAC	TGTGTATACA	CGTTTGAAG	TGACGTCTGG	2580
	TCCTATGGGA	TTTTTCTTTG	GGAGCTGTTT	TCCTTAGGAA	GCAGCCCCCTA	TCTTGGAAATG	2640
	COGTCGATTT	CTAAGTTCTA	CAAGATGATC	AAGGAAGGCT	TCCGATGCT	CAGCCTGAA	2700
45	CACGCACTGT	CTGAATGTGA	TGACATAATG	AAGACTTGCT	GGGATGCAGA	TCCCCTAAAA	2760
	AGACCAACAT	TCAAGCAAA	TGTTGAGCTA	ATTGAGAAGC	AGATTTCAGA	GAGCACCAAT	2820
	CATATTACT	CCAGCTTAGC	AAACTGCAGC	CCCAACCGAC	AGAAGCCCGT	GGTAGACCAT	2880
	TCTGTGCGGA	TCAATTTCTG	CGGCAGCACC	GCTTCTCCT	CCCAGCCTCT	GCTTGTGCAC	2940
	GACGATGCT	GAGCAGAATC	AGTGTTTGGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCTTCCATGA	TGGTTATTTT	CTTTTCTTTC	AACTTGCATC	CAACTCCAGG	ATAGTGGGCA	3060
	CCCCACTGCA	ATCCGTCTCT	TCTGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTCATCAGC	3120
	CACCATCTCA	TTGCAAGGTT	TCCAACCTGA	TATATTCCCA	ATAGCAACGT	AGCTTCTACC	3180
	ATGAACAGAA	AACATTCTGA	TTTGGAAAAA	GAGAGGGAGG	TATGACTGAG	GGGCCAGAGT	3240
	CCTTTCCAAG	GCTTCTCCAA	TTCTGCCCAA	AAATATGGTT	GATAGTTTAC	CTGAATAAAT	3300
55	GSTAGTAATC	ACAGTTGGCC	TTCAGAACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
	AGCTGAAAC	CTAAGTCTCT	TATGTGGAAA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAAG	AATCTAGTAT	TTTATGCTGG	GAATGAGACA	TAGGCCATGA	3480
	AAAAATGAT	CCCCAAGTGT	GAACAAAAGA	TGCTCTTCTG	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGGTTTT	TAAATAGAGT	TTGCTATTAG	AGCATTGAAT	TGGAGAGAAG	3600
60	GCCTCCCTAG	CCAGCACTTG	TATATACGCA	TCTATAAATT	GTCGTTGTTT	ATACATTGTA	3660
	GGGGAACAA	CCATAAGGTT	TGTTTCTGT	ATACAACCTT	GGCATTATGT	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACAG	TTAATACCAT	TTTTAAGGA	3780
	AACAATATAA	CCACAAGCA	CAGTTGAAC	AAAATCTCCT	CTTTAGCTG	ATGAACCTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAATG	GCATTGTACT	CAATGGATT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCAC	GCATGGCTCC	CACAGGAGTG	GGMAAACACT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAAATAAAGT	ATAGGTTTAG	CCTCCTTCGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTACGTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGGCCC	TGAGTCCAAG	AGGGTCTTCT	AGTACCTGAA	4140
	AAGTAACTTG	GCTTTCATTA	TTAGTACTGC	TCTTGTCTCT	TTTACATAG	CTGTCTAGAG	4200
70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCACTTC	ACCTGCACTT	AAGGCACCTT	GTTATTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTTAGACT	4380
	GTAGCCTGGA	TATTATTCTT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
	AACTCCCCCT	CCTCAGTCCC	CAATATAAAA	GGCAAAATGT	TACATGGCAG	AGTTTGTGTG	4500
75	TGTCCTTGAA	AGATTTCAGG	ATGTTGCCTT	TATGGTTTCC	CCCTTCTACA	TTTCTTAGAC	4560
	TACATTATAGA	GAACGTGGGC	CGTTATCTGG	AAGTAACCAT	TTGCACTGGA	GTTCTATGCT	4620
	CTCGCACTT	TCCAAAGTTA	ACAGATTTTG	GGGTTGTGTT	GTACCCCAAG	AGATTGTTGT	4680
	TGCCCATACT	TGTCCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4800
80	TTGCCATACT	TTGCTGAGAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4920
	AATGCTTTTT	GAATATTCCC	AAGCCCATGA	GTCCTTGAAA	ATATTTTATA	TATATACAGT	4980
	AACTTTATGT	GTAAATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
	TTATTCCTGT	ATGTTGTCCA	ATTGTTGACA	GTCTGAAGA	ATTC		

Seq ID NO: B74 protein sequence  
Protein Accession #: NP\_000213.1

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MRGARGANDF LCVLLLLLRV QTGSSQPSVS PGEPSPPSIH PGKSDLIVRV GDEIRLLCTD 60
PGFVKNTFEI LDETENKNQN EWITEKAEAT NTGKYCTCNK HGLSNSIYVF VRDPAKFLFV 120
DRSLYKEDN DTLVRCPLTD PEVTNYSKLG CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAPKA VPVVSVKAS YLLREGEFT VTCTIKDVSS 240
SVYSTKREN SQTKLQEKYN SWHHGDFNFE RQATLTISSA RVNDSGVFMC YANNTFGSAN 300
VTITLEVVDK GFNIIFPMIN TTVFVNDGEN VDLIVEYEF PKPEHQWIY MNRTFTDKWE 360
DYPKSENESE IRYVSELHLT RLKGTGEGTY TFLVNSDVN AALAFNVYVN TKPEILTYDR 420
LVNGLQCVQA AGFPEPTIDW YFCPTGEQRC SASVLPVDVQ TLNSSGPPFG KLVVQSSIDS 480
SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIEPHT LFTPLLIGFV IVAGMMCIIV 540
MILTYKYLQK PMYEQWQVW EEINGNNTYV IDPTQLPYDH KWEFFRNRLS FGKTLGAGAP 600
TKVVEATAYG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLSYLGNH MNIVNLLGAC 660
TIGGPTLVIT EYCCYGDLLN FLRRKRDSPI CSKQEDHAEA ALYKILLHSE ESSCSDSSTNE 720
YMDMKPGVSY VVPTKADKRR SVRIGSYIER DVTPAIMEDD ELALDLEDDL SFSYQVAKGM 780
AFLASKNCHL RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPE 840
IFNCVYTFES DVWSYGIWLF ELFSLGSSPY PCMPVDSKPY KMIKEGFRML SPEHAPAE 900
DIMKTCDWAD PLKRPFTKQI VQLIEKQISE STNHIYSNLA NCSPNRQKPV VDHVSIRINSV 960
GSTASSSQPL LVHDDV

```

Seq ID NO: B75 DNA sequence  
Nucleic Acid Accession #: NM\_004456  
Coding sequence: 58..2298

```

30      1      11      21      31      41      51
|      |      |      |      |      |
GAATTCGGGG CGACGCGCGG GAACAACGCG AGTCGGCGCG CGGGACGAAG AATAATCATG 60
GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTTGTG GCGGAAGCG TGTAAAATCA 120
GAGTACATGC GACTGAGACA GCTCAAGACG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCA ATCGTCAGAA AATTTTGGA AGAACGGAAT TCCTAAACCA AGAATGGAAA 240
CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 300
GAGTGTTCGG TGACAGTGA CTGTGATTTT CCAACACAAG TCATCCCAT TAAAGACTCTG 360
AATGCAGTTG CTTCACTACC CATAATGTAT TCTTGGTCTC CCCTACAGCA GAATTTTATG 420
GTGGAAGATG AAAGTGTTTT ACATAACATT CCTTATATGG GAGATGAAGT TTTAGATCAG 480
GATGTACTCT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAGTACA CGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAATTTTGT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAGCAGAGAA 660
GATCTGGAGG ATCAGCGAGA TGATAAGAA AGCCGCCAC CTCGAAAT TCCTCTGAT 720
AAAAATTTGG AGGCCATTTT CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAATAAAG 780
GAAAAATATA AAGAACTCAC CGAACAGCAG CTCCAGGCG CACTTCTCC TGAATGTACC 840
CCCAACATAG ATGGACAAA TGCTAAATCT GTTCAGAGAG AGCAAGCTT ACCTCCTTT 900
CATAGCTTTT TCTGTAGCGG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTATGCA 960
ACACCCAACA CTTATAAGCG GAAGAACA CAACAGCTC TAGACAACA ACCTTGTGGA 1020
CCACAGTGTT ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCACACAAA ACGTCCAGGA GCGCGCAGAA GAGGACGGCT TCCCAATAAC 1140
AGTAGACAGG CCAGCACCCC CACCATTAA TGTCTGGAAT CAAAGGATAC AGACAGTGAT 1200
AGGGAAGCAG GGAATGAAC GGGGGGAGAG AACAATGATA AAGAAGAAGA AGAGAAGAAA 1260
GATGAAACTT CGAGCTCTCT TGAAGCAAA TCTCGTGTCT AAACACCAAT AAAGATGAAG 1320
CCAAATATTG AACCTCTGTA GAATGTGGAG TGGAGTGGTG CTGAGCCTC AATGTTTGA 1380
GTCTCTATTG GCATCTACTA TGACAATTTC TGTGCCATTG CTAGGTTAAT TGGACCAAA 1440
ACATGTAGAG AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
GCTGAGGATG TGGATCTCC TCCAAGGAAA AAGAAGAGGA AACACCGGT GTGGGCTGCA 1560
CACTGCAGAA AGATACAGCT GAAAAGGAG GGCCTCTCTA ACCATGTTTA CAACTATCAA 1620
CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTGCTGCC CTGTGTGAT AGCACAATA 1680
TTTTGTGAAA AGTTTGTGTA ATGTAGTTCA GAGTGTCAAA ACGCTTTCC GGGATGCCG 1740
TGCAAGCAC AGTGCAACAC CAAGCAGTGC CGTGCTACC TGGCTGTCG AGAGTGTGAC 1800
CCTGACTCT GTCTTACTTG TGGAGCCGCT GACCATGGG ACAGTAAAAA TGTGCTCTG 1860
AAGAACTGCA GTATTACAGG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGAOCTG 1920
GCAGGCTGGG GGAATTTTAT CAAAGATCCT GTGCAGAAA ATGAATTCAT CTCAGAATAC 1980
TGTGGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTA TGATAAATAC 2040
ATGTGCAGCT TTCTGTTCAA CTTGAACAA TATTTGTGG TGGATGCAAC CCGCAAGGT 2100
AACAAAATTC GTTTTGCAAA TCATTGCGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCACAGGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCG CATCGAAGA 2280
GAAATGGAAA TCCCTTGACA TCTGCTACCT CCTCCCTCT CTTGAAACA GCTGCCTTAG 2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGT TGAATTTCTG 2400
AATTTGCAAA GACTGTGAAG AATAATTTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCCTCTCAC CAGCTGCAAA GTGTTTGTGA CAGTGAATT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAATTTGAA AAAAAAATA AAAAAA

```

Seq ID NO: B76 Protein sequence  
Protein Accession #: NP\_004447

```

80      1      11      21      31      41      51
|      |      |      |      |      |
MQQTGKKEK GPVCRKRKVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL ERTILNQEW 60
KQRIQPVHII LTVSSSLRGT RECSVTSDDL PPTQVPLKLT LNAVASVPLM YSWSPQLQNF 120
MVEDETVLHN IPYMGDEVLD QDGTFFIELI KNYDGKVDGD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDPEEREKEQ KLEHHRDDK ESRPPRKFPK DKILEALISM FPDKGTADEL 240
KEKYKELTEQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRCP KYDCFLHPH 300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GRRRRGLPN 360

```



NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEEEK KDETSSSSEA NSRCQTPIMM 420  
KPNIEPPENV ENSGAEMSMF RVLIGTYIDN FCAIARLIGT KTCRQVYEFR VKESSIIAPA 480  
PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPVIAQ 540  
NPCEKFCQCS SEQNRFPFGC RCKAQCNKQK CPCYLAVREC DPLCLTCCGA ADHWDKSNVS 600  
CKNCSIQRGS KKHLLLPSPD VAGWGIFIKD PVQKNEFISE YCGEIIISQDE ADRRGKVYDK 660  
VMCSFLEFNLN NDFVVDATRK GNKIRFANHNS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720  
ELFVDYRYSQ ADALXYVGIE REMEIP

Seq ID NO: B77 DNA sequence  
Nucleic Acid Accession #: NM\_007015  
Coding sequence: 1..1005

1 11 21 31 41 51  
| | | | |  
15 ATGACAGAGA ACTCCGACAA AGTTCGCCATT GCCCTGGTGG GACCTGATGA CGTGAATTC 60  
TGCAGCCCC CGGCGTAGCG TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120  
AAGGTGGGAG CCGTGGTCTT CATTCGGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180  
GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240  
ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300  
20 TTTAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCGA GAATGGCATC 360  
ACAGGAATTC GTTTTGTCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420  
ATTCTGTAGG TGGGCGCCCT GACCAACAG AGCATCTCCT CCAACTGGA AGGCAAGATC 480  
ATGCCAGTCA AATATGAAGA AAATTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540  
GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTTCTGG 600  
25 CTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660  
GTCCCAACTA CCACAAAAG ACCACACAGT GGACCAAGGA GCAACCCAGG CGCTGGAAGA 720  
CTGAATAATG AAACAGAGCC CAGTGTTCAG GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780  
CCTTATCATC AGCAGGAAGG GGAAGCATG ACATTGAGC CTAGACTGGA TCACGAAGGA 840  
ATCTGTGTTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900  
30 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960  
ATCCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT 1020  
CAGTGTCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTG 1080  
ATGCTGATGG GACCATAAAA TATTTTACAA CGCAGCCTGA GCGGTTATTC TTGCACTCT 1140  
TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAAATGCA CTGAAAGGGT 1200  
35 AGTTCAAGTC TAAATGCCA TAAACCCGTT ATTTGTTATT TTTTATTTCG ATTGATTTCG 1260  
CATAAGTCTT CCCTTGCTTG CATCTTCAA AGCTATTTCG AAATAAACAC GAAATTTAC 1320  
AGTTTGCC

Seq ID NO: B78 Protein sequence  
Protein Accession #: NP\_008946

1 11 21 31 41 51  
| | | | |  
45 MTENSDKVP I ALVGDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60  
AFYFWKSDS HIYNVHYTMS INGKLQDGS EIDAGNNLET FRMGSGAEZA IAVNDFQNGI 120  
TGIRPAGGEK CYIKAKVKAR IPEVGAVTKQ SISKLEGGI MPVKYEENSL IWVAVDQPVK 180  
DMSFLSSKVL ELCDGLPIFW LKPTYPKEIQ RERREVRKI VPTTTRKPHS GPRSNPGAGR 240  
LNNETRPVSQ EDSQAFNPDN FYHQEGESM TFDPRLDHEG ICCIECRSY THQKICEPL 300  
50 GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: B79 DNA sequence  
Nucleic Acid Accession #: NM\_012449.1  
Coding sequence: 66..1085

1 11 21 31 41 51  
| | | | |  
55 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60  
AATTAATGGA AAGCAGAAA GACATCACAA ACCAAGAAGA ACTTTGGAAG ATGAAGCCTA 120  
GGAGAAATTT AGAAGAAGAC GATTATTGCG ATAAGGACAC GGGAGAGACC AGCATGCTAA 180  
60 AAGACCTGT GCTTTTGCAT TTGCACCAA CAGCCCATGC TGATGAATT GACTGCCCTT 240  
CAGAACTTCA GCACACACAG GAATCTTTC CACAGTGCCA CTTGCCAATT AAAATAGCTG 300  
CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTCTGAG GGAAGTAATT CACCTTTAG 360  
CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTATCAAC AAAGTCTTGC 420  
CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480  
65 TCCAACCTTA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540  
TAACAAGAAA GCAGTTTGGG CTTCTCAGT TCTTTTTCG TGTACTGCAT GCAATTTATA 600  
GTCTGTCTTA CCCAATGAGG CGATCCCTACA GATACAAGTT GCTAACTGG GCATATCAAC 660  
AGGTCCAACA AAATAAGAA GATGCCCTGA TTGACCATGA TGTTTGGAGA ATGGAGATT 720  
ATGTGTCTCT GGGAAATGTG GGATGGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780  
70 CATCTGTAGG TGACTCTTTG ACATGGAGAG AATTTCACCTA TATTCAGAGC AAGCTAGGAA 840  
TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCTGGAAT AAGTGGATAG 900  
ATATAAACA ATTTGTATGG TATACACCTC CACTTTTAT GATAGCTGTT TTCCTTCAA 960  
TTGTTGTCCT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA 1020  
75 AGATTAGACA TGGTTGGGAA GACGTACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080  
TGTAAGATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140  
TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence  
Protein Accession #: NP\_036581.1

1 11 21 31 41 51  
| | | | |  
80 MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60  
LQHTQELFPQ WHPPIKIAAI IASLTFLYTL LREVIHPLAT SHQYFYKIP ILVINKVLPM 120

VSITLLALVY LPGVIAAIVQ LHNQTKYKKP PHWLDKWLMT RKQFGLLSFF FAVLHAIYSL 180  
 SYPMRRSYRY KLLNWAYQQV QONKEDAWIE HDVWRMEIVV SLGIVGLAIL ALLAVTSIPS 240  
 VSDSLTWREF HYIQSKLGIV SLLGTIHAL IFANNKWIDI KQFVWYTPPT FMAVFLPIV 300  
 VLIFKSILEFL PCLRKKILKI RHGWEDVTIKI NKTEICSQL

Seq ID NO: B81 DNA sequence  
 Nucleic Acid Accession #: NM\_000684  
 Coding sequence: 87..1520

1 11 21 31 41 51  
 TGCTACCCCG GCCCGGGCTT CTGGGGTGTG CCCCAACCAC GGCCACAGCC TGCCACACCC 60  
 CCCGCCCCCG GCCTCCGAG CTGCGCATGG GCGCGGGGT GCTCGTCTG GCGCCTCCG 120  
 AGCCCGGTAA CCTGTCTCG GCGCACCAG TCCCAGACGG CGCGCCACC GCGCGCGGC 180  
 TGCTGGTGCC CGCGTCCCG CCGCCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCCGAGC 240  
 CGCTGTCTCA CGAGTGGACA GCGGGCATGG GTCTGCTGAT GGCGCTCATC GTGCTGCTCA 300  
 TGTGGCGGG CAATGTCTG GTGATCGTGG CCATCGCCAA GACCGCGCG CTGCAGACGC 360  
 TCACCAACCT CTTTCATATG TCCCTGGCCA GCGCGACCT GGTGATGGG CTGCTGGTGG 420  
 TGCCGTTCGG GGCCACCATC GTGGTGTGG GCGCTGGGA GTACGGCTCC TTCTTCTGCG 480  
 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540  
 TTGCCCTGGA CGCTACCTC GCCATCACCT CGCCTTCCG CTACCAAGAG CTGCTGACGC 600  
 GCGCGCGGG GCGGGGCTC GTGTGACCG TGTGGCCAT CTGCGCCCTG GTGCTCTTCC 660  
 TGCCCATCT CATGCACTG TGGCGGCGG AGAGCGACGA GCGCGCGCG TGCTACAACG 720  
 ACCCAAGTG TGGCACTTC GTACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT 780  
 CCTTCTACGT GCCCTGTGC ATCATGGCCT TCGTGTACCT GCGGGTGTG CCGCAGGCCC 840  
 AGAAGCAGTG GAAGAAGATC GACAGCTGCG AGCGCGGTT CCGCGCGCG CCAGCGCGGC 900  
 CGCCTCGCC CTGCGCCTC CCGTCCCG GCGCGCGCC GCGCGCGGA CCGCGCGCC 960  
 CCGCGCGCG CCGCGCCAC GCGCGCTGG CCAACGGGG TGGGGTAA GCGCGCGCT 1020  
 CGCGCTCGT GGCCCTACGC GAGCAGAAG CGCTCAAGAC GCTGGGCATC ATCATGGCGG 1080  
 TCTTCAACGT CTGCTGGCTG CCTTCTTCT TGGCCAACGT GGTGAAGGC TTCCACGCG 1140  
 AGCTGGTGG CGACCGCCTC TCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCT 1200  
 TCAACCCAT CATCTACTG CGCAGCCCG ACTTCCGCA GGCCTTCCG GACTGTCTCT 1260  
 GCTGCGCGG CAGGGCTGCC CCGCGCGCC ACGGACCCA CGGAGACCG CCGCGCGCT 1320  
 CGGGCTGTCT GCGCGCGCC GGACCCCGC CATCGCCCG GCGCGCTCG GACGACGAG 1380  
 ACGAGCATGT CGTGGGGCC ACGCGCGCG CGCGCTGCT GGAGCCCTG GCGCGCTGCA 1440  
 ACGCGGGGG GCGCGGGAC AGCGACTCGA GCCTGGACGA CCGGTGCGC CCGGCTCG 1500  
 CCTCGAATC CAAGTGTAG GCGCGCGC GGGCGCGGA CTCGGGCAC GGTCTCCAG 1560  
 GGGAAAGAG AGATCTGTG TTACTTAAGA CCGATAGCAG GTGAATCGA AGCCCAAT 1620  
 CTCGTCTGA ATCATCGAG GCAAAGAGAA AAGCCACGA CGTTGCACA AAAAGGAA 1680  
 TTTGGGAGG GATGGAGAG TGGCTGTG ATGTTCCTG TTG

Seq ID NO: B82 Protein sequence  
 Protein Accession #: NP\_000675.1

1 11 21 31 41 51  
 MGAGVLVGA SEPNLSSAA PLEDGAATAA RLLVPASPPA SLLPPASESP EPLSQWNTAG 60  
 MGLMALIVL LIVAGNVLVI VAIKTPRLQ TLNLFIMSL ASADLVMGLL VVPFGATIVV 120  
 WGRWEYGSFP CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSL TRARAGLVC 180  
 TVWALSALVS FLPLMHWRW AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240  
 AFVYLRVFE AQKQVKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAATAP 300  
 LANGRACKRR PSRLVALREQ KALKTLGIIM GVFTLCWLEP FLANVVKAFH RELVPRDLFV 360  
 FFWNLGYANS AFNPIIYCRS PDERKAFQGL LCCARRAARR RHATHGDRPR ASGLARPGP 420  
 PPSPGAASDD DDDVVGATP PARLLEPWAG CNGGAADSD SSLDEPCRFG PASESKV

Seq ID NO: B83 DNA sequence  
 Nucleic Acid Accession #: NM\_000729.2  
 Coding sequence: 2..421

1 11 21 31 41 51  
 GGCTCAGCTG CCGGGCTGCT CCGGTGGAA ACGCCAAGCC AGCTGCGTCT CTAATCCAAA 60  
 AGCCATGAAC AGCGCGTGT GCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCT 120  
 GACGACGCG GTGCTCCCG CAGATCCCG GGGCTCGGG CTGCAGCGG CAGAGGAGC 180  
 GCGCCGTAGG CAGCTAGGG TATGCGAGAG AACGGATGG GAGTCCGAG CGCACTGGG 240  
 CGCCCTGCTG GCAAGATACA TCCAGCAGG CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300  
 CGTTAAGAAC CTGCAGAAC TGGACCCAG CCACAGGATA AGTGACCGGG ACTACATGG 360  
 CTGGATGGAT TTTGGCGCTC GCAGTGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420  
 GCGCCATCA GCGCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAA AAGACAACAA 480  
 TCACACTCAT AACTATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540  
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCACTGCAAC CACACAGCT CACCAGAAGT 600  
 TGTGCAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660  
 TATGCTATTA AAGGATTTC ATTCGTC

Seq ID NO: B84 Protein sequence  
 Protein Accession #: NP\_000720.1

1 11 21 31 41 51  
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRLRVSQRT DGESRAHLGA 60  
 LLARYIQQAR KAPSGRMSIV KNLQNLDP SH RISDRYMGW MDFGRSAEE YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	<b>A1 DNA SEQUENCE</b>	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Gene name:	Hs.154210
	Unigene number:	M31210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	251-1396
	Coding sequence:	
15	TCTAAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCGG TACAGATCCC GGGCTCTCCG	60
	AACGCAACTT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA	120
	AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT	180
	CTCGCTCGC CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CGGCTTCTCT GGGGACACAG	240
	GGTTGGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCACCGCA GCTCGGTCTC	300
	TGACTAGCTC AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT	360
	CAGGCGGAG AAGGAGAACA GCATTAAACT GACCTCGGTG GTGTTCAATC TCATCTGCTG	420
20	CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCOA	480
	CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTGUG CAGGAGTAGC	540
	CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CCGCCCACTG	600
	GTTTCTCGCG GAAGGAGATA TGTTTGTGGC CCTGTCAAGC TCCGTGTTC A GTCTCTCTG	660
	CATCGCCATT AAGGCGTATA TCACAATGCT GAAATGAAA CTCCACAACG GGAGCAATAA	720
25	CTTCGGCTCT TTCTGCTAA TCAGCGCTCG CTGGGTCTAT TCCCTCATCC TGGGTGGCCT	780
	GCCTATCATG GGCTGGAATC GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCCGCT	840
	CTACCAAGC CACTATATCC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT	900
	CGTCACTCTG TACTCGAGAA TCTACTCCTT GGTCAAGACT CGGAGCGGCC GCCTGACGTT	960
30	CCGCAAGAAC ATTTCGAAG CCAGCGCGAG CTCTGAGAAT GTGGCGCTCG TCAAGACCGT	1020
	AATTATCGTC CTGAGCGTCT TCATCGCCTG CTGGGCACCG CTCTTCATCC TGCTCTGCT	1080
	GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCCTCTTC AGAGCGGAGT ACTTCTGGT	1140
	GTAGCTGTG CTCAACTCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT	1200
	GGGTGGGGCC TTCACTCGGA TCATGTCTCG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG	1260
	CAAAATCAAG CGACCCATCA TCGCGGCGAT GGAATTGAGC CGCAGCAAT CGGACAATTC	1320
35	CTCCCAACCC CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAACCGT	1380
	CAACTCTTCT TCCTAGAACT GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTCG	1440
	CTGGCCACCC CAGTGTGTTG AAAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT	1500
	GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGCTGGTGT CGGCTGTGG	1560
	TGGGTAGAGT TAGTTCCTGT GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCT	1620
40	GGAATATATA TTCTACCCCC CTGGAGCTTT GATTTTGAC TGAGCCAAAG GTCTAGCATT	1680
	GTCAAGCTCC TAAAGGTTTC ATTTGGCCCC TCCTCAAGA CTAATGTCCC CATGTGAAAG	1740
	CGTCTCTTGT TCTGGAGCTT TGAGGAGATG TTTTCTTCA CTTTAGTTTC AAACCCAGT	1800
	GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCCCTGTACA TCCACACCC CACCTCCCT	1860
	TCCCTTCATA CCCTCTCTCA AGTTCCTTT ACTTTATACT TTAACCTACT GAGAGTTATC	1920
45	AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAAT AGGCTATGTT GAGTAAGTAG	1980
	GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAACAAT GTCCTTCCCT GAGGCCAAG	2040
	TTTCCATGTA AGCGGGATCC GTTTTGTGGA ATTTGGTTGA AGTCACTTTG ATTTCTTTAA	2100
	AAAACATCTT TTCAATGAAA TGTGTTACCA TTTCATATCC ATTGAAGCCG AAATCTGCAT	2160
50	AAGGAAGCCC CTTTATCTTA AATGATATTA GCCAGGATCC TTGTTGTCCT AGGAGAAACA	2220
	GACAAGCAAA ACAAGTGAA AACCGAATGG ATTAACTTTT GCAACCAAG GGAGATTCT	2280
	TAGCAATGA GTCTAACAAA TATGACATCC GTCTTCCCA CTTTGTGTA TGTATTTC	2340
	AGAACTCTGT GTGATTCAIT TCAAGCAACA ACATGTTGTA TTTTGTGTG TTAAGAGTAC	2400
	TTTTCTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTTATGGA TTTTCTAAC	2460
	CCGTGTTAAC TTTTCTAGAA TCCACCTCT TGTGCCCTTA AGCATTACTT TAACGGTGA	2520
55	GGAAACGCCG AACTTTTAAG TCCAGCTATT CATTAGATAG TAATGAAGA TATGTATAAA	2580
	TATTACAAG AATAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC	2640
	CGAGAGATGT CTTGTTTTT TAAAAAGAAT AGTATTTAAT AGGTTTCTGA CTTTGTGGA	2700
	TCATTTTGCA CATAGCTTTA TCAACTTTTA AACATTAATA AACTGATTTT TTAAAG	
60	<b>A2 Protein sequence:</b>	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Gene name:	Hs.154210
	Unigene number:	M31210
	Probeset Accession #:	AAA52336
65	Protein Accession #:	none found
	Signal sequence:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Transmembrane domains:	plasma membrane
	Cellular Localization:	
70	1 11 21 31 41 51	
	MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSV VFILICCFII	60
	LENIFVLITI WKTKFHRPM YFIGNLALS DLLAGVAYTA NLLLSGATTY KLTPAQWFLR	120
75	EGSMFVALSA SVFSLIAIAI ERYITMLQMK LHNGSNNFRL PLLISACWVI SLILGGLPIM	180
	GNICISALSS CSTVLPVLYHK HYILFCTTVF TLLLLSIVIL YCRIYSLVRT RSRRLTFRKN	240
	ISKASRSSEN VALLKTVIIV LSVFIACWAP LFILLLLDVG CKVKTCIDILF RAELYFLVLAV	300
	LNSGTNPPIY TLNKMERRA FIRIMSCCKC PSGDSAGKFK RPIIAGMEFS RSKSDNSSHP	360
	QKDEGDNPET IMSSGNVNSS S	
80	<b>A3 DNA SEQUENCE</b>	G protein-coupled receptor 51
	Gene name:	Hs.198612
	Unigene number:	AA452928
	Probeset Accession #:	NM_004624.1
	Nucleic Acid Accession #:	

Coding sequence:

1-2826 (underlined sequences correspond to start and stop codons)

```

5      1      11      21      31      41      51
|      |      |      |      |      |
ATGGCTTCCC CGCGGAGGTC CGGGCAGCCA GGGCGGCCGC CGCCGCCGCC ACCGCCGCC 60
GGCGCGCTGC TACTGCTACT GCTGCTGCCG CTGCTGTGCG CTCTGGCGCC CGGGGCTGG 120
GGCTGGGGGC GGGGCGCCCC CGGCGCGCGC CCAGCAGGCC CGCGCTCTC CATCATGGGC 180
CTCATGCGCG TCACCAAGGA GGTGGCCAAG GGCAGCATCG GCGCGGTGT GCTCCCGCC 240
GTGGAATGCG CCATCGAGCA GATCGGCAAC GAGTCACTCC TGCGCCCTTA CTCTCTCGAC 300
CTGCGGCTCT ATGACACGGA GTGCGACCAAC GCAAAAGGGT TGAAAGCCTT CTACGATGCA 360
ATAAATAACG GGCAGAACCA CTGATGGTGT TTTGGAGGCG TCTGTCCATC CGTCACATCC 420
ATCATGTCAG AGTCCCTCCA AGGCTGGAAT CTGGTGACGC TTTCTTTGCG TGCAACCAAG 480
CCTGTTCTAG CCGATAAGAA AAAATACCCT TATTTCTTTC GGACCGTCCC ATCAGACCAAT 540
GCGGTGAATC CAGCCATTCT GAAGTTGCTC AAGCACTACC AGTGAAGGCG CGTGGGCACG 600
CTGACGCAAG ACGTCTCAGG GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCTGTAT 660
GGCGAGGACA TTGAGATTTC AGACCCGAG AGCTTCTCCA ACGATCCCTG TACCAAGTGT 720
AAAAAGCTGA AGGGGAATGA TGTGCGGATC ATCCTTGGCC AGTTTGACCA GAATATGGCA 780
GCAAAAGTGT TCTGTTGTGC ATACGAGGAG AACATGTATG GTAGTAAATA TCAGTGGATC 840
ATTCCGGGCT GGTACGAGCC TTCTTGGTGG GAGCAGGTGC ACACGGAAGC CAACTCATCC 900
CGCTGCTCTC GGAAGAATCT GCTTGTCTGC ATGGAGGGCT ACATTTGGCG GGATTTCGAG 960
CCCTGAGCTC CCAAGCAGAT CAAGACCATC TCAGGAAAGA CTCACAGCA GTATGAGAGA 1020
GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGGTA CGCTACGAT 1080
GGCATCTGGG TCATGCGCAA GACACTGCAG AGGGCCATGG AGACACTGCA TGCCAGCAGC 1140
CGGCACCGAG GGAATCCAGG CTCTCACTAC ACGGACCACA CGCTGGGCGG GATCATCTCT 1200
AATGCCATGA ACGAGACCAA CTCTCTGGGG GTACCGGGTC AAGTTGTATT CGGAATGGG 1260
GAGAGAATGG GGACCATTA ATTTACTCAA TTCAAGACA GCAGGGAGGT GAAGGTGGGA 1320
GAGTACACAG CTGTGGCCGA CACACTGGAG ATCATCAATG ACAACATCAG GTTCCAAGGA 1380
TCCGAACCA CAAAGACAAA GACCATCATC CTGGAGCAGC TGCAGAGAT CTCCCTACCT 1440
CTCTACAGCA TCCTCTCTGC CCTCAACATC CTCGGGATGA TCATGGCCAG TGCTTTTCTC 1500
TTCTTCAACA TCAAGAACCG GAATCAGAAG CTCATAAAGA TGTCGAGTCC ATACATGAAC 1560
AACCTTATCA TCCTTGGAGG GATGCTCTCC TATGCTTCCA TATTTCTCTT TGGCCTTGAT 1620
GGATCCTTTG TCTCTGAAA GACCTTTGAA ACACCTTGCA CGTCAAGGAC CTGGATTCTC 1680
ACCGTGGGCT ACACGACGCG TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCAAGCC 1740
ATCTTCAAAA ATGTGAAAT GAAGAAGAAG ATCATCAAGG ACCAGAACT GCTTGTGATC 1800
GTGGGGGCGC TGCTGCTGAT CGACCTGTGT ATCTGATCT GCTGGCAGCG TGTGGACCCC 1860
CTGCGAAGGA CAGTGGAGAA GTACAGCATG GAGCGGAGCC CAGCAGGAGC GGATATCTCC 1920
ATCCGCCCTC TCCTGGAGCA CTGTGAGAAC ACCCATATGA CCATCTGGCT TGGCATCGTC 1980
TATGCTTACA AGGGACTTCT CATGTTGTTC GGTGTGTTCT TAGCTTGGGA GACCCGCAAC 2040
GTCAGCATCC CGCACTCAA CGACAGCAAG TACATCGGGA TGAGTGTCTA CAACGTGGGG 2100
ATCATGTGCA TCATCGGGGC OGCTGTCTCC TTCTGACCC GGGACAGCC CAATGTGCAG 2160
TTCTGCATCG TGGCTCTGTT CATCATCTTC TGCAAGCACA TCACCTCTG CTGTGTATTC 2220
GTGCGGAAGC TCATCAACCT GAGAACAAAC CCAGATGCAG CAACGCAGAA CAGCGGATTC 2280
CAGTTCACTC AGAATCAGAA GAAAGAAGAT TCTAAACCT CCACCTCGGT CACCAGTGTG 2340
AACCAGCCCA GCACATCCCG CCTGAGGGGC CTACAGTCAG AAAACCATG CCTGCGAATG 2400
AAGATCAGAG AGCTGGATAA AGACTTGGAA GAGGTCAACA TGCAGCTGCA GGACACACCA 2460
GAAAAGACCA CCTACATTAA ACAGAACCA TACCAAGAGC TCAATGACAT CCTCAACCTG 2520
GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATT TAAAAATCA CCTCGATCAA 2580
AATCCCCAGC TACAGTGGAA CACAACAGAG CCTCTCGAA CATGCAAGA TCCTATAGAA 2640
GATATAAATC CTCCAGAAAC CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCTCCAC 2700
CAGCGCTACC TCCATCCAT GAGAGGCGTG GACGCCAGCT GTGTCAAGCC CTGGTCAAGC 2760
CCCACGCCCA GCCCGGCCA CAGACATGTG CCACCTCTCT TCCGAGTCAT GGTCTCGGGC 2820
CTGTAA

```

**A4 Protein sequence:**

Gene name: G protein-coupled receptor 51  
 Unigene number: Hs.198612  
 Probeset Accession #: AA452928  
 Protein Accession #: NP\_005449.1  
 Signal sequence: 1-42  
 Pfam domains: 7tm\_3 [481-754], ANF\_receptor [130-204]  
 Transmembrane domains: 22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744  
 Cellular Localization: plasma membrane

```

65      1      11      21      31      41      51
|      |      |      |      |      |
MASPRRSQGP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP PSSPPLSIMG 60
IMPLTKEVAK GSIGRGVLPV VELAIEQIRN ESLLRPYPLD LRLYDTECDN AKGLKAFYDA 120
IKYGNHLMV FGVCPSVTS IIAESLQGNW LVQLSPAATT PVLADKKKYP YPFRTVPSDN 180
AVNPAILKLL KHYQKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SPSNDPCTSV 240
KKLKGNDVRI ILQDFQDMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS 300
RCLRNKLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQOYER EYNNKRSVG PVSKFHGYAYD 360
GIWVIKTLQ RAMETHLASS RHQRIQDFNY TDHTLGRIL NAMNETNFFG VTGQVFRNG 420
ERMGTIKFTQ FQDSREVRVG EYNNAVATLE IINDTIRFQG SEPPKDKTII LEQLRKISLP 480
LYSILSALTI LGMIMASAFI PFNIKRNQK LKIMSSPYMN NLIIIGGMLS YASIFLFGLD 540
GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTHRVHA IFKIVKMKKK IIKDQKLLVI 600
VGGMLLIDLC ILICWQAVDP LRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660
YAYKGLMLF GCLLAWETR VPSPALNDSK YIGMSVYVNG IMCIIGAAS FLTRDQFNQ 720
FCIVALVIIIF CSTITLCLVF VPKLITLRN PDAATQNRFF QFTQNKQKED SKTSTSVTSV 780
NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMQLQDTP EKTITYIKQNH YQELNDILNL 840
GNFTSTGGG KALLKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLFILH 900
HAYLPSIGGV DASCVSFVCS PTASPRHRHV PPSFRVWVSG L

```

A5 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

```

10 1      11      21      31      41      51
    |      |      |      |      |      |
    AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GCGCGCTGTG 60
    CCTGCTGCTG AGCAGCGCGG CGGAGAGGCC GCTGCTCCCG GGGAACTACT TCACCAATGA 120
    GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCAATCCGG GCGCCTGGCA 180
    GTGTGAOCGG CTGCTGACTG GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
    GTGCAAAATGT GGCCTCAACT TCTTCCCTGT TGCCAGCGCG ATCCATTGCA TCATTGGTCG 300
    CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
    AAACCTCTCT CTTTGCTCCA CGCCCGCTCA CCACTGCAAG AACGGCTCT GTATTGACAA 420
    GAGCTTCATC TGCATGTGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
    AAGTTCTCAA GAACCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
    TTACCCAGC ATCACCATAT CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
    CTGCTGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
    GCACCGGCTG CAGCACCCTG TGCTGTGTTC CCGCTGGTG GTCTGAGAC ACCCCACCA 720
    CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
    GAATGCGTCG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840
    TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
    CGACCTGCCC CCGTACCGCT CCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
    CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
    GGGCAGCTCT GAGCCACGGG ACTCTGAGCC CAGCCAGGCG ACTGAAGAAG TATAAGTCCC 1080
    AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140
    TGCTCATGGG AAGCTCTTTA AGCACCCTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
    AACTATCTCT GCATTCCCTC CTCCCCAGC ACTTCAGAGA TGTTTTCTG CGCTCTCAGT 1260
    TGACATGATC TGTGTGCGT CTTTCTGTCT AGGTCACTCT TCCCTGGGA CCCGAGATCA 1320
    CACCCTCATT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
    AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
    CGCTGGACCC AATTCCTCTC GCTGGGTAGT TACCTTAGAG CATTGGGGA TTGGGTTAG 1500
    ATGATCTAAC CAGGAGGCCA TCACTGGATG GTACCCCCCG CAAAAAATT CCATTGAGC 1560
    ATCAAAACCT GCTTTCACA ATCCTATTG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
    AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTTATTG TGTTTTGTG 1680
    AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTG CCAAGAAATG 1740
    CTCAATTCTA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGC 1800
    GAGCCCTCTC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAAGCT GCCAAGACCC 1860
    TACACCTGCC CTGGCTCTAC AGCCACITAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920
    ACCTGCCCTG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
    GTATGTCCTG GTGGCCCAAC CCCAGCCTGT CTGCTCAATT CATGCAGCCT CAACACTGGC 2040
    CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTCCTCT GTGCATTGAG ACTTGAGGAC 2100
    ACTGGTTTCT TTTTGTGTTT TTCCCTTCTA GTTAAGGAGC TATTTATATG TGTATAGGAA 2160
    CTGCACGTG CAGCTCCTC TTCCCAAGGT CCAATACCA GCACTCTAG TTAGAGTTAG 2220
    GGTGAGGTC AGGCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
    AGACAATTG GAGTCAAGAT TTCCATTG GATCTATT TTAACTTTTA GAAATGCATT 2340
    TGAAACAGT TGTGTGTTT TTCCCTTCTA GTTAAGGAGC TATTTATATG TGTATAGGAA 2400
    AGCTGTCTCT TTTTGTGTTT TTCCCTTCTA AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460
    ACACCTTGC CCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
    ACATTGTGTC ATTGTGTCAC TTTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580
    AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTCTTTTTT 2640
    TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700
    AGGTGTGTTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760
    CCACCTCGGG CAGCTGTGAC CCATTGAGAA CTCTTTCCG CAGCTGAAGA AATGTTAGT 2820
    AACCTGTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGCTAAAG TGCATTTCAG 2880
    TGATCCCTGT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTACAGAA 2940
    AAGCTAGCCA CTGGTATTTT GTTTGTTTAA AAAAAAATAA GAAAGAAAGA AAGAAAGAAA 3000
    AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
    CTGAGTAATC CAATAAGGAA CTTTGTATGA CAGCCAGAA GTGTTAGAAC TCTGGCTGAA 3120
    CATTTCATCT CCGTGTGATC AGAAGGCTT TATTTCTCCC TTTGATGGGG CCGCTTCTC 3180
    TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
    GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT 3300
    AGATAAGGGA TGCTACTAA TGCTTTTAA AAACAAACAG GGACATTTT ATTATAGATT 3360
    TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGG GGCAGGGTTT 3420
    TTTTGGGGG GAGGGGGTTT GTTTTCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
    TTTTAACTC ATTTCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCA 3540
    AAAATAGTCT CATCTCTTTT TTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600
    AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
    TTTTAAAAA ATGCAACTAA GTGTTAATA GTGTGTGAGC CTCAAGTTA ATGTAAACTG 3720
    GAAAGGTTGT GTGTCGTGTC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAAT 3780
    TTATACCTTC TAATAAATTT GCAGTTTCAT TCTTCTGTTT TGTGCAAAWG GWMCTAMARM 3840
    AAMMAAAAC AWWTGGGG GGGCTGGGC CTCGGAAAAA GTTTTAAACA CCATCTCGGG 3900
    TGGGGCGCG GGGCCCAAGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAA 3960
    GAAACCTGG CCAAGAAAAA GGTGGCGAGA ATTCCTCCCA CCAGAAAAA ACGCGCGGG 4020
    GGAACCGCA GAGTGTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGC 4080
    GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G
  
```

A6 Protein sequence:

Gene name: ESTs

Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51  
 MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECPKAKSK CGPTFFPCAS GIHCIIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSP ICDGQNNQD NSDEESSCESS QEPGSGQVVF TSENQLVYVP SITYAIIGSS 180  
 15 VIFVLVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VLDHPHHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

20 A7 DNA SEQUENCE  
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Nucleic Acid Accession #: NM\_002205  
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51  
 ATGGGGAGCC GGACGCCAGA GTCCCTCTC CACGCCGTGC AGCTGGGCTG GGGCCCCCGG 60  
 CGCGACCCCG CGCTSSSTGCC GCTGCTGTG CTGCTSSSTG CGCCGCCACC CAGGGTCGGG 120  
 GGCTTCAACT TAGACGCGGA GGCCCCAGCA GTACTCTCGG GGCCCCCGGG CTCTTCTTC 180  
 GGATTCTCAG TGGAGTTTAA CCGCCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240  
 CCCAAGGCTA ATACCAAGCA GCCAGGAGTG CTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCTCGGCTC 300  
 35 TGGGGTGCCA GCCCCACACA GTGCACCCCC TCGTCCATCT TGGCATGCGC TCCACTGTAC 420  
 CTGGAGTCTC CACTGTCCAG CTGAGAGGGA GAGGAGCCCT TGGAGTACAA GTCCCTGTAC 480  
 TGGTTGCGGG CAACAGTTCC AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 540  
 AGCTGGGGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 600  
 GATAACTTCA CCCGAATTCT GGAGTATGCA CCTGCGCGCT CAGATTTTCA CTGGGAGGCA 660  
 40 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGGAGTTCA CCAAGACTGG CCGTGTGGTT 720  
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 780  
 ATTGCAGAA CTATTATCCC GAGTATCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 840  
 CGCCAGGCCA GTTCCATCTA TGTATGACGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 900  
 TTCACTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 960  
 45 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGCATCCC TCTACAATT CTGAGGGGAA 1020  
 CAGATGGGCT CCTACTTTGG CTATGCAATG GCGGCCACAG AGCTCAATGG GAGCGGCTCAG 1080  
 GATGACTTCT TGGTGGGGGC ACCCTGTCTC ATGGATCGGA CCCCTGAGCG GCGGCTCAG 1140  
 GAGGTGGGCA GGGTCTACGT CTACCTGAGC CACCCAGCCG GCATAGAGCC CAGCCGCCAC 1200  
 50 CTTACCTTCA CTGGCCATGA TGAGTTTGGC GGCATCGGG CTCCCTTTGG TGGGAGAGCC 1260  
 GACCTGGACC AGGATGGCTA CAAATGATGT GCCATCGGG CTCCCTTTGG TGGGAGAGCC 1320  
 CAGCAGGGAG TAGTGTGTGT ATTTCTGGG GGGCCAGGAG GGCTGGGCTC TAAGCCTTCC 1380  
 CAGGTTCTGC AGCCCTCTGT GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1440  
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCCTTTGG 1500  
 55 GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CCGCTAGTGC CTCCCTCACC 1560  
 ATCTTCCCGC CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1620  
 GCCTGCATCA ACCTTAGCTT CTGCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1680  
 GGTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1740  
 CTGTCTCTGG CCTCCAGGCA GGCAACCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1800  
 60 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAAG AGTCAGAAAT TCGAGACAAA 1860  
 CTCTCGCCGA TTCACTGCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1920  
 CACGGCCTCA GGCACGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1980  
 ATCTGTCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGT 2040  
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC 2100  
 65 CAGAAATGTG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCAACGC CCCTCCAGAG 2160  
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2220  
 TTTGCGGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGAGGGA 2280  
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2340  
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2400  
 70 TCCTTTGGCC TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCGAAGCCT 2460  
 GAGGCACTGC TATTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2520  
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCC CAGCTCCATT 2580  
 AGCCAGGGTG TGCTGGAAT CAGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT 2640  
 GTGACCAGAG TTACGGGACT CAATGTCACC ACCAATCACC CCATTAAACC AAAGGSCCTG 2700  
 GAGTTGGATC CCGAGGGTTC CCTGCAACAC CAGCAAAAAC GGGAACTGCC AAGCCGAGC 2760  
 75 TCTGCTTCTT CGGACCTTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTC CAGGCTGCGC 2820  
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTTGCA TTTCCAGTGC 2880  
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCTGCAAGT TGAGGCTGTG 2940  
 TACAAGGCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCCA AAAGAGCGGT 3000  
 CAGGTGGGCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGGCT CCACTGTGG 3060  
 80 ATCATCATCC TAGCCATCCT GTTGGGCTTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3120  
 TACAAGCTTG GATTCTTCAA ACCTCCCTC CCATATGGCA CCGCATGGA AAAAGCTCAG 3180  
 CTCAGCCCTC CAGCCACCTC TGATGCTGA

**A8 Protein sequence:**

5 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Protein Accession #: NP\_002196  
 Signal sequence: 1-42  
 Transmembrane domains: 998-1020  
 10 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036  
 Cellular Localization: plasma membrane

15 1 11 21 31 41 51  
 MGSRTPESEL HAVQLRWGPR RRPPLLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGGSFF 60  
 GPSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WNASPTQCTP IEFDSKGSRL 120  
 LESSLSSSSG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVTCTYLSL 180  
 20 DNPTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ QQILSATQEQ 240  
 IAESYYPEVL INLVQQLQQT RQASSIYDSS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300  
 GYVITLNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DLLLVGAPLL MDRTDPGRPQ 360  
 EVGRVYVYL HPAGIEPTPT LTLTGHDFFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420  
 QQGVVVFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDNGG YPDILVGSFG 480  
 25 VDKAVVYRGR PIVSASASLT IFPAMFNPPE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540  
 GFTVELQLDW QKQKGGVRRR LFLASRQATL TQTLLEIONGA REDCREMKIY LRNESEFRDK 600  
 LSPHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAP ILLDCGEDNI CVPDLQLEVF 660  
 GEQNHVYLGD KNALNLTFAH QNVGEGGAYE AELRVTPAPE AEYSGLVHRP GNFSLSLCDY 720  
 FAVNQSRLLV CDLGNPMKAG ASLWGGRLPT VPHLRDTKKT IQDFQILSK NLNNSQSDVV 780  
 30 SFRLSVEAQA QVTLLNGVSKP EAVLFFVSDW HPRDQPKQEE DLGPAVHHVY ELINQGPSSI 840  
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QOKREAPSR 900  
 SASSGPGILK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960  
 YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020  
 35 YKLGFFKRSL PYGTAMEKAQ LKPPATSDA

**A9 DNA SEQUENCE**

40 Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Nucleic Acid Accession #: NM\_002211.1  
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 ATGAATTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT 60  
 CAACACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120  
 CGAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180  
 50 TCTGCACGAT GTGATGATTT AGAAGCCTTA AAAAAGAAGG GTTGCCCTCC AGATGACATA 240  
 GAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAAACCA CCGTAGCAAA 300  
 GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCA CAAGTTGGTT 360  
 TTGCGATTAA GATCAGGGGA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC 420  
 TATCCCATGT ACCCTTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTGGAG 480  
 55 AATGTAAAAA GTCTTGAAGT AGATCTGATG AATGAAATGA GGAGGATTAC TTCGGACTTC 540  
 AGAATTGCGT TTGCTCTATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600  
 GCTAAGCTCA GGAACCTCTG CACAAGTGAA CAGAACTGCA CCAGCCCAT TAGCTACAAA 660  
 AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGG AAAACAGCGC 720  
 ATATCTGAA ATTGGATTG TCCAGAAAGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780  
 60 TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840  
 GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAAA TGAATGGACAA 900  
 TGTCACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960  
 CACCTTGTCC AGAACTGAG TGAATAAAT ATTACAGCAA TTTTGCAGT TACTGAAGAA 1020  
 TTTACAGCTG TTTACAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080  
 65 TCTGCAAAAT CTAGCAATGT AATTCAGTTG ATCATTGATG CATACAATTC CCTTTCCTCA 1140  
 GAAGTCATT TCTGAAAACG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200  
 TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCCATT 1260  
 GGAGATGAGG TTCAATTTGA AATTAGCATA ACTTCAAATA AGTGTCCAAA AAAGGATTCT 1320  
 GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGTTTAT TCTTCAGTAC 1380  
 70 ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440  
 AATGGGACAT GTGATGTGGG GCGTGCAGG TGCAATGAAG GCGCTGTTGG TAGACATTGT 1500  
 GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560  
 AGTTCAGAAA TCTGCAGTAA CAATGGAGAG TGCCTCTGCG GACAGTGTGT TTGTAGGAAG 1620  
 AGGGATAATA CAAATGAAAT TTATTCTGGC AAATCTGCG AGTGTGATAA TTTCAACTGT 1680  
 75 GATAGATGCA ATGGCTTAAT TTGTGGAGGA AATGGTGTGT GCAAGTGTG TGTGTGTGAG 1740  
 TGCAACCCCA ACTACATCGG CAGTGCATGT GACTGTTCTT TGGATACTAG TACTGTGAA 1800  
 GCCAGCAACG GACAGATCTG CAATGGCCCG GGCATCTCGG AGTGTGTGT CTGTAAGTGT 1860  
 ACAGATCCGA AGTTTCAAGG GCAAACGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920  
 GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980  
 80 TGCAACAGG AATGTTCTTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTATCC 2040  
 CAGCGGTTC AACCTGATCT TGTGTCCCAT TGTAAAGGAGA AGGATGTGTA CGACTGTGG 2100  
 TTCTATTTTA CGTATTCACT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAA 2160  
 CCAGAGTGTC CCACTGGTCC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220

GTTCTTATTG GCCTTGCAAT ACTGCTGATA TGAAGCTTT TAATGATAAT TCATGACAGA 2280  
 AGGGAGTTTG CTAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAAT 2340  
 CCTATTATA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGG AAAATGA

# **A10 Protein sequence:**

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Protein Accession #: NP\_002202.1  
 Signal sequence: 1-21  
 Transmembrane domains: 732-754  
 INB domain: 34-464  
 PSI domain: 26-76  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 1 MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60  
 2 SARCDDLEAL KKKGCPPDDI ENPRGSKDIK KKNVNTNRSK GTAELKLPED ITQIQPQQLV 120  
 3 LRLRSGEPT FTLKPKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180  
 4 RIGFGSFVEK TVMPIYSTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKE VFNELVKGQR 240  
 5 ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFSFDA GFHFAGDGKL GGIVLPNDGQ 300  
 6 CHLENNMYTM SHYDYPSIA HLVQKLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGT 360  
 7 SANSNNVIQL IIDAYNSLSS EVILENGKLS EGVITISYKSY CKNGVNGTGE NGRKCSNISI 420  
 8 GDEVQFEISI TSNKCPKIDS DSFKIRPLGF TEEVEVILQY ICECECQSEG IPESPKCHEG 480  
 9 NGTFECGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVCRK 540  
 10 RDNTEIYSG KFCECDNFNC DRNGLICGG NGVCRCRCE CNFNYTGSAC DCSLDTSTCE 600  
 11 ASNGQICNGR GICEGVCCKR TDPKFQGGTC EMCQTCGLVC AEHKECVQCR AFNKGEKKDT 660  
 12 CTQECSEYFNI TKVESRDKLP QPVQPDVSH CEKEDVDDCW FYFTYSVNGN NEVMVHVVEN 720  
 13 PECPTGPDII PIVAGVVGAI VLIGLALLLI WKLLMIHNR REFAPKEKEK MNAKWDVTGEN 780  
 14 PIYKSAVTTV VNPKEGK

## **All DNA SEQUENCE**

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 1 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60  
 2 GCTCGGTCTT ACACACCTTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120  
 3 CAGCAAAAGT ACACACACCT GGTTCGAATT CAAACAAAG AAGAGATTGA GTACCTAAAC 180  
 4 TCCATATTGA GCTATTCAAC AAGTTATTAC TGGATTGGA TCAGAAAAGT CAACAATGTG 240  
 5 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAAGTG GGCTCCAGGT 300  
 6 GAACCCACAA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360  
 7 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 8 GCTGCCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 9 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAAGTGT 540  
 10 ACAGCCCTGG AATCCCTCTG GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAAACTTC 600  
 11 AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 12 ACCATCAGT GTATGTCCTG TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGTTT 720  
 13 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGGA 780  
 14 AGCTTCCCAT GGAACACAA CTGTACATTT GACTGTGAAG AAGGATTGA ACTAATGGGA 840  
 15 GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 16 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAAATGCT CTGTGAGGTG CAGCCATTCC 960  
 17 CCTGCTGGAG AGTTCACTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020  
 18 TTGCAGGGAC CAGCCAGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCCA 1080  
 19 GTTGTGAAG CTTTCCAGT CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140  
 20 CTTCCTAGTG CTCTGGCAG TTTCOGTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200  
 21 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC 1260  
 22 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320  
 23 GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTCTG TGCCCTTCAGC 1380  
 24 TGTGAGGAGG GATTGTAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440  
 25 TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAAATGTT CAAGCCTGSC AGTTCGCGGA 1500  
 26 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGA CTGTGTGCAA GTTCGCTGTG 1560  
 27 CCTGAAGGAT GGAAGCTCAA TGGCTCTGCA GCTCGGACAT GTGAGGCCAC AGGACACTGG 1620  
 28 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
 29 CTTTCTGCTG CTGACTCTC CTCTCTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740  
 30 TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAGCCT TGAATCAGAC 1800  
 31 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

## **A12 Protein sequence:**

Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 Transmembrane domains: 555-573  
 C-lectin domain: 23-139



Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKEEIEYLN 60  
 SILSYSPSY WIGIRKVVNV WVVGTQKPL TEEAKNWAPG EPNRQKDED CVEIYIKREK 120  
 DVGMMNDERC SKKILALCYT AACTNTSCSG HGEVETINN YTCKDPGFS GLKCEQIVNC 180  
 10 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
 ECDAVTNPAN GFVECFQNPQ SFPWNTTCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNFTCEEGFM LQGPQVVECT TQGGWTQIIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GPVLKGSKRL QCGPTGEWDN 420  
 EKPTCEAVRC DAVHQPPLKGL VRCASPIGE FTYKSSCAPS CEEGFELYGS TOLECTSQGQ 480  
 15 WTEVPSCQV VKCSSLAVPG KIMMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
 SGLLPTCEAP TESNIPLVAG LSAAGLSLIT LAPFLWLRLK CLRRAKKFVP ASSCQSLESD 600  
 GSYQKFSYIL

**A13 DNA SEQUENCE**

20 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60  
 CCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCTTA TTCTGGTGA CCTGATCATC 120  
 TTCGTGATGG GCTTCTGGG GAACAGCGCC ACCATTGGG TCACCCAGGT GCTGAGAAG 180  
 30 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGACATC 240  
 TTGTGTTC TCATCGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC 300  
 ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360  
 GCTACGCTGC TGCACTGTCT GACACTCAGC TTGAGCGCT ACATCGCCAT CTGTACCCC 420  
 35 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATGG CTTCGTCTGG 480  
 GTCACCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGTACTGA GTACCCCTG 540  
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGC CCACCCAGAG 600  
 CAGCCCGAGA CCTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660  
 CAGTCCAGCA TCTTCGGGCG CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720  
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780  
 ACGCGGCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGCGAG 840  
 ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACAG 900  
 ATTGAGGGA TCATGGCTGC GGCCAAACCC AAGCAGACT GGACGAGTTC CTACTTCCG 960  
 CGTACATGA TCTCTCTCCC CTTCGCGAG AGTTTTTCT ACCTCAGTTC GGTCAATCAAC 1020  
 45 CGCTCTCTGT ACACGGTGTCT CTGCGAGCAG TTTCGGCGGG TGTTCTGTGA GGTGCTGTGC 1080  
 TGCCGCTGT CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGCTGACA TGCGCACTCC 1140  
 ACCACGACA GCGCCCGCTT TGTGAGCGC CGTTGCTCT TCGCGTCCG GCGCCAGTCC 1200  
 TCTGCAAGGA GAACAGTGA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260  
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAAGCC 1320  
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

**A14 Protein sequence:**

55 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm 1 [72-172, 224-344]  
 60 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 Cellular Localization: plasma membrane

65 1 11 21 31 41 51  
 MASPSLPDSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTOVLQK 60  
 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120  
 ATLLHLVTL FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTREYPL 180  
 VNVPSHRLT CNRSSTRHHE QPETSNNMSIC TNLSSRWTVF QSSIFGAFV YLVVLLSVAF 240  
 70 MCMNMQVLM KSQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIV TLAVCWMPNQ 300  
 IRRIMAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFQVLC 360  
 CRLSLQHANR EKRLRVHAHS TDSARFVQR PLLFASRRQS SARTEKIPL STPOSEAEPO 420  
 SKSQSLSLES LEPNSGAKPA NSAAENGFOE REV

**A1 Prostate****A15 DNA sequence**

80 Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75

```

GGGTCGCGG CACACCTCCC CGGCGCGCG CGGCCACGCG CCGCACTCCG CCGCCTCTGC 60
CCGCAACCGC TGAGCCATCC ATGGGGGTGG CGGCGCGCAA CCGTCCCGGG GCGGCTGGG 120
CGGTGCTGCT GCTGCTGCTG CTGTGCGCG CACTGCTGCT GCTGGCGGGG GCGCTCCGCG 180
CGGTGCGGG CCGTGCOCG GGGCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
ATGACTGCCA TGCGAGCGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300
AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360
TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATGST TGCATTGTGT 420
TGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480
AGAACAATGG CCGCTGCCAG CATACCTGTG TCAACGTGAT GGGAGCTAT GAGTGTCTGT 540
GCAAGGAGGG GTTTTTCTGT AGTGACAATC AGCAGCCTG CATTACCGC TCGGAAGAGG 600
GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
TCTTGACCTG TAACCATGGG AACGGTGGT GCCAGCCTC CTGTGACGAT ACAGCCGATG 780
GCCAGAGTGG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
AGCGAGAGGA CACTGTCTGT GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACRAA GGAGGCTGTG 960
ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCGC TTGTCTCTGT GSATTCACTC 1020
TGCAATGGGA TGGGAGAGCA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080
GTGATCATTT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CCGGTGCAAG AAAGGATTTA 1140
AATTATTAAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200
GTGACCACAG CTGCATCAAC CACCTTGSCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA 1260
CCCTGTATGG CTTCACCAC TGTGAGAGCA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CAGTGCCAC CCTGGGTACA 1380
AGCTCCACTG GAATGAAAAA GACTGTGTGG AAGTGAAGGG GCTCTGCGCC ACAAGTGTGT 1440
CACCCCGTGT GTCCCTGCAC TCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500
GTCACTCTGG CATTCACTTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA 1560
AGCTAAATGA AGGCAAGTGT AGTTTGAATA ATGCTGAGCT GTTTCGCGAG GGTCTGCGAC 1620
CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGTACGTA AACCTTACAT 1680
GCAGCTCTGG CAATCAAGTC CAGGAGCGCC CTGGCCGACC AAGCACCCTT AAGGAATATG 1740
TTATCACTGT TGAGTTTGAAG CTTGAAACTA ACCAAAGGA GGTGACAGCT TCTTGTGACC 1800
TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860
AGGCCGTCCT CAGGGAGCAG TTTCACTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920
AAAAGCCTCC CAGAACATCT GAAGCCGAGG CAGAGTCTTG TGGAGTGGGC CAGGGTCACT 1980
CAGAAAAACA ATGTGTCACT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040
GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100
GCCAAGACC AGGAAATCTT GGGGCCCTGA AGACCCAGA AGCTTGAAT ATGTCTGAAT 2160
GTGGAGTCT GTGTCAACT GGTGAATATT CTGCAGATGG CTTTGACCTT TGCCAGCTCT 2220
GTGCCCTGGG CAGTPTCCAG CCTGAAGCTG GTGCAACTTC CTGCTTCCCT TGTGGAGGAG 2280
GCCTTGCCAC CAACATCAGT GGAGCTACTT CTTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340
GTTCACTGGG ACATTTCTAC AACACCACCA CTCACOGATG TATTCGTGTC CCAGTGGGAA 2400
CATACCAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAT ACTACGACTG 2460
ACTTTGATGG CTCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520
GAGATTTTAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
AGGTACCTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATGCTG GTCCCTGAGA 2640
TCTTCCTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT 2700
CCATTTCTGT GACAACATAT GAAACCTGCC AGACCTACGA AGCCCCATC GCCTTCACCT 2760
CCAGTCAAA GAAGCTGTGG ATTCAAGTCA AGTCAATGA AGGGAACAGC GCTAGAGGGT 2820
TCCAGTCCCA ATACGTGACA TATGATGAGG ACTACAGGGA ACTCATTGAA GACATAGTTC 2880
GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAT ACTTAAGGAT AAGAACTTA 2940
TCAAGGCTCT GTTTGATGTC CTGGCCATC CCCAGAACTA TTTCAAGTAC ACAGCCAGG 3000
AGTCCCGAGA GATGTTTCCA AGATGTTTCA TCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060
TTTTGAGACC TTACAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
GGTGTGGGG ACAGAGCTGT CTCTCTCTG CATGTGAGCA CAGTGGGTA TTGCTGCCTC 3180
CGTATACCT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGTTAAATT 3240
GAACCTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
CAGCTTCTCA CTGCTGTGGG CCGATGTCTT GGATAGATCA CCGGCTGGCT GAGCTGGACT 3360
TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTCTC TCAAGGAGTC 3420
TGTAGTCCAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCCTTAGC 3480
COGGCCCTCT CTAAGGGGAG CCTCTGCAT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540
CAAGAGGGGA GGAAGGAGGA CCGCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG 3600
ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
AGTTCTAAGC AGTGTCTGCTG AAAAAAAGAA TTAGAAATAA ATAAAACTA 3720
AGCACTTCTG GAGACAT

```

## A16 Protein sequence

Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like\_domains [49-84,132-167,177-213,286-321,407-442]  
 CUB\_domain [809-918]  
 Cellular Localization: may be secreted

80  
1 11 21 31 41 51  
 MGVAENRFG AANAVLLLLL LLPPLLLLAG AVPPGRGRGA GPQEDVDECA QGLDDCHADA 60  
 LQNTPTSYK CCKPGYQGE GRQCEIDEC GNELNGGCVH DCLNIPGNYR CTCFDGFMLA 120  
 HDGSHCLVD ECLNNGGQ HTCVNMGSY ECKCKEGFPL SDNQHTCIHR SEEGLSGMNK 180  
 DHGCSHICAE APRGSVACEB RPFPELAKNQ RDCILTCNHG NGGQHSQDD TADGPECSCH 240  
 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDRTCKDT 300

STGVHCSPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGPTH CGDTNECSIN NGGCOQVCVN 420  
 TVGSYEQCH PGYKLHNKK DCVEVKGLLP TSVSPRVLH CGSGGGGDC FLRCHSGIHL 480  
 SSDVTIITS VTFKLNKGK SLKNAELFPE GLRPALEKH SSVKESFRYV NLTCSSGKQV 540  
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSICVIR TEKRLKAIK TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPRTS ERQAESCGVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660  
 TFQNEEGQMT CEPKPRPGNS GALKTPEAWN MSECGLQCP GEYSADGFAP COLCALGTFQ 720  
 PEAGRTSCFP CGGGLATKHQ GATSPQDCET RVQCSPGHFY NTTTHRCIRC PVGTIYQPEFG 780  
 KNNCVSCPGN TTIDFDGSTN ITQCKNRRCG GELGDFTYI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSVTTY ETCQTYERPI APTSRSKLW 900  
 IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960  
 LAHPQNYFKY TAQESREMF RSPFIRLLRSK VSRFLRPYK

**A17 DNA sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

1 11 21 31 41 51  
 CAAAAGAAA TAGATAAAAT AAATGGAATA TTAGAAGAGT CTCTGTGATA TGATGGTTTT 60  
 CTGAAGGCTC CTGCAGAAAT GAAAGTTTCT ATTCCAATAA AAGCCTTAGA ATTGATGGAC 120  
 ATGCAAACTT TCAAAGCAGA GCTCCCGAG AAGCCATCTG CTTTCGAGCC TGCCATTGAA 180  
 ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240  
 GATCAGATGT TCCTTTCAGA ATCAAAACAA AAGAASGTTG AAGAAATTC TTGGGATTCT 300  
 GAGAGTCTCC GTGAGACTGT TTCACAGAAG GATGTGTGTG TACCCAAGGC TACACATCAA 360  
 AAAGAAATGG ATAAATAAAG TGGAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420  
 GATACAGTTC ATTCTTGTGA AAGAACAAGG GAACCTCAAA AAGACCCCTG TGACCCACGT 480  
 TCAGAAAA

**A18 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Protein Accession #: none found  
 Signal sequence: none  
 Transmembrane domains: none  
 Cellular Localization: nuclear

1 11 21 31 41 51  
 QKEIDKINGK LEESPDNDGF LKAPCRMVVS IPTKALELMD MQTFKAEPPE KPSAFEPALIE 60  
 MQKSVENKAL ELKNEQTLRA DQMFPSKQ KXVEENSWDS ESLRETYSQK DVCVPKATHQ 120  
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPDPR SGK

**Breast****A19 DNA SEQUENCE**

Gene name: TMPSR33a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ACCGGGCACC GGACGGCTCG GGTACTTTGG TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGAGGGCGGA GCGGATGTC 180  
 AGAGGTCTCG AATAGTCTAC CATGGGGGAA AATGATCCG CTGCTGTTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGG CCTGTGATGAT TTGAAATAA GTCCCTGTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATGCTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCGGTGC TCCAGGTGTT CACAGCTGCT TGCTGGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGT TGCTGTGCTC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAAECTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGGT TACCTTGACG TGACACGCT GTGCTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTAGTTCC AGGCTACCA CCTGTGCGGG GGCTCTGTCA TCAAGCCCTG GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTA TGACTGTGAC CTCCCAAGT CATGGAACAT CCAGTGGGT 1020  
 CTAGTTTCCC TGTGGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080  
 ACGAAGTACA AGCAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGT GCCTGGGACA 1140  
 CTCACGTCA ATGAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGGAAGG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAG AGGTGACGCC 1260  
 TCCCTGTCC TGAACCAAGC GGCCTGCTCT TTGATTTCCT ACAAGATCTG CAACCAAGG 1320  
 GAGGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380

5 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCACT CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCGGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCOOGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGT CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 10 TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT 1920  
 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAATGA TGTGCTGCT TCAGCTCCC ACAGTGTGG GATTACAGGC ATGGGCCACC 2040  
 ACGCTAGCC TCAGCTCCT TTCTGATCT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTCG AAAATTCCTG 2160  
 ACGAGATAAG CAGTTATGTG AACTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 15 AGCCAGGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAAGAA 2280  
 CCAAAACCCAC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCTTAT TTTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400  
 TTGTCCTTGG ATTCCAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAAAA

A20 Protein sequence:  
 Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 25 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 30 Cellular Localization: not determined

35 1 11 21 31 41 51  
 MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFPF IIVIGIALI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVILQVF 120  
 TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180  
 VTALHHSYVV REGCASGHV VTLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240  
 40 LCGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCMT SGWGATEDGA GDASFVLNHA 360  
 AVPLISNKIC NHRDVGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWLKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

45 A21 DNA SEQUENCE  
 Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Nucleic Acid Accession #: AA428090  
 Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG 60  
 CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120  
 55 TTTTCAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT 180  
 GATCTGTTG GCTTCTCTGG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240  
 GGAAAAACAA CTAACTCAG CCATTGCCCC AATTCCACC TTGCTAGTTA TCAGAGTTCA 300  
 CTATTGTTTA AGCTCCAGGG GTCACTACTAT GGCAATCTAC TGGTGAATTT TATCTGAGC 360  
 60 AAGTGTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAC ATTGCCTCCA GCTGCAAGC 420  
 AAGGGCATTG CCATTATGAA AGCCCCCTCA AGACTCTCTG CTATTTTCAA AACATGGAAA 480  
 GAAAAAGGGA AAAAAAGAAA AAAAAATAATA ATTAGAAGGA TTTGTTCTCT AATTGGGGCT 540  
 CCCAAAAATG AGAAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATATT TTAACCTCTC 600  
 CAAGCAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTATT 660  
 65 TTTCTTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCTTTCTCT ATCTGGATCT 720  
 GTTCTGCTC ATTTCTCTTT CAAAGTCATC TTTCAGGGAA CTGCGCCTGA TTAATTGAT 780  
 TTTAACCAAA CAAATAAGAT ATTTGATATA TTAATTTAAA CTTTGTGAGA TGATTGATTA 840  
 GGAATTGCAT CATGTTTACA TGAGTATACC GAATTCRAAG TTAACCTTCA TAAGCAGGAG 900  
 TTTTACACA TCGTAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA 960  
 70 CTGAATGTTT TTGAAATAAA CACATTTTTA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020  
 CTTTTTACAC AAAATATATC AGTGAGAGAG TGTGTTTGA AGAAAAAAA TCAAAGCACA 1080  
 ACAGATTGAG CAGATCCAGG CTTTATCAAT ATAAGTAATA ATTTTGTAGA ATGGTGATT 1140  
 GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200  
 TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCCTATTGC TAGAAGGATG 1260  
 75 AAAGTGAATC CATATAAAC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAACTTTAT 1320  
 TATTCAGATT TAGATGTAAAC AGACATCTTT GCTGCGCTGA GATGTTTGC ATAGAAATA 1380  
 CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACCTA TGAAAAACAA ATAAATAAAA 1440  
 ACCAAAAAAT TTCATGTGTT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA 1500  
 ATCAGGACTA CAAATTGAAT TCTTTTCTT AGCAACATGA AATCATTCCA TATGAAGAC 1560  
 80 ATTTCTGCT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTTT GAGATGTTC 1620  
 CCCCTCATGC CTCCCCCAA GTTTTCCATG TGGTTGTCAA ATAGTCCGC

A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 113-129  
 Cellular Localization: not determined

10 1 11 21 31 41 51  
 MKPSLKHWD IKMFSEIDQR QVVGEEIHLQ VVSVSYLEN PSDTDDLMSI VEESDSCYNR 60  
 DSVGLPGRAG DRLQPKTKPR GKTTNLSHLP NFHLASYQSS LLFKLQSSYY GNLLVEFILS 120  
 KCFVQLAVLK QKGHCLQLQS KGIAIMKAPQ RLSAIFKTKW EKGKKEKKII IRRICSLIWA 180  
 PKNEK

#### A23 DNA SEQUENCE

20 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Nucleic Acid Accession #: AL133619  
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 ATGAGCGGTG CCGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCGGGGTCT 60  
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG 120  
 CTCAGGCAGA GCGAGCCGCA GAAACGGAACT CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCTCCCA GCACACTCA 300  
 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCACT CCAGCACAGC CCTGGGCTCA 360  
 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTG CCCACCTGGC TGCACTGGCC 420  
 CTTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGTACCTCT 480  
 AGCCGTGGCT GGAACATGTT ATGCAGCCAA GCACAGCAGC TGCTGTCTCT GGGAGGCCCA 540  
 GGGCTGTAGG TCATTGCAGG GCGGCAGGTG GCCACAGGCT GCTCCCCAGA CTTCCCTCCT 600  
 CCAAGTAGAG CTGAATGGG AAGGAACCCC TGGGACAGCC CTTGCCCTCT TAGATCTTTG 660  
 CTTCAATTTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGCT TTCTTGCCA CTTGTCCAAG 840  
 GCACTTCACT ATCTCTACAG CGGCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATTATCTTT GGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960  
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TCCCAGGGA 1020  
 GACATGGAGA AGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CTTGCACTGC TGGGGAAGCT 1140  
 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTGGGACCT GCTGTCCAT GTGTCCCAAG 1200  
 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTTG 1260  
 GGGCTCTGCT GGTCTGCTAT CAACGAGTG TGGGTAGAGC CGGAGGACC CAGCCCTGCC 1320  
 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1380  
 GCGGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCATCTCTAA TTCAAGCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCTTCAACA AGCAAGATTG AAGAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560  
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTTGGG TACAAGGCA GGCAGAAAG 1620  
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680  
 AGGCAGATGG GGGCGGGGCG ACACCCCCCA ATGATCTTGC CCCTTCCCTC GCGAAAGCCC 1740  
 ACCACACTTA GGCAGTGCCA AGTGCTCATC CGCGAGCTGT GGAATAACCA CCTCTGCG 1800  
 ACCCAAGAGC TGCGGCACCT CAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCCAGC 1860  
 CCGGAGGAAG CTAGCTTTCC CAGGACCAA GAAGCCACGC ATTTCCCAA GGTCTTCCAC 1920  
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980  
 CTGAAGCAGA CCCGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCATGCGAG 2040  
 AACCGCGGCC TGCATCGCTC AGTGCTTGA

#### A24 Protein sequence:

65 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Protein Accession #: T43457  
 Signal sequence: none found  
 Transmembrane domains: 303-322  
 Cellular Localization: not determined

75 1 11 21 31 41 51  
 MSGAGVAAAT RPPSSPTPGS RRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60  
 QQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPQAH S TLPLPQHRNT AINSSTRLGS 120  
 GGTQDGEPLQ TVLAHLAALA FVCPQSGYRF WGTWDAATS SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAQRQV ATGCSFDLPP PSRAEMGRNP WDSPPCFARSL PQIAAVARER ISSPMALSPH 240  
 MLGAQGIWTH SIQGSPLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300  
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGEGP FPSRCGNSSE 360  
 LFWAKCGFSR PQPQCSAGDA DRTREBAMLS LGTCCSMCPK PSCFPDGPSP NHLRSASAPL 420  
 GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPKGKRGRLA GGSADTVRSP ADSLSMSSFQ 480  
 SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEE PLLHNSKLDK VPGVQQAARK 540

EKAEASNAGA ACMGNSQHQG ROMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600  
 TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTPKNFPA ERQKRLQAMQ KRRLHRSVL

**A25 DNA SEQUENCE**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Nucleic Acid Accession #: NM\_000949  
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 15 GGAGGCTGAA ATCCCCAGAC GCGGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACCTCTT 60  
 CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTCCACACA ATGGAGCTTC 120  
 ATGTCTCGT GCAGGAAGTA CTATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180  
 TAAAGAACTC TCCTATTCTT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCTGTAA 240  
 GTGAACCTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAAATGTGG 300  
 20 CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT 360  
 TACCTCTCGG AAAACCTGAG ATCTTTAAAT GTCTTCTCC CAATAAGGAA ACATTCACTT 420  
 GCTGTGGAG GCCTGGGACA GATGGAGGAC TTCTACCAA TTATTCAGT ACCTACCACA 480  
 GGGAGGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAACTCCT 540  
 25 GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600  
 CTAACAGAT GGGAGCAGT TTCTCGGATG AACTTTATGT GGAGCTGACT TACATAGTTC 660  
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACA GCCAGAAGC AGAAAAACCT 720  
 ACCCTGTGGT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAAGCTGT TGGTTTCAAGC 780  
 TCCTGTATGA AATTTCGATT AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG 840  
 GGCAGCAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900  
 30 TTGCTGCAAC ACCAGACCAT GGATACCTGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960  
 TACCTAGTGA CTTCAACATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCTTTCTG 1020  
 CTGTCTCTG TTTGATTATT GTCTGGGAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080  
 GCATCTTTCC GCAGATTCTT GGGCCAAAAA TAAAGGATT TGATGCTCAT CTGTGGGAGA 1140  
 AGGCAAGTC TGAAGAATA CTGAGTGCCT TGGGATGCCA AGACTTTCTT CCCACTTCTG 1200  
 35 ACTATGAGA CTTGCTGGT GAGTATTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260  
 TGTCAGTCCA TTCAAAAGAA CACCCAAGTC AAGGTATGAA ACCCACTAC CTGGATCCTG 1320  
 ACATGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380  
 AACCCAGGC CAATCCCTCC ACATTCTATG ATCTGTAGGT CATTGAGAAG CCAGAGAATC 1440  
 CTGAACAAC CCACACCTGG GACCCCAAGT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500  
 40 TTCACTGCTG TGGATCCAAA TGTTCAACAT GGCCTTACC ACAGCCAGC CAGCACAAAC 1560  
 CCAGATCCTC TTACCACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGG CCTGCAGGTG 1620  
 CACCGGCCAC TCTGTTGAAT GAAGCAGTA AAGATGCTTT AAAATCTCT CAAACCATTA 1680  
 AGTCTAGAGA AGAGGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA 1740  
 CTGACCAAGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800  
 45 CCTGTGATTA TGTGGAGATT CACAAGTCA ACAAGATGG TGCATTATCA TTGCTACCAA 1860  
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGAC TCCTGAGAAC AATAAGGAGT 1920  
 ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGTGCCA GATCCACATG 1980  
 CTAAAAACGT GGCTTGCTTT GAAGAATCAG CCAAGAGGC CCCACATCA CTTGAACAGA 2040  
 50 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100  
 TGGGTGCTTT GGAATACCTG GATCCCGCAT GTTTTACACA CTCCCTTACC TGATAGCTTG 2160  
 ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTAGCTGA 2220  
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGGCTC CCAGCTCCTT TCATGCTCCA 2280  
 TTTTAAACCA CTGCTCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCTT 2340  
 55 AACTGTGATT TGTAGATTTA CTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400  
 AAAAGCACAC TGTCTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG 2460  
 GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA 2520  
 AAGATGACAA AAGAAAATT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAAC 2580  
 AACTGCATAA CCTTTACACT CCTGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640  
 60 AAAGAAAGAA TGCATTCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700  
 TGTCTGATAT GCAAGTAAAG AAT

**A26 Protein sequence:**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Protein Accession #: NP\_000940  
 Signal sequence: 1-23  
 Transmembrane domains: 237-253  
 70 FN3 domains: 28-112, 127-215  
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51  
 MKENVASATV FTLLFLNLC LLNQQLPPGK PEIFKCRSPN KETFTCWWRP GTDGGLPNTY 60  
 SLTYHREGT LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVNATNQMG SSFSDELYVD 120  
 80 VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW 180  
 EIHFAQQOTE FKLLSLHPGQ KYLVQVRCKP DHGYSWAWSP ATFIQIPSDF TMDTTTWNIS 240  
 VAVLSAVICL IIVVAVALKG YSMVTCIPFP VPGPKIKGFD AHLLEKKGSE ELLSALGCQD 300  
 FPPTSDYEDL LVEYLEVDDG EDQHLMSVHS KEHPSQGMKP TYLDPDTSRG RGSQDPSPLL 360  
 SERKEEPQAN PSTFYDPEVI EKPNPETTH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420

PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQOREVE 480  
 SFHSETDQDT PWLLPQEKTP FGSAPKLDYV EIHKNVDGA LSLLPKQREN SGKPKKPGTP 540  
 ENNKEYAKVS GVMNNILVL VDPHAKNVA CFEESEAKEAP PSLEQNAQAEK ALANFTATSS 600  
 KCRLQLGGGLD YLDPACTHFS FH

**A27 DNA SEQUENCE**

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Nucleic Acid Accession #: NM\_000909.1  
 Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60  
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTGGT AAATGGATT CAAATACGGG 120  
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180  
 ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTGAAAA 240  
 TCATTAGTC CACTCTAATT TCTCAGAGAA GAATGCCAG CTTCGGCTT TTGAAAATGA 300  
 TGATTGTCTAT CTGCCCCCTG CCATGATATT TACCTTAGCT CTTCGCTATG GAGCTGTGAT 360  
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420  
 GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTGCCAT 480  
 CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGCTT TTGGTGAGGC 540  
 GATGTGTAAAG TTGAATCCCT TTGTGCAATG TGTTCATC ACTGTGTCCA TTTTCTCTCT 600  
 GGTTCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660  
 TAATAGACAT GCTTATGTAG GTATTGCTGT GATTGGGCT CTTCGCTGAG CTTCCTCTTT 720  
 GCCTTTCTCTG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGATGC 780  
 GTACAAAGAC AAATACGCTG GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTCTA 840  
 TACCACTCTC CTCTTGGTGC TGCAGTATT TGGTCCACTT TGTTTTATAT TTATTTGCTA 900  
 CTTCAAGATA TATATACGCC TAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960  
 TAAGTACAGG TCCAGTGAAG CCAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020  
 ATTTGACATC TGCTGGCTCC CTCTTACCAT CTTAACACT GTGTTTGATG GGAATCATCA 1080  
 GATCATTTGT ACCTGCAACC ACAATCTGTT ATTCCTGCTC TGCCACCTCA CAGCAATGAT 1140  
 ATCCACTTGT GTCAACCCCA TATTTATGG GTTCCTGAAC AAAAATCTCC AGAGAGACTT 1200  
 GCAGTCTTTC TTCAACTTTT GTGATTCCCG GTCTCGGGAT GATGATTATG AAACAATAGC 1260  
 CATGTCCAGG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320  
 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380  
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACTACTCTT GATTACCTGT 1440  
 TCTCCCAAGG AATGGGGTGG AAATCATTGG AAAATGACTA AGATTTCCTT GTCTTGCTTT 1500  
 TTAAGTCTTT TGTGTAGTGT GTCAATAATTA CATTGGAAC AAAAGGTGTG GGCTTTGGGG 1560  
 TCTTCTGGA AATAGTTTGA CCAGACATCT TTGAAGTGCT TTTTGGAAT TTATGCATAT 1620  
 AATATAAAGA CTTTATACT GTACTTATTG GAATGAAATC TCTTAAAGT ATTACGATGC 1680  
 GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCAATTG ATTGGGTCAT CTTGATTAGA 1740  
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800  
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTG AGGAGCCGAA AGATAGTCTT 1860  
 GAAGTCATC AGAAGTGGTT TGAGGTTTCT GTTTTGTGTT GGTTTTGTGTT TGTTTTGTGTT 1920  
 TTTTTCAC CTTAAGGGAGG CTTTCATTTC CTCCCGACTG ATTGTCACTT AAATCAAAAT 1980  
 TTAATAATGA ATAAAAAGAC ATACTTCTCA GCTGCAATA TTATGGAGAA TTGGGCACCC 2040  
 ACAGGAATGA AGAAGAAAG CAGCTCCCCA ACTTCAAAAC CATTTTGGA CCGACACA 2100  
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAAGT ATTGCTGCA ATAGCTAAAT 2160  
 TATATTATT TGAATTGATG GTCAAGAGAT TTTCCATT TTTTACAGAC TGTTCAGTGT 2220  
 TTGTCAAGCT TCTGGTCTAA TATGACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280  
 ACAAATATCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTTCAATGTC 2340  
 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTACCTAGC 2400  
 AGGAAAAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT 2460  
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTAAGTAATA GTTGTGTCAT 2520  
 GTTAATGTGC CTAATTTCAT GTATCTGTGA ATCATGATTG AGCCTCAGAA TCATTGAGAG 2580  
 AAATATATT TTAAGAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640  
 TGTTTGATTT TAAAGGGCG GACATTTTAT TAAATCAAT ATTGTTTTTG CTTTTCGTA 2700  
 GGAGTCTCTT TCAATTTCAT TTTTCTCAT CCCATGACTT CCCTCCGATG GT

**A28 Protein sequence:**

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Protein Accession #: NP\_000900.1  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [57-91]  
 Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MNSTLFSQVE NRSVHSNFSE KNAQLLAFEN DDCHLPLAMI FTILAYGAV IILGVSGNLA 60  
 LIIILLKQKE MRNVNITLIV NLSFSDLLVA IMCLPPTFVY TLMHWVFE AMCKLAPFVQ 120  
 CVSTTVSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180  
 DEPPQNVTL D AYKQKYVCFD QPPSDSHRLS YTTLLVLQY FGPLCFIFIC YPKIYIRLKR 240  
 RNNMDKMRD NKYRSSETR INIMLLSIVV AFVAVCHLPLT IFNTVFDWNH QIIATCNHNL 300  
 LFLILCHLTAM ISTCVNPIFY GFLNKNFQRD LQFFNFNCFD RSRDDDYETI AMSTMHTDVS 360

KTSLKQASPV AFKINNND NEKI

A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC 60
GGCTGCCCGG GCTGTGGCGC CAACGCCTCG GACGGCCAG TCCCTTCCG GCGGGCCGTG 120
GAGCCTGGCG TCGTGGCGCT CTCTTCCGCG GCGCTGATGC TGCTGGGCCT GGTGGGAAC 180
TCGCTGGTCA TCTACGTCAT CTGCGGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
ATGCCCAACC TGGCGGCCAC GGACGTGACC TTCCTCCTGT GCTGCGTCCC CTTCACGGCC 300
CTGCTGTACC CGTGCCTCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT GGTCAACTAC 360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCATAGAG TGTGGACCGC 420
TGGTAGGTGA CGTGTGTCCC GTTGGCGGCC CTGCACCGCC GCACGCCCGC CTGGGCGCTG 480
GCTGTAGCCG TCAGCATCTG GTTAGGCTCT GCGGCGGTGT CTGCGCGGCT GCTGCGCCTG 540
CACCGCCTGT CACCCGGGCC GCGCGCCTAC TGCAGTGAGG CCTTCCCGAG CCGGCGCCTG 600
GAGCGGCGCT TCGCATCTGA CAACCTGCTG GCGCTGTACC TGCTGCGGCT GCTGCGCAC 660
TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGTGGCG CCGCGCGCCC 720
GCGGATAGCG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCGGT GCGGGCCAAAG 780
GTCTCGCGCG CTGCTGCGCG CTGTGCTCTG CTCTTCCGCG CCTGCTGGGG CCCCATCCAG 840
CTGTTCTGCG TGTGTCAGCG GCTGGGCCCC GCGGGCTCCT GGCACCCACG CAGTACGCC 900
GCCTAGCGCG TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCGG 960
CTGCTCTACG CCTTCTGGG CTGCACTTTC CGACAGGCGT TCCGCGCGT CTGCCCTTGC 1020
GCGCGCGCGC GCCCGCGCGG CCGCGCGCGG CCGGAGCCCT CGGACCCCGC AGCCCCACAC 1080
GCGGAGCTGC ACGCCCTGGG GTCCACCCCG GCCCGGCCCA GGGCGCAGAA GCCAGGGAGC 1140
AGTGGGCTCG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAAACCCCC TCTCTGA

```

A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

Pfam domains: 7tm\_1 [59-323]

Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA ALMLLGLVGN 60
SLVIYVICRH KPMRTVINFY IANLAATDVT FLCCVPFTA LLYPLPGWVL GDFMCKFVNY 120
IQQVSQVQAT ATLTAMSVD R WYVTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAL 240
ADSLAQQVQL AERAGAVRAK VSRILVAAVVL LFAACWPIQ LFLVLQALGP AGSWHFRSPA 300
AYALKTNAHC MSYSNSALNP LLYAFLGSHF RQAFRRVCPC APRRRPRRRR PGPSDFAAPH 360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL

```

A31 DNA SEQUENCE

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM\_014246

Nucleic Acid Accession #: NM\_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCGCGC CGCGCGCGCC CGTGTGCCCC GTGCTGCTGC TCCTGGCCGC GCGCGCGGCC 60
CTGCGCGCGA TGGGGCTGCG AGCGGCGCGC TGGGAGCCGC GCGTACCCGG CGGGACCGCC 120
GCCCTGCGCC TCGGCGCGCG CTGTACCTAC GCGGTGGGCG CCGCTTGACG GCCCGGGGCG 180
CGCGGGGAGC TGCTGGAAGT GGGCGCGGAT GGGCGGCTGG CAGGACGTGG GCGGCTCTCG 240
GGCGGGGGGG GCCCGCTGCC GCTGCAAGTC CGCTTGGTGG CCGCAGTGGC CCGGACGGGG 300
CTGAGCGGCC GCGTGGCGGC GTTCCCGGCT CCGGAGCCCG TGCCCGGCTC 360
TGCGGAACCG GTGCGCGGCT CTGCGGGGCG CTCTGCTTCC CCGTCCCGCG CGGCTGCGCG 420
GCGGCGCAGC ATTGCGCGCT CGCAGCTCCG ACCACCTTAC CCGCTGCGCG CTGCGCGCGG 480
CGCCCCAGCG CCGCTGTGCC CGGCGGTCCC ATCTGCTGCG CGCGGGCGGG CTGCGTCCGC 540
CTGCGCTGCG TGTGCGCCCT GCGGCGCGCG GCTGGCGCGG TCCGGTGGGG ACTGGCGCTG 600
GAGGCGGCCA CGCGGGGGAC GCCCTCCGCG TCGCATCCCG CATGCGCGCC CCGCGCGCGG 660
AACTTGCCTG AAGCCCGGGC GGGGCGGGCG CGACGGGGCC GCGGGGGCAC GAGCGGCAGA 720
GGGAGCCTGA AGTTTCCGAT GCCCAACTAC CAGGTGGCGT TGTGTGAGAA CGAACCGGGG 780
GGCACCTCTA TCCTCCAGCT GCACGCGCAC TACACCATCG AGGGCGAGGA GGAGCGCGTG 840
AGCTATTACA TGGAGGGGCT GTTCGACGAG CGCTCCCGGG GCTACTTCCG AATCGACTCT 900
GCCACGGGCG CCGTGAGCAC GGACAGGTGA CTGGACGCGG AGACCAAGGA GACGACGCTC 960
CTCAGGGTGA AAGCCGTGGA CTACAGTACG CCGCGCGCGT CCGCCACCAC CTACATCACT 1020
GTCTTGGTCA AAGACACCAA CGACCAAGC CCGGTCTTGG AGCAGTCCGA GTACCGCGAG 1080
CGCGTGGGG AGAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCCGCGC CAGCGACCGC 1140

```



	GACTCGCCCA	TCAACGCCAA	CTTGCGTTAC	CGCGTGTGG	GGGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAACG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGCGG	TGCTGGACCG	GGAGGAGGCG	1260
	GCCGAGTACC	AGCTCCTGGT	GGAGGCCAAC	GACCAGGGCG	GCAATCCGGG	CCCGCTCAGT	1320
5	GCCACGCCCA	CGGTGTACAT	CGAGGTGGAG	GACGAGAACG	ACAACCTACCC	CCAGTTTCAGC	1380
	GAGCAGAACT	ACGTGGTCCA	GGTGCCCGAG	GACGTGGGGC	TCAACACGGC	TGTGCTGCGA	1440
	GTGCAGGCCA	CGGACCGGGA	CCAGGGCCAG	AACGCGGCCA	TTCACTACAG	CATCCTCAGC	1500
	GGGAACGTGG	CGGCGCAGTT	CTACCTGCAC	TCGCTGAGCG	GGATCCTGGA	TGTGATCAAC	1560
	CCCTTGGAAT	TCGAGGATGT	CCAGAAATAC	TCGCTGAGCA	TTAAGGCCCA	GGATGGGGGC	1620
	CGGCCCCCGC	TCATCAATTC	TTCAAGGGTG	GTGTCTGTGC	AGGTGCTGGA	TGTCAACGAC	1680
10	AACGAGCCTA	TCCTTTGTGAG	CAGCCCTTTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTCTG	1740
	GGCTACCCCG	TGGTGACAT	TCAGGCGGTG	GACGCGGACT	CTGGAGAGAA	CGCCCGGCTG	1800
	CATCATCGCC	TGGTGGACAC	GGCTCCACC	TTTCTGGGGG	GCGGACGGC	TGGGCTTAAG	1860
	AATCCTGCCC	CCACCCCTGA	CTTCCCTTTC	CAGATCCACA	ACAGCTCCGG	TTGGATCACA	1920
15	GTGTGTGCCG	AGCTGGACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGGCGGTG	1980
	GACCACGGCT	CGCCCCCATC	GAGCTCCTCC	ACCAGCGTGT	CCATCACGGT	GCTGGACGCTG	2040
	AATGACAAAG	ACCGGGTGT	CACGACGGCC	ACCTACGAGC	TTCTGTCTGA	TGAGGATGCG	2100
	GCGGTGGGGA	GGAGCGTGCT	GACCTGCAG	GCCCGGACG	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACGAGC	TCACAGGCGG	CAACACCCGG	AACCGCTTTG	CATCAGCAG	CCAGAGAGGG	2220
20	GGCGGCTCA	TCACCTTGGC	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	GTACGTGCTG	2280
	GCGGTGACAG	CTATCGACGG	CACACGGTCG	CACACTGCGC	ATGTCTTAAT	CAACGTCAC	2340
	GATGCCAACA	CCCAAGGCGT	TGTCTTTCAG	AGCTCCCAT	ACACAGTAGA	TGTGATGAG	2400
	GACAGGCTCG	TGGGCACCTC	CATTGTACCC	CTCAGTGCCA	ACGATGAGGA	CACAGGAGAG	2460
	AATGCCCGCA	TCACCTAAGT	GATTGAGGAC	CCCGTCCCGC	AGTTCGCGAT	TGACCCCGAC	2520
25	AGTGGCACCA	TGTACACCAT	GATGGAGCTG	GACTATGAGA	ACCAGGTGCG	CTACAGCTG	2580
	ACCATCATGG	CCGACGAGCA	CGGCTCCCG	CAGAAATCAG	ACACCAACCA	CCTAGAGATC	2640
	CTCATCTCTG	TGCCCAATGA	CAATGCACCC	CAGTTCTGTG	GGGATTCTTA	CCAGGGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTGACACAGC	ATCTCTCCAG	TCTCTGCCAC	GGACCGGGAC	2760
	TCAGGTCCCA	ATGGGCGTCT	GCTGTACACC	TTCCAGGGTG	GGGACGACGG	CGATGGGGAC	2820
30	TTCTACATCG	AGCCCCACGT	CGGTGTGATT	CGCACCCAGC	GCGGCTGGA	CCGGAGAGAT	2880
	GTGGCCGTGT	ACAACTTTTG	GGCTCTGGCT	GTGGATCGGG	CGATGCCAC	TCCCTTTAGC	2940
	GCCTCGGTAG	AAATCCAGGT	GACCATCTTG	GACATTAATG	ACAATGCCCC	CATGTTTGAG	3000
	AAGGACGAAC	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGGTCCGT	GGTGGCAAAG	3060
	ATTCGTGCTA	ACGACCCCTGA	TGAAGGCCCT	AATGCCCAGA	TCATGTATCA	GATTGTGGAA	3120
35	GGGACATGTC	GGCATTTCTT	CCAGCTGGAC	CTGCTCAACG	GGGACCTGCG	TGCCATGGTG	3180
	GAGCTGGAAT	TTGAGGTCCG	GCGGGAGTAT	GTGCTGGTGG	TGCAGGCCAC	GTGCGCTCGG	3240
	CTGGTGAGCC	GAGCCACGGT	GCACATCCTT	CTCGTGGACC	AGAATGACAA	CCCGCTGTG	3300
	CTGCCGACT	TCCAGATCCT	CTTCAACAAC	TATGTCAACA	ACAAGTCCAA	CAGTTTCCCC	3360
	ACCGGCGTGA	TCGGCTGCAT	CCCGGCCCAT	GACCCGACG	TGTACAGACG	CCTCAACTAC	3420
40	ACCTTCGTGC	AGGGCAACGA	GCTGCGCCTG	TTGCTGCTGG	ACCCCGCCAC	GGGCGAACTG	3480
	CAGCTCAGCC	GCGACCTGGA	CAACAACCGG	CCGCTGGAGG	CGCTCATGGA	GGTGTCTGTG	3540
	TCTGATGGCA	TCCACAGGCT	CAOGGCTTTC	TGCAACCTGC	GTGTCAACAT	CATCACGGAC	3600
	GACATGTCTG	CCAACAGCAT	CACGTGCGCG	CTGGAGAAC	TGTCACAGGA	GAAGTTCTCG	3660
	TCCCGCTGCG	TGGCCCTCTT	CGTGGAGGGG	GTGGCGCGCG	TGCTGTCCAC	CACCAAGGAC	3720
45	GACGTCTTGG	TCTTCAACGT	CCAGAACGAC	ACCGAGCTCA	GCTCCAACAT	CCTGAACGCTG	3780
	ACCTTCTGCG	CGCTGTCTGC	TGGCGGGTGC	CGCGGCCAGT	TCTTCCCGTC	GGAGGACCTG	3840
	CAGGAGCAGA	TCTACTGAAA	TGGAGCGCTG	CTGACCAACA	TCTCCAACGA	GCGCGTCTG	3900
	CCCTTCGAGG	ACAACATCTG	CCTGCGGAG	CCCTGCGAGA	ACTACATGAA	GTGCGTGTCC	3960
	GTCTGCGAT	TCGACAGCTC	CGCGCCCTTC	CTCAGCTCCA	CCACCGTGTCT	CTTCCGGCCC	4020
50	ATCCACCCCA	TCAACGGCCT	GCGCTGCCGC	TGCCCGCCCG	GCTTCCCGCG	CGACTACTGC	4080
	GAGAGCGGGA	TCGACCTCTG	CTACTCGAGC	CCGTGCGGCG	CCAACGGCGG	CTGCGCGAGC	4140
	CGCAGGGCGG	GCTACACCTG	CGAGTGCTTC	GAGGACTTCA	CTGGAGAGCA	CTGTGAGGTG	4200
	GATGCGCGCT	CAGGCGCGTG	TGCCAACGGG	GTGTGCAAGA	ACGGGGGAC	CTGCGTGAAC	4260
	CTGCTCATCG	GCGGCTTCCA	CTCGTGTGT	CCTCTGCGG	AGTATGAGAG	GCCCTACTGT	4320
55	GAGGTGACCA	CCAGGAGCTT	CCCGCCCCAG	TCCTTGTGTA	CCTTCCGGGG	CCTGAGACAG	4380
	CGCTTCAACT	TCAACATCTC	CCTCACTGTT	GCCACTCAGG	AAAGGAACCTG	CTTGTCTCTC	4440
	TACAACGGCC	GCTTCAATGA	GAAGCACGAC	TTCACTCGCC	TGGAGATCGT	GGAGGAGCAG	4500
	GTGACGTCTA	CCTTCTCTGC	AGGCGAGACA	ACAACGACCG	TGGCACCGAA	GGTTCCTCAGT	4560
	GGTGTGAGTG	ACGGGCGGTG	GCACTCTGTG	CAGGTGCAGT	ACTACAAACA	GCCCAATATT	4620
60	GGCCACCTGG	GCCTGCCCCA	TGGGCGGTCC	GGGAAAAGA	TGGCGGTGTT	GACAGTGGAT	4680
	GATTGTGACA	CAACCATGGC	TGTGCGCTTT	GGAAAGGACA	TGGGAAGTCA	CAGCTGCGCT	4740
	GCCCAGGGCA	CTCAGACCGG	CTCCAAGAAG	TCCCTGGATC	TGACCGGCCC	TCTACTCCTG	4800
	GGGGGTGTCC	CCAACCTGCC	AGAAGACTTC	CCAGTGACCA	ACCGGACGTT	CGTGGGCTGC	4860
	ATGCGGAACC	TGTCACTGGA	CGGCAAAAT	GTGGACATGG	CCGGATTCTAT	CGCCAAATAT	4920
65	GGCACCGGGG	AAGGCTGCGC	TGCTCGGAGG	AATCTCTGCG	ATGGGAGCGG	GTGTGAGAA	4980
	GGAGGCACTT	GTGTCAACAG	GTGGAAATAT	TATCTGTGTG	AGTGTCCACT	CCGATTCCGC	5040
	GGGAAGAACT	GTGAGCAAGC	CATGCCCTAC	CCCCAGCTCT	TCAGCGGTGA	GAGCGTCTGT	5100
	TCCTGGAGTG	ACCTGAACAT	CATCATCTCT	GTGCGCTGTT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCCGGAAGG	AGGACAGCGT	TCTGATGGAG	GCCACCAATG	GTGGGCCCCC	CAGCTTTCCG	5220
70	CTCCAGATCC	TGAACAACTA	CCTCCAGTTT	GAGGTGTCCC	ACGGCCCCCTC	CGATGTGGAG	5280
	TCGCTGATGC	TGTCCGGGTT	GCGGGTGACC	GACGGGGAGT	GGCACCACTT	GCTGATGAG	5340
	CTGAAGAATG	TTAAGGAGGA	CAGTGAGATG	AAGCACTGG	TCAACATGAC	CTTGGACTAT	5400
	GGGATGGACC	AGAACAAGGC	AGATATCGGG	GGCATGCTTC	CGGGGCTGAC	GGTAAGGAGC	5460
	GTGGTGTGCG	GAGGCGCTTC	TGAAGACAAG	GTCTCGGTGC	GCGGTGGATT	CCGAGGCTGC	5520
75	ATGACGGGAG	TGAGGATGGG	GGGGACGCCC	ACCAACGTGC	CCACCTTGAA	CATGAACAC	5580
	GCACTCAAGG	TCAGGGTGAA	GGACGGCTGT	GATGTGGAGC	ACCCCTGTAC	CTCGAGCCCC	5640
	TGTCCCCCCA	ATAGCCGCTG	CCAOGAOGCC	TGGGAGGACT	ACAGCTCGGT	CTGTGACAAA	5700
	GGGTACCTTG	GAATAAAGCT	TGTGGATGCC	TGTCACTTGA	ACCCCTGCGA	GAACATGGGG	5760
	GCTGCGTGC	GCTCCCGCGG	CTCCCGCAG	GGCTACGTGT	GCGAGTGTGG	GCCCACTCAC	5820
80	TACGGGCGCT	ACTGTGAGAA	CAAACTCGAC	CTTCCGTGCC	CCAGAGGCTG	GTGGGGGAAC	5880
	CCCGTCTGTG	GACCTTGCCA	CTGTGCGCTC	AGCAAAGGCT	TTGATCCCGA	CTGTAATAAG	5940
	ACCAAGCGCC	AGTGCCCAAT	CAAGGAGAA	TACTACAAGC	TCCTAGCCCA	GGACACCTGT	6000
	CTGCCCTGCG	ACTGCTTCCC	CCATGGCTCC	CACAGCCGCA	CTTGCGACAT	GGCCACCGGG	6060
	CAGTGTGCTC	GCAAGCCCGG	CGTCACTGGC	CGCCAGTGCA	ACCGCTGCGA	CAACCCGTTT	6120
	GCGGAGGTCA	CCACGCTCGG	CTGTGAAGTG	ATCTACAATG	GCTGTCCCAA	AGCATTGAG	6180

5 GCGGCGATCT GGTGGCCACA GACCAAGTTC GGGCAGCCGG CTGCGGTGCC ATGCCCTAAG 6240  
 GGATCCGTTG GAAATGCGGT CCGACACTGC AGCGGGGAGA AGGGCTGGCT GCCCCAGAG 6300  
 CTCTTTAACT GTACCAACAT CTCCTTCGTG GACCTCAGGG CCATGAATGA GAAGCTGAGC 6360  
 CGCAATGAGA CGCAGGTGGA CGGCGCCAGG GCCCTGCAGC TGGTAGGGGC GCTGCGCAGT 6420  
 GCTACACAGC ACACGGGCAC GCTCTTTGGC AATGACGTGC GCACGGCCTA CCAGCTGCTG 6480  
 GGCCACGTCC TTCAGCACGA GAGCTGGCAG CAGGCTTCG ACCTGGCAGC CACGCAGGAC 6540  
 GCGCACTTTC ACGAGGACGT CATCCACTCG GGCAGCGCCC TCCTGGCCCC AGCCACCAAG 6600  
 GCGGCGTGGG AGCAGATCCA GCGGAGCGAG GCGGCGACGG CACAGCTGCT CCGGCGCCTC 6660  
 10 GAGGGCTACT TCAGCAACGT GGCAGCGAAC GTGCGGCGGA CGTACCTGCG GCCCTTCGTC 6720  
 ATCGTACCG CCAACATGAT TCTTGCTGTC GACATCTTTC ACAAGTTCAA CTTTACGGGA 6780  
 GCGAGGGTCC GCGATTTCGA CACCATCCAT GAAGAGTTCC CCAGGGAGCT GGAGTCCTCC 6840  
 GTCTCCTTCC CAGCGCACTT CTTAGACCA CTTGAAGAAA AAGAAGGCCCT CCTGCTGAGG 6900  
 CCGGCTGGCC GGAGGACCAC CCGCGAGACC ACGCGCCCGG GCGCTGGCAC CGAGAGGGAG 6960  
 15 GCCCGCATCA GCAGGCGGAG GCGACACCTT GATGACGCTG GCCAGTTGCG CGTCTGCTCTG 7020  
 GTCATCATTT ACCGCAACCT GGGGCGAGCT CTGCGCGAGC GCTACGACCC CGACCGTCCG 7080  
 AGCCTCCGGT GCGCTACCGT GCGCATCATT AATAACCCGA TGGTAGAGCA GCTGGGTGAC 7140  
 AGCGAGGGGG CTCGCTCCCT GAGACCCCTG GAGAGGCCCG TCCTGGTGGG GTTGGCCCTG 7200  
 CTGAGGTTGG AGGAGCGAAC CAAGCCTGTC TGGCTGTTCT GGAACCACTC CTTGGCGGTT 7260  
 20 GGTGGGACGG GAGGTTGGTC TGCCCGGGGC TGCGAGCTCC TGTCAGGAAA CCGGACACAT 7320  
 GTGCGCTGCC AGTGCGAGCA CACAGCCAGC TTTGCGGTGC TCATGGATAT CTCAGGGGTG 7380  
 GAGAACGGGG AGGTCCTGCC TCTGAAGATT GTCACTATG CCGCTGTGTC CTTGTCACTG 7440  
 GCAGCCCTGC TGGTGGCCTT CGTCTCCTG AGCCTGTGTC GCATGCTGCG CTCACACCTG 7500  
 CACAGCATTC ACAAGCACTT CGCGTGGCG CTCTCTCTCT CTCAGCTGGT GTTCTGTATT 7560  
 25 GGGATCAACC AGACGGAAAA CCGGTTTCTG TGACAGTGG TTGCCATCCT CTCCTACTAC 7620  
 ATCTACATGA GCACCTTTGC CTGGACCCCT GTGGAGAGCC TGCTGTCTTA CCGCATGCTG 7680  
 ACCGAGGTGC CCAACATGCA CACGGGGGCC ATGCGGTTCT ACTACGTCGT GGGCTGGGGC 7740  
 ATCCCGGCCA TTGTACAGG ACTGGCGGTC GGCCTGGACC CCCAGGGCTA CGGGAACCCC 7800  
 GACTTCTGCT GGCTGTGCT TCAAGACACC CTGATTGGA GCTTTGCGGG GCCCATCGGA 7860  
 30 GCTGTTATAA TCATCAACAC AGTCACCTCT GTCTTATCTG CAAAGGTTTC CTGCCAAAGA 7920  
 AAGCACCATT ATTAGGGAAA AAAAGGGATC GTCTCCCTGC TGAGGAGCCG ATTCTCTCTG 7980  
 CTGCTGCTCA TCAGCGCCAC CTGGCTGCTG GGGCTGCTGC CTGTGAACCG CGATGCACTG 8040  
 AGCTTCACT ACCTCTTCCG CATCTTCAGC GGCTTACAGG GCCCTTCTGT CCTCTTTTC 8100  
 CACTGCGTGC TCAACAGGA GGTCCGGAAG CACCTGAAGG GCGTGTCTCG CGGGAGGAAG 8160  
 35 CTGCACCTGG AGGACTCCGC CACACACAGG GCCACCTGCT TGACGCGCTC CCTCAACTGC 8220  
 AACACCACTT TCGGTGACGG GCCTGACATG CTGCGCAGAG ACTTGGGCGA GTCCACCGCC 8280  
 TCGCTGGACA GCATCGTCAG GGATGAAGGG ATCCAGAAGC TCGGCGGTGC CTCTGGGCTG 8340  
 GTGAGGGGCA GCCACGGAGA GCCAGACGCG TCCTCATGCG CCAGGAGCTG CAAGGATCCC 8400  
 CCTGGCCACG ATTCGACTC AGATAGCGAG CTGTCCCTGG ATGAGCAGAG CAGCTCTTAC 8460  
 40 GCCTCTCAC ACTCGTCAGA CAGCGAGGAC GATGGGGTGG GAGCTGAGGA AAAATGGGAC 8520  
 CGCGCCAGGG GCGCGCTCCA CAGCACCCCG AAAGGGGAGC CTGTGGCCAA CCACGTTCCG 8580  
 GCGCGCTGGC CGACGACAGG CTTGGCTGAG AGTGACAGTG AGGACCCGAG CGGCAAGCCC 8640  
 CGCCTGAAGG TGGAGACCAA GGTACGCGTG GAGCTGCACC GCGAGGAGCA GGGCAGTCAC 8700  
 CTGGGAGAGT AGCCCCCGGA CCAGGAGAGC GGGGGCGCAG CCAGGCTTGC TAGCAGCCAG 8760  
 45 CCCCCAGAGC AGAGGAAAGG CATCTTGAAA AATAAAGTCA CCTACCCGCC GCGCTGACG 8820  
 CTGACGGAGC AGACGCTGAA GGGCGGCTC CGGAGAGAAG TGGCCGACTG TGAGCAGAGC 8880  
 CCGCATCTCT CGCGCACGTC TTCCCTGGGC TCTGGCGGCC CCGACTGCGC CATCAGATC 8940  
 AAGAGCCCTG GGAGGGAGCC GGGGCGTGAC CACCTCAACG GGGTGGCCAT GAATGTGCGC 9000  
 ACTGGGAGCG CCCAGGCCGA TGGCTCCGAC TCTGAGAAAC CGTGAGGCAA GCCCGTCAAC 9060  
 50 CCACACAGCG TGCGGCATCA CCTCAGACC TTGGAGCCCA AGGGGCCACT GCCCTTGAG 9120  
 TGGAGTGGGC CAGAGATGTC GCGGTCCCCA TGGTGGCAGC CCCCCGACTG ATCATCCAGA 9180  
 CACAAGGTTC TTGGTTCTCC CAGGAGCTCA GGGCTGTGTA GACCTGTGTA CAAGTGCCAA 9240  
 AGGCCACAGG CATGAGGGAG GCGTGGACCA CTGGGCGAGC ACCGCTGAGT CCTAAGACTG 9300  
 CAGTCAAAGC CAGAACTGAG AGGGGACCCC AGACTGGGCC CAGAGGCTG CCAAGATTCA 9360  
 55 GGAACGCCGG GCACAGACCA AAGACCGGGG TCCAGCCCCG CCCAGSGGG CATCTCATGG 9420  
 CAGTGGCGAG CCGTGGCTGG CAGCCCGGCG AGTCCTTTGC AAAGGCACCC CTGTCTTAA 9480  
 AATCACTGCG CTATGTGCGA AAGGTGGAGA TACTTTTATA TATTGTATG GGACTCTGAG 9540  
 GAGGTGCAAC CTGTATATAT ATTGCATTG TGCTGACTTT GTTATCCCGA GAGATCCATG 9600  
 CAATGATCTC TTGCTGTCTT CTCTGTCAAG ATTGCACAGT TGTACTTGAA TCTGGCATGT 9660  
 60 GTTGACGAAA CTGCTGCCCT AGCAGATCAA AGGTGGGAAA TACGTGAGCA GTGGGGCTAA 9720  
 AACCAAGCGG CTAGAAGCCC TACAGCTGCC TTGGGCCAGG AAGTGAGGAT GGTGTGGGCC 9780  
 CTCCCGCGCG GCCCCCTGGG TCCCCAGTGT TGCTGTGTG TGCGTTTGTG CTCTGCTGCC 9840  
 ATCTGCCCGG GCTGTGTGAA TTCAAGACAG GGCAGTGAC CACTAGGCAG GTGTGAGGAG 9900  
 CCTGTCTGAG GTCACTGTGG GGCACGGTTG CCAACGGCT GTCATTTTT ACCTGGTCAT 9960  
 65 TCTGTACCA CACCCCCCTC CCTCACCAG CTCCAGGTG GCGCGGAGC TGCAGGTGG 10020  
 GATGGCTTTG TCCTTTGCTC CTGCTCCCGG TGGGACCTGG GACCTTAAAG CGTTGAGGT 10080  
 TCCTGATTG GACAGAGGTG TGGGGCCTTC CAGGCGGTTA CATACCTCTC GCCAATTCTC 10140  
 TAACTCTCTG AGACTGCGAG GATCTCCAGG CAGGGTTCTC CCTCTGGAG TCTGACCAAT 10200  
 TACTTCAATT TGCTTCAAT GGCCAAATTG GCAGAGGGAC AAAGCCACAG CCAACTCTT 10260  
 70 CAACGTTAC CAACTGTTT TTGGAATTC ACACCAAGGT CGGCCCCACT GCAGGCAGCT 10320  
 GGCACAGCGT GGGCGAGGG GCTGTGGAAAC GGGTCCCGGA ACTGTGAGC ATGTTTGATT 10380  
 TAGCGTTTC CTTTGTCTT CAAATCAGGT GCCCAATAA GTGATGACCA CAGCTGCTTC 10440  
 CAAATAGGAG AAACCATAAA ATAGGATGAA AATCAAGTAA AATGCAAGA TGTCCACACT 10500  
 GTTTTAAAT TGACCTGAGT GAAAATGTA GCACTGTTAG CAGATGCCCTA TGGGAGAGGA 10560  
 75 AAAGCGTATC TGAAAATGGT CCAGGACAGG AGGATGAAAT GAGATCCCG AGTCCTCACT 10620  
 CCGTAATGAA TTATACATGT GCCTTACCAG GTGAGTGTG TTTGGAAGAT AAAAAGTCT 10680  
 AGTCCCTTTA AACGTTTGGC CTTGGCGTTT CCTAAGTACG AAAAGGTTTT TAAGTCTTCG 10740  
 AACAGTCTCC TTCTAGTACT TTAACAGGAT TCTGCCCCCT GAGGTGTAAAT TTTTGTGTT 10800  
 TATTTTTTTC CAGCTACTTC ACAGCCAACA TCACGAGGTG TAATTTTTAA TTTGATCAGA 10860  
 80 ACTGTTACCA AAAACAACCT GTCAGTTTTA TTGAGATGGG AAAAATGTAA ACCTATTTTT 10920  
 ATTACTTAAG ACTTATGAG AGAGATTAGA CACTGGAGGT TTTTAAACAGA ACSTGTATTT 10980  
 ATTAATGTTT AAAACACTGG AATTACAAAT GAGAAGAGTC TACAATAAAT TAAGATTTTT 11040  
 GAATTTGTAC TTCTGCGGTG CTGGTTTTTC TCCACAAACA CCCCCCCCC TCCCCATGCC 11100  
 CAGGTTGGCC GTGGAAGGGA CGGTTTACGG ACGTGCAGCT GAGCTGTCCG TGTCCATGC 11160  
 TCCCTCAGCC AGTGAACGCT GCGGGAACCT TTTGTCCATT CCCTAGTAGG CTTGCCACAG 11220

CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTTGAGGAC TTTTTTTTTT TGCCATTATT 11280  
 TCTTCAGTTT TCTTTTCTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340  
 AGACGTTAGA CCTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTC

### 5 A32 Protein Sequence

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo  
 (Drosophila) homolog (CELSR1),  
 Hs.252387  
 Unigene number: NP\_055061  
 Protein Accession #: 1-20  
 Signal sequence: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,  
 1110-1199  
 Cadherin domains: Pfam domains: Laminin\_EGF [2003-2048], 7cm\_2 [2465-2708]  
 Latrophilin/GPS domains: 2407-2460  
 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704  
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51  
 MAPPPPPVLP VLLLLAAAA LPAMGLRAAA WEPRVPGGTR AFALRPGCTY AVGAACTPRA 60  
 PRELLDVGRD GRLAGRRRVS GAGRPLPQV RLVARSAPTA LSRLRLRARTH LPGCGARARL 120  
 CGTGARLGA LCFPPVPGGCA AAQHSALAAP TTLPACRCPP RPRPCPCGRP ICLPPGGSVR 180  
 25 LRLLCALRAA AGAVRVGLAL EAATAGTPSA SPSPSPPLPP NLPEARAGPA RRARRGTSGR 240  
 GSKLFFMPNY QVALFENEP A GTLILQLHAH YTIEGEEERV SYMEGLFDE RSRGYFRIDS 300  
 ATGAVSTDSV LDRETKETHV LRVKAVDYST PPRSATTYIT VLVKDTNDHS PVFEQSEYRE 360  
 RVRENLEVG EYLITRASDR DSPINANLRY RVLGGAADVQ QLNESGVS TRAVLDREA 420  
 AEYQLLVEAN DQGRNPGPLS ATATVYIEVE DENDNYPQFS EQNYVVQVPE DVGLNTAVLR 480  
 30 VQATDRDQGG NAAIHYSILS GNVAGQFYH SLSGILDVIN PLDFEDVQKY SLSIKAQDGG 540  
 RPPLINSSGV VSVQVLDVND NEPIFVSSPF QATVLENVPL GYPVVIQAV DADSGENARL 600  
 HYRLVDAST FLGGGSAGPK NPAPTDFPP QIHNSSGWIT VCAELDREEV EHYSGVEAV 660  
 DHGSPMSSS TSVSITLVLD NDNDPVFTQP TYELRLNEDA AVGSSVLTLO ARDRDANSVI 720  
 TYQLTGNTR NRPALSSQRG GGLITLALPL DYKQEQYVL AVTASDGRS HTAHLINVT 780  
 35 DANTRHPVQ SSHYTVSVSE DRFVGTISIAT LSANDEDTGE NARITYVIQD PVQFRIDPD 840  
 SGTMYTMEL DYENQVAYTL TIMAQDNGIP QKSDTTTLEI LILDANDNAP QFLWDFYQGS 900  
 IFEDAPPSTS ILQVSATDRD SGPNGRLLYT FQGGDDGDDG FYIEPTSGVI RTQRLRDREN 960  
 VAVYNLWALA VDRGSPTPLS ASVEIQVITL DINDNAPME KDELELFVEE NNPVGSVVAK 1020  
 IRANDPDEG NQAIMYQIVE GDMRHFFQLD LLNGDLRAMV ELDFEVREYR VLUVQATSAP 1080  
 40 LVSRAVTHIL LVDQNDNPPV LPDFQILFNN YVTNKSNSFP TGVIGCIPAH DPVDSDSLNY 1140  
 TFVQGNELRL LLLDPATGEL QLSRDLDNRR PLEALMEVSV SDGHSVTAP CTLRVITIITD 1200  
 DMLTNSITVR LLMQSQKFL SPALLFVEG VAAVLSTTKD DVFFVNVQND TDVSSNIIAV 1260  
 TFSALLPGGV RQGFPPSEDL QEQIYLNRTL LTTISTQRVL PFDDNICLRE PCENYMKCVS 1320  
 LRFDSNAPR LRSTTVLFRP IHPINGLRCR CPPGFTGDYC ETEIDLCSYD PCGANGRCRS 1380  
 45 REGGYTCECF EDFTGEHCEV DARSRCRANG VCRNGGTVCN LLIGGFHCVC PPGEYERPVC 1440  
 EVTTSPFPQ SPVTFRGLRQ RFHTITSLTF ATQERNGLLL YNGRFNEKHD FIALEIVDEQ 1500  
 VQLTFSAGT TTTVAPKVPS GVS DGRWHSV QVQYINKPMI GHGLPLHGFS GEKMAVTVTD 1560  
 DCDTMAVRF GKIDIGNYSCA AQGTQTGSKK SLDLTGPLLL GGVENLPEDF PVHNRQFVGC 1620  
 MRNLSVDGKN VRMAGFIANN GTREGCAARR NPDGRRQCN GGTCVNRWNN YLCECPLRF 1680  
 50 GNCCEQAMPH PQLPFGESV SWSDLNIIIS VPHYGLMFR TRKEDSVLME ATSGGPTSPR 1740  
 LQILNNYLPQ EYSHGSPDVE SVMLSGLRVT DGEWHLLIE LKNVKEDSEM KHLVTMTLDY 1800  
 GMDQKADIG GMLPGLTVRS VVVGASEDK VSVRRGFRGC MQGVRMGGTP TNVATLNMNN 1860  
 ALKVRVKDGC DVDDPCTSSP CPFNRSCHDA WEDYSCVCDK GYLGINCVDA CHLNPCENMG 1920  
 ACVRSPGSPQ GYVCEGSPSH YGPYCENKLD LPCPRGWMGN PVOCPCHCAV SKGFDPDCNK 1980  
 55 TNGQCQCKEN YYKLLAQDTC LPDCPPPHGS HSRTCDDMAT QCACKPGVIG RQCNRCDNPF 2040  
 AEVTLGCEV IYNGCPKAFE AGIWWQTKF QGPAAVPCPK GSVGNVVRHC SGEKGNLWPE 2100  
 LFNCITISFV DLRAMNEKLS RNETQVDGAR ALQLVRLARS ATQHTGLTFG NDVRTAYQLL 2160  
 GHVLQHSWQ QGFDLAATQD ADFHEDVIHS GSALLAPATR AAEQIQRSB GGTAQLRLRL 2220  
 EGYFSNVARN VRTTYLRPFV IVTANMILAV DIFDKFNFTG ARVERFDTH EEPRELESS 2280  
 60 VSFPADFFRP PEEKSGPLL R PAGRRITPQT TRPGPQTERE APISRRRRHP DDAGQFAVAL 2340  
 VIYRTLGQL LPERYDPDRR SLRLPHRP II NTPMVSTLVY SEGAPLPRPL ERPVLVEFAL 2400  
 LEVEERTKPV CVPMNHS LAV GGTGWSARG CELLSRNTH VACQCSHTAS FAVLMDISRR 2460  
 ENGEVLPKI VTYAAVLSL AALLVAFVLL SILVRMLRSNL HSIKHLAVA LFLSQLVFI 2520  
 GINQTNFPL CTVAAILLHY IYMSTFAWTL VESLHVYRML TEVRNIDTGP MRFYVVGWG 2580  
 65 IPAIVTGLAV GLDPQGYGNP DFCWLSLQDT LIWSPAGPIG AVIIINTVTS VLSAKVSCQR 2640  
 KHYYGKKG I VSLRLTAPLL LLLISATWLL GLLAVNRDAL SPHYLFAIPS GLQGPVLLF 2700  
 HCVLNQEVKR HLKGVLGGRK LHELSATTR ATLLTRSLNC NTTFGDGPDM LRTDLGESTA 2760  
 SLDIVRDEG IQKLGVSGL VRGSHGEPDA SLMPRSCKDP PGHDSDSSE LSLDEQSSSY 2820  
 ASSHSSDSE DGVAEEKWD PARGAVHSTP KGDAVANHPV AGWPDQLAE SDESDEPSGK 2880  
 70 RLKVTKVS ELHREBQGS RGEYPPDQES GGAARLASSQ PFEQRKGILK NKVTYPPPLT 2940  
 LTEQTLKRL REKLADCEQS FTSRTSSSLG SGGPDCAITV KSPGREGRD HLGAVAMNVR 3000  
 TGSQAQDGS SEKP

### 75 A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Probeset Accession #: X95876  
 Nucleic Acid Accession #: X95876  
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 CCAACCAAA GCACCAAGC AGAGGGGCG AGAGCACACC ACCAGCAGC CAGAGCACCA 60  
 GCCACGCCAT GGTCTTGAG GTGAGTGACC ACCAAGTGCT AAATGAGGCC GAGGTTGCCG 120

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

CCCTCCTGGA  GAACCTCAGC  TCTTCTATG  ACTATGGAGA  AAACGAGAGT  GACTCGTGCT  180
GTACCTCCCC  GCCCTGCCCA  CAGGACTTCA  GCCTGAACTT  CGACCGGGCC  TTCTTGCCAG  240
CCCTCTACAG  CCTCTCTTT  CTGCTGGGGC  TGCTGGGCAA  CGCGCGGTG  GCAGCOGTGC  300
TGCTGAGCCG  GCGGACAGCC  CTGAGCAGCA  CCGACACCTT  CTTGCTCCAC  CTAGCTGTAG  360
CAGACACGCT  GCTGGTGTGC  AACTTGCCGC  TCTGGGCAGT  GGACGCTGCC  GTCCAGTGGG  420
TCTTTGGCTC  TGGCCTCTGC  AAAGTGGCAG  GTGCCCTCTT  CAACATCAAC  TTCTACGCAG  480
GAGCCCTCCT  GCTGGCCTGC  ATCAGCTTTG  ACCGCTACCT  GAACATAGTT  CATGCCACCC  540
AGCTCTACCG  CCGGGGGCCC  CCGGCCCGCG  TGACCCCTAC  CTGCCTGGCT  GTCTGGGGGC  600
TCTGCCTGCT  TTTGCGCCCT  CCAGACTTCA  TCTTCTGTGC  GGGCCACCAC  GACGAGCGCC  660
TCAACGCCAC  CCACTGCCAA  TACAACCTCC  CACAGGTGGG  CCGCACGGCT  CTGCGGGTGC  720
TGCAGCTGGT  AGGCGCTTTC  CTGCTGCCCC  TGCTGGTCAT  GGCCTACTGC  TATGCCACA  780
TCTTGGCCGT  GCTGCTGGTT  TCCAGGGGCC  AGCGGGCGCT  GCGGGCCATG  CGGCTGGTGG  840
TGGTGGTCTG  GGTGGCCTTT  GCGCTCTGCT  GGACCCCTTA  TCACCTGGTG  GTGCTGGTGG  900
ACATCCTCAT  GGACCTGGGC  GCTTTGGCCC  GCAACTGTGG  CCGAGAAAGC  AGGGTAGACG  960
TGGCCAAATC  GGTCACTTCA  GGCGTGGGCT  ACATGCACGT  CTGCCTCAAC  CGGCTGCTCT  1020
ATGCGTTTGT  AGGGGCTCAAG  TTCCGGGAGC  GGATGTGGAT  GCTGCTCTTG  CGCCTGGGCT  1080
GCCCCAACCA  GAGAGGGGCTC  CAGAGGCAGC  CATCGTCTTC  CCGCGGGGAT  TCATCTGGT  1140
CTGAGACCTC  AGAGGCTCTC  TACTCGGGCT  TGTGAGGCGG  GAATCGGGC  TCCCTTTTCG  1200
CCACAGTCT  GACTTCCCCG  CATTCACGGC  TCCTCCTCTC  CTCTGCGGCG  CTGCGCTCTC  1260
CCCAATATCC  TGCTCCCCGG  GACTCACTGG  CAGCCCCAGC  ACCACAGGT  CTCCCGGGAA  1320
GCCACCTGCT  CAGCTCTGAG  GACTGCACCA  TTGCTGCTCC  TTAGCTGCCA  AGCCCATATC  1380
TGCCGCCCGA  GGTGGCTGCC  TGGAGCCCCA  CTGCCCTTCT  CATTTGGAAA  CTAAACTTTC  1440
ATCTTCCCA  AGTGGCGGA  GTACAAGGCA  TGGCGTAGAG  GGTGCTGCC  CATGAAGCCA  1500
CAGCCCCAGC  CTCCAGCTCA  GCAGTGACTG  TGGCCATGGT  CCCCAGACC  TCTATATTG  1560
CTCTTTTATT  TTTATGTCTA  AAATCTGTCT  TAAACTTTT  CAATAACAA  GATCGTCAGG  1620
ACCAAAAAAA  AAAAAA      AAAAAA      AAAAAA      AAAAAA      BHCLITERAT  1680
UREBHCBLAS  TPBHCORTHO  LOGUESMOUS  ECKRMYLEV  SERQVLASD  FAFLENSTIS  1740
PYDGENESD  FSDSPPCPD  FSLNFDRTFL  PALYSLLFL  GLLNGAVAA  VLLSQRTALS  1800
STDFTLLHLA  VADVLLVLT  PLNAVDAVQ  WVFGPGLCKV  AGALFNINFY  AGAFLLACIS  1860
FDRYLSIVHA  TQYRRDPRV  RVALTCIVVM  GLCLLFPALP  FIYLSANYDQ  RLNATHCQYN  1920
FPQVGRALR  LLVAVGFL  PLLVMAYCYA  HILAVLLVSR  GQRRFRAMRL  VVVVAAFAV  1980
CWTPLYHLVL  VDILMDVGV  ARNCGRESHV  DVAKSVTSGM  GYMHCCLNPL  LYAFVGVKFR  2040
EQMWMLFTRL  GRSDQRGPQR  QPSSSRRESS  WSETTEASYL  GL
  
```

**A34 Protein sequence**

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Protein Accession #: P49682  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [70-318]  
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323  
 DRY box: 148-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MVLEVDHQV LNDAEVAALL ENFSSSYDYG ENESDSCTTS PPCPDQFSLN FDRAFLPALY 60  
 SLLFLGLLG NGAVAVLLS RRTALSSTDT FLLHLAVADT LVLTLPLWA VDAAVQWVFG 120  
 SGLCKVAGAL FNINFYAGAL LLACISFDXY LNIIVHATQLY RRGPPARVTL TCLAVWGLCL 180  
 LFLALPDFIFL SAHDERLINA THQYNFPQV GRTALRVLQL VAGFLPLLV MAYCYAHILA 240  
 VLLVSRGQRR LRAMRLVVVV VVAFALCWTP YHLVVLVDIL MDLGLALRNC GRESRVDAVK 300  
 SVTSGLYGYM CCLNPLLYAF VGVKFRERMW MLLRLGLCPN QRGLQRQPSS SRRDSSWSET 360  
 SEASYSGIL

**A35 DNA SEQUENCE**

Gene name: Differentially expressed CO16 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 Probeset Accession #: AA447522  
 Nucleic Acid Accession #: BC001291  
 Coding sequence: 44-541 (start and stop codons are underlined)

65  
 70  
 75  
 80

```

1 11 21 31 41 51
| | | | |
GGGGGCGCCG CGCGCTGACC CTCCTGGGCG ACCGCTGGGG ACGATGGCGC TGCTCGCCTT 60
GCTGCTGGTG GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120
AGATCCAGAG GACTCCCAGC GAACGACGGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
TGAGAGAGAA AACACTTTTC AGTGCCAGAA CCCAAGGAGG TGCAATAGGA CAGAGCCATA 240
CTGCGTTATA CGCGCCGTGA AAATATTTC ACCTTTTTTC ATGGTTGCGA AGCAGTGCTC 300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
GCCATGCCCT TCTTTTACC TCAAGTGTG TAAATTCGC TACTGCAATT TAGAGGGGCC 420
ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
GCTGTGGCTG GCCATCTCTC TGCTGCTGGC CTCATTGCA GCGGCGCTCA GCCTGTCTTG 540
AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTGTGC 600
ACCTGTTGCA TTAACCTTGT TTTCTGTTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT 660
GGGATGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
ACATTACAGG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTTC 780
AAATCAAACC TTGTAACCTA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCCCTCTG 840
CCTCTGAGGG CTCTCAGTAT GATGGGGAGG GAGGCCTAAG TACCCTCAT GCAGAGTATG 900
TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATG 960
GGGTGAAGAC ATCCCTGAGG TGAAGGACTC CTCAGCATGG GGGGCGATGG GGCACACGTT 1020
AGGGCTGCCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC 1080
  
```

5 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140  
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200  
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260  
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAACAAAT ACAAGGGGAC 1320  
 TTCAAAGTT CACGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

10 A36 Protein sequence:  
 Gene name: Differentially expressed CO16 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 Probeset Accession #: AA447522  
 Protein Accession #: AAH01291  
 Signal sequence: 1-17 (first underlined sequence)  
 Transmembrane domain: 146 - 162  
 Cellular localization: plasma membrane

20 1 11 21 31 41 51  
 MALLALLLVV ALPRVWTDAN LTARQRDPED SQRTDEGDNR VVCHVCEREN TFEQNPERRC 60  
 KWTEPYCVIA AVKIPPRFFM VAKQCSAGCA AMERPKPEEK RFLLEPPMPF FYLKCKCKIRY 120  
 CNLEGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSL

25 A37 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

30 1 11 21 31 41 51  
 35 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60  
 CCGTCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120  
 GTGCAACATA CCAGGCAACT TCATGTGCGA CAATGGACGG TGCAATCCCG GCGCCTGGCA 180  
 GTGTGACGGG CTGCGTGAAT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTCGAAATGT GGCCCAACT TCTTCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG 300  
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTCTG CTTTGTCTCA CGCCCGGCTA CCACTGCAAG AACGGCTCT GTATTGACAA 420  
 GAGCTTCATC TCGATGTGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 AAGTTCTCAA GAACCCGACA GTGGGCAAGT GTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 TTACCCACGC ATCACTATG CCACTCATCG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCGTCTGGCA CTGGCTTTCG ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCGCGT 660  
 45 GCACCGGCTG CAGCAGCGTG TGCTGTCTGC CGGCTGGTGG GTCTTGGACC ACCCCACCA 720  
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 GAATGCGCTG GAAGTACGCT CCCCACCTC CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840  
 TGGTGGTATG GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
 50 CGACCTGCCC CCCTACCGCT CCGGTCGCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960  
 CAGCAGCTCT CAGCAGGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020  
 GGGCAGCTCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACT GTTGCCATTG TAACAATTTG 1140  
 TGCTCATGGG AAGCTCTTGA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 55 AACTATCTCT GCATTCCCTC CCTCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260  
 TGACATGATC TGTGTGCGT CTTTCTGTC AGGTCACTCT TCCCTTGGGA CCGGAGATCA 1320  
 CACCCTCAT TTTCACTATA TTCTGTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380  
 AAATAGGCTG GAGAGAGACA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500  
 60 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAAT CCATTTGAGC 1560  
 ATCAAAACCT GCTTGCACA ATCCTATTG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620  
 AAGAAACTT TGGACGTGAG TAACACCTT CAGCAGTGGC AAGCTTATTG TGGTTTGTG 1680  
 AAGGACTCTG AAACCATCTA CCGTGTATAA ATTCTGGCT TAGAAATTTG CCCAAGAAATG 1740  
 CTCATTCTGA GAGCTTCTC CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800  
 65 GAGCCCTCC CATGAGTTTA TCCAAGTCT CAGCTCTTAA AATGCAGGCT GCCAAGACCC 1860  
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCACAGCTG 1920  
 ACCTGCCCCG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAGTCT TGACCTGGCT 1980  
 GTATGTCCTT GTGGCCACCA CCCAGCCTGT CTGTCTCATT CATGCAGCCT CAACACTGGC 2040  
 CTCCAAAGTT CCCTAACACG TTGCAAGTCT CTTTCTACCT GTGCATTGGG ACTTGAGGAC 2100  
 70 ACTGPTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTGAGGGT AGGCTCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340  
 TGAAACAGTG TGTGTGTTT TTCCCTTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400  
 75 AGCTGTCTCT TTTTGTGTT TTCTTTTAA AAGTCCAAA GAAAGATGCA AAGGAGATC 2460  
 ACACCCCTGC CCCCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520  
 ACATTGTGTC ATTTGTGACG TTTGAGGTTA TTATTATCA AGTCTTTGAA GGAAGCAGAA 2580  
 AGAGGCACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640  
 TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAACGTT 2700  
 80 AGGTGTGTTG TGGCAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGTAGAG 2760  
 CCACTCGGG CAGCTGTAC CCATTGAGAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820  
 AACCTGTGTT ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAGG TGGCATTGAC 2880  
 TGATCCGTGT CTGTAGACTT TCTTTCTTT TTTTAAACAA ATCCAAAGGA TGTATACGAA 2940  
 AAGCTAGCCA CTGTATTTT GTTTGTGTTA AAAAAAAGA GAAAGAAAGA AAGAAAGAAA 3000

AACGGAAGG AACCTAGCTG CTTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTCATCT CTTGTAGATC AGAAGGGCTT TATTCTCCC TTTGATGGG CCCCTCTCTC 3180  
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATAGT 3300  
 AGATAAGGGA TGCCCTACTAA TGCCTTTTAA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACAG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTTACCTT GAAATTGACA 3660  
 TTTTAAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTTGT GTGTGCTTGC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780  
 TTATACTTTC TAATAAAATT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GNMCTAMARM 3840  
 AAMMAAAAC AMYWTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGCGCGG ICDGQNNQD NSDEESCESS QEPGSGQVFF TSENQLVYYP SITYAIIGSS 3960  
 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAAAAAA ACCGCGCGGG 4020  
 GGAACCGCA GAGTGTGCG TAAACCAAC CCAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

**A38 Protein sequence:**  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MWLLGFLCLL LSSAAESQLL PGNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECFKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSF ICDGQNNQD NSDEESCESS QEPGSGQVFF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHFN VTYNVNNGIQ 240  
 YVASQAQNA SEVGSPSYS EALLDORPAW YDLPPFPYSS DTESLNQADL PPRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

**A39 DNA sequence**  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGCTGCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60  
 GGAAGAAAC TTCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCGAGC 120  
 GACCGGAGGA GGGAGAGCG GCGGAGGCT GCGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGAGGCGG AGAAGGGGAA CCGGGCGAG CGCCCGCCT GATCCGCGC CCAGCAGCAG 240  
 CCGCGGCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCG CTGGGGGCGC GCAGGACCTC 300  
 CGCTCGCTC CTGGACCTTC CCGGGGAGG GTCCGCTTGC CAGTGAATC TCCAGAGGCT 360  
 TCGGAGCAG AGCCCCGGG GCCTTCTGAC TGATCCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAGG CAGTCCCTAA GGGGACGGG CCACCGGCTG AGGACGGGA TGGCTTAGGA 480  
 GCTCTGAGC CTAGGGCCCG GGTGCTGTC CTCTGGGCG TCGCGCAGA GGGGAGTGCC 540  
 CCGCGCGGA AGCGCGCGG GACAGTCAGT GACGAGGCC GGGGGTCCG GGGGCCACGA 600  
 CTTCTCGAG ACCGTCTGC GCTCTCTGA GACGCGCTGT CCGCGGCCAG GGTGGTGCA 660  
 TGTGGGGGCG TCGCGCTCG TCGCTCTCT CATCTTGAA CGCGCTTCG CTCTGCAGC 720  
 TGCTGCTGC TGCGCTGCT GCGGCGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGC 780  
 TGGCTGGAG CGCAGGGGT CTGGGCGATC GGCTTCCAGT GTCCGAGCG CTTCGACGC 840  
 GCGGACGCA CATCTGCTG CGGCAGCTGC GCTTGCCTC ACTGCTGCTC CAGCGCGAG 900  
 GCGCGCTCG ACCAGGGCG CTGGGACAAT GACCGCGAG AGGGCGCTG CGAGCTGCG 960  
 CCGGGGACA AAGACGGGC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGG AGGGTGCGCC CCCACCGGTG AGGGCTGGC AGCGGTGCTC CCCTGAAGGC 1080  
 TCCCGAAAG GAAGGCGCT CCTCAGGCT TCCCGGGGCG TGTGCCCCG TGCCAGACGC 1140  
 CGCGGATTCC CATCTCTCC AGCGCGCGC CCTCTTCCC TGCAGCGCC CGCCTTGCC 1200  
 ATCTACGTG CGTCTCTCAT TGTGGCTCC GTGTTGTGC CTTTATCAT CTTGGGGTCC 1260  
 CTGTGGGAG CAGTGTCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320  
 GCGGAGGGG GTAAACCGCT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACTCC 1380  
 CGGGGGTCT CCTACGCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CCGCACTCC 1440  
 GGGGCGCGG CGCCCCAAC AAGGTACAG ACCAAGTGT GCTTGCCGA AGGGACCATG 1500  
 AACACGTGT ATGTCAACAT GCGCAGAAAT TTCTCTGTG TGAAGTGA GCAGGCCACC 1560  
 CAGATTGTG CACATCAAG GCAATATCTG CATCCCCAT ACGTGGGTA CAGGGTGA 1620  
 CAGCACTCT TGCCCATGAC AGCTGTGCCA CCTTTCATG ACAGGCTGCA GCCTGGCTAC 1680  
 AGGCAGATT AGTCCCCCT CCTCACACC AACAGTGAAC AGAAGATGA CCGAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCA TGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTG GTGGTATTTA TGGCAGGATT CTTTGGATG 1860  
 GCTTATTGT CCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTCT GGATATGTT 1920  
 CATCCAGGT ATCATTGAT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TGTGATGG GTGTATAACA AATGCTTGTG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGATTTTA TAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTT 2100

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75

TTGTTGTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160  
 TTTTITTTTT TTTTITTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG 2220  
 TGGTGGGATC TGGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCTCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TGTATTTTTT 2340  
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGTGCTCTC ACTCTCTGA CCTCAAGCAA 2400  
 TCTGCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC 2460  
 TGAGCCTTTT TTTTCTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAA TAACAGGACT 2520  
 ATTCTAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580  
 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640  
 GGGCTATTTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700  
 TTAAGAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760  
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCACTT CATCCCCTTC 2820  
 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCCTTTT 2880  
 TATATTGAAA TCATAAACTA TCACCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940  
 TGGTTATGGT TTGGCGTTTC CTTCGTTTG GTTTTCAGAG CCCCCTGTCT ATATAGTCCT 3000  
 GAGTGCAGT ACTTCTATA CTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060  
 AAAAAATTTT TGTCTTAGT TATAAAATT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCTTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTTT 3180  
 GGAGATCAT AAGCTTTTAA TACTCTGTT ATCAAAATGG CTTATTTTTC AGGCACCTAG 3240  
 GATTGTTAAG AGAAAGCTT TTCAACGAAG GATTGCTTTT CTTCTCCAC ACTGTTCTTG 3300  
 ATTTCTCTC TCTTTCAGG CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360  
 CAAATTCAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480  
 GTATGGTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540  
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAAT GGTATCATCA ATGATACTCA 3600  
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGAATAAATA AAAAAAATA AAAAAAATA

#### A40 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular localization: not determined

1 11 21 31 41 51  
 MLSEFLMSPS QHRAQYTPG GKLPWEASI GAHRSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKNRGE PPWIRAOQQ PRPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPFPA 120  
 SGRQPRGPSD CIPRFPASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEBSGS 180  
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVV CGALAARPS HPPTPLRSCS 240  
 CNWLRCWRRG RGPSPGEYCHG WLDAQGVWRI GFQCPERFDG GDATCCGSC ALRYCCSSAE 300  
 ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTO GDGBGAPPPV RAWQRCSPFG 360  
 SPKGRQLLRA PPGLLPRARR RGFPSPPRGG PSLQRPALP IYVPFLIVGS VFAVFIILGS 420  
 LVAACCCRLC RPKQDPQQR APGGRNRLMET IFMIPASSTS RGSSSRQSSST AASSSSSANS 480  
 GARAPPTRSQ TNCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGYL HPFYVGYTVQ 540  
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQMYPV TV

#### A41 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTACAG TTTCTTCCAA CTTTGCCATT 120  
 GCAATAAAAA AGGAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 ATGTTTATTC ATCACCTTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300  
 CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420  
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGCCTC GGGATTATAC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540  
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAAGT CAAATTTTCA 600  
 GAAGAAACCC TCTGGCATAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660  
 TTACTATTTA GTTTTITTA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTITTA 720  
 TCTGAAAAAA AAAAAAATA AAAAAAATA

#### A42 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

1 11 21 31 41 51  
5 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60  
PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTIDKNLS PDGQYVPRIM 120  
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

10 A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
Unigene number: Hs.106778  
Probeset Accession #: N51919  
Nucleic Acid Accession #: AF189723  
15 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51  
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
ATTCTCCAAG CTGATCITCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTCTGGCCTT CTGCAGTCAT CAGTGTTTTA 240  
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
25 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTGAAG AATTGAGTAA ACTTGTGCCA 360  
CCAGAATGCC ATTGTGTGCG TGAAGGAAAA TTGAGCATA CACTTGCCCG AGACTTGGTT 420  
CCAGGTGATA CAGTTTGCTT TCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTIT 480  
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTICT 540  
AAGGTGACAG TCCTTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
30 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTGTGTCAT TGGACAGGA 660  
GAAATTCCTG AATTGTGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
CCTCTGCAGA AGAGCATGGA CCTCTAGGA AAACAACCTT CTTTACTCT CTTTGTGATA 780  
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840  
ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTACACAGT 900  
35 ACGCTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAGGG CCATTGTGAA AAAGCTGCCT 960  
ATTGTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGG AACACTGAGC 1020  
AAGAATGAAA TGACTGTATC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTACT 1080  
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTC 1140  
40 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAAAT 1200  
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCATGAAG 1260  
ATTGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTAGCTCT 1320  
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
TGTTTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
45 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500  
ATGGGCTCAG CCGGACTCAG AGTTCTTCTT TGGCTTCTG GTCCCTGAAT GGGCAGAGCT 1560  
ACATTCTTGT GCTTGGTGGG AATCAATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620  
ACAACACTCA TGGCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTG ACAGGAGACT 1680  
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCAAAAA CTTCCTCAGT AGTCTCAGGA 1740  
50 GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTCTACAAA TAGTACCAA GGCTGCAGAC 1800  
TTTTACAGAG CTAGCCCAAG GCACAGATG AAAATATTA AGTCGTACA GAAGAAGCGT 1860  
TCAGTTGTAG CCAATGACAG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920  
ATGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980  
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGAATTTAT 2040  
55 AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100  
ATCTCATGGG CTACATTAAT GAACCTTCTT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160  
ATCAATATTA TTATGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAAC AGTGATATAA 2220  
GATGTCTTTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAATCTGATA 2280  
CTTAAATATC TTGTTTCATC AATAATCATT GTTGTGGGA CTTTGTGTTT CTCTGGCGT 2340  
60 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400  
TTTTTGACA TGTTCAATGC ACTAAGTCC AGATCCCGA CCAAGTCTGT GTTTGAGATT 2460  
GGACTCTGCA GTAATAGAAAT GTTTGTCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520  
CTAGTTATTT ACTTCTCTCC GCCTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
GATCTGTGTT TCTTTTGGG TCTCACCTCA TCACTGTGCA TAGTGGCAGA AATTATAAAG 2640  
65 AAGGTTGAAA GGAGCAGGGA AAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700  
CTTGAAGTAT GA

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
Unigene number: Hs.106778  
70 Probeset Accession #: N51919  
Protein Accession #: AAF27813  
Signal sequence: none found  
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
75 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
Cellular Localization: not determined

80 1 11 21 31 41 51  
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FRGWNEFDIS EDEPLWKKYI 60  
SQFNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQYRSEK SLEELSKLVP 120  
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180  
KVTAQPAAT NGDLASRNI AFMGTIVRCG KAKGVVIGTG ENSEPGEVFK MMQAEAPKT 240  
PLQKSMOLLG KQLSPYSFGI IGIIMLVGWL LKGDILEMFT ISVSLAVAAI PEGLPIVVTV 300



5 TLALGVMRMV KKRAIVKILP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360  
 GVGYNQFGEV IVDGDVVHGF YNPVSRIVE AGVCNDAVI RNNTLMGKPT EGALIALAMK 420  
 MGLDGLQQDY IRKAEYFFSS EQKWMVAVKV HRTQODRPEI CFMKGAYEQV IKYCTTYQSK 480  
 10 GQTLTLTQQQ RDVYQOEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV 540  
 TLLIASGVST KMITGDSQET AVAIA SRLGL YKSTQSQSVSG BEIDAMDVQQ LSQIVPKVAV 600  
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADMI 660  
 LVDDDFQTTM SAIEEGKGIY NNINFNVRFP LSTSLAALT ISLATLMMFP NPLNAMQILW 720  
 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780  
 ELRDNVITPR DTTMTFTCFV PFDMEALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMQQL 840  
 15 LVYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVEREREKIQ KHVSTSSSF 900  
 LEV

**A45 DNA sequence**

15 Gene name: ESTs  
 Unigene number: Hs.157601  
 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

20  
 1 11 21 31 41 51  
 25 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60  
 TTTTATTTCG AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120  
 CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180  
 ACATAACAGT GTCCCAAGTG GCAGCCGCGC CCGGGGCGCC CTTCTGTGA TCCCGTAGCG 240  
 CCCCCTGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGCGAC CGAGCGCTGG 300  
 TCGCCGCTCT CCTTCGGTTA TATCAACATG CCCCCTTTC TGTGTCTGGA GGCCGTCTGT 360  
 30 GTTTTCTCTT TTTCCAGAGT GCGCCCATCT CTCCTCTCC AGGAAGTCCA TGTAAAGCAA 420  
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480  
 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAAG 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600  
 GCATTCCAGT TCAGTTCAC TCCTCATCTG GAATTCCTCT TGGATTCATT TTCAACCCAA 660  
 35 CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720  
 CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCTGGAG GCAGAAATGC TTCTGTGCCC 780  
 CAGATCCTCA TCATCGGTAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900  
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGCAGCACG TGCTGTGGC TGAGCAGGTG 960  
 40 GAGGATGCCA CCAACGCCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCAGCGGCC 1020  
 ACGCCAGACT GCAGGGTCCA GGCTCACCCC TGTGAGCACA GACCGCTGGA GATGGTCCGG 1080  
 GAGTTGCTCG GAAATGCCCC ATGCTGGAGA GATCGCGGCC GACCCCTTGC GGTGCTGGCT 1140  
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTCTCTAA CCCACCTTGC CACTGCTTAC 1200  
 45 AGGACCACTT GCCCAGGCCCT CTGTGACTCG CAGCCCTGCC AGAATGAGG CACATGTGTT 1260  
 CCAGAGGAC TGAGCGGCTA CCAAGTGCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320  
 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCTGCTT GGACAGCTCT 1380  
 GCGGGCACCA CTCTGGACGG CTTCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGGCG 1440  
 GCGTCTCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500  
 CTGGTGGCGG TGCTGTGGGG GGAGTACCAG GATGTGCTCG ACCTGGTCTG GAGCCTCGAT 1560  
 50 GGCATTCCCT TCGGTGTGCG CCCACCCCTG ACGGGCAGTG CCTTGGGCA GGCGGCAGAG 1620  
 CGTGGCTTGG GAGAGGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTGT 1680  
 CTCAGTGAAT CACTCTCCGA GGATGAGGTT GCGGGCCCGC CGCGTCAACG AAGGGCGCGA 1740  
 GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800  
 GGCAAGCCAA AGCATGTGAT GGTCTACTCG GATCTCAGG ATCTGTTCAA CCAAATCCCT 1860  
 55 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGGT GCGGACACA AGCCCTGGAC 1920  
 CTGCTCTTCA TGTTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980  
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGG 2040  
 CTGCTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGACACCAA ACCCAACCGG 2100  
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGTGGG CTGACCCGGC 2160  
 60 ACCGCCCTGC TGACATCTTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220  
 GTCCCAAGAG CTGTGGTGGT GCTCACAGGC GGGAGAGCGG CAGAGGATGC AGCCGTTCCT 2280  
 GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGTGCG TGGGCGTGGG GCCTGTCTTA 2340  
 AGTGAGGGTC TGCGAGGGCT TGACAGTCCC CGGGATTCCC TGATCCAGCT GGCAGCTTAC 2400  
 GCGACCTGCG GGTACCAACA GGACGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460  
 65 CAGTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCTG CCTGCAGAA 2520  
 GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCTACTGCGA GAACCGTGAG 2580  
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATTG TTGAGACGCC CCTGAGGCAC 2640  
 ATGGCTCCCG TGACGAGGGG CAGCAGCCGT ACCCCTCCCA GCAACTACAG AGAAGGCCTG 2700  
 GGCACTGAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760  
 70 TTCCCGCGST GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCAACA AACGATGTTG TTGAAAAGTT 2880  
 TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CTTTGTGAG GCTATGTCT 2940  
 CTGCCACCTT TCCTTGGAGG ATAAACAAGG GGTCTCTGAG ACTTAAATTT AGCGGCTGTA 3000  
 CGTTCTCTTG CACACAATCA ATGCTGCGCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060  
 75 AGGCTTTTAC TAGAGCATCC TTTGGAGGCG GAAGGCCACG GCCTTTCAAG ATGGAAGGCA 3120  
 GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTG GCATTGAGTC TGAAAGGGGG 3180  
 CTTGAGGAGC GTTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAAGA GACTTGGAAA 3240  
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTGTG TGATGGGGGA GGGGCTGAGT 3300  
 80 TGTGATGGG CCCAGGTCTG GAGGGCCACG TAAATCGTGT CTGAGTCTGG AGCAGTGTCC 3360  
 ACCTGAAGG TCCTC

**A46 Protein sequence**

Gene name: ESTs

Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

10 1 11 21 31 41 51  
 | | | | | |  
 MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60  
 SVKGSGSPERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120  
 15 MVFKGGRTRT ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180  
 FAVGVRFRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCM RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360  
 RAKVVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVFDLVNSL DGIFPRGGPT 420  
 20 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480  
 EAVRAELEEE TGSPKHVMVY SDPQDLFNQI PELQGLKCSR QRPGRCTQAL DLVFMLDTS 540  
 SVGPENFAQM QSFVRSCALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLGGVGSA GTALLHIYDK VMTVQRGARF GVPKAVVVLT GGRGAEDAAV PAQKLRRNGI 660  
 SVLVVGVGVF LSEGLRRLAG PRDSLHVA YADLRVHQDV LIENLCGEAK QPVNLCKPSP 720  
 25 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENTR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFW NVCAQGP

## COLON

30 A47 DNA SEQUENCE:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 35 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 | | | | | |  
 CGGCACCAAG AGCACTGGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120  
 GCATAAAAA AGGAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 45 ATGGTTATTC ATCACTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300  
 CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCTAGAAAT CATGTTTGT 420  
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGCTC GGGATTATACC CCTATTGATA GAAACATGA AGAAGCATT AAGACTTATT 540  
 50 CAGTCAGACC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAGAGAT CAAATTTTAT 600  
 GAAGAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660  
 TTACTATTTA GTTTTITTA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTITTA 720  
 TCTGAAAAA AAAAAA AAAAAA

55 A48 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 60 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

65 1 11 21 31 41 51  
 | | | | | |  
 MMLHSALGLC LLLVTSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAQKSKK 60  
 PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETDKNLS PDGQVYVPRIM 120  
 70 FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A49 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 56  
 75 Unigene number: Hs.6527  
 Probeset Accession #: AA478599  
 Nucleic Acid Accession #: NM\_005682  
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | | |  
 CGGCAGCAGG GTCTCGCTCT GTACACAGG CTGGAGTGCA GTGGTGTGAT CTTGGCTCAT 60  
 CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120  
 ATTACAGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CAGTCGCTG 180

CTGCAGACGA CACTGTTCCT GCTGAGTCTG CTCTTCCTGG TCCAAGGTGC CCAACGCGAGG 240  
 GGCCACACAGG AAGACTTTGG CTCTGTCAGC CAGCGGAACC AGACACACAG GAGCAGCCTC 300  
 CACTACAAAC CCACACCAGA CCTGCGCATC TCCATCGAGA ACTCCGAAGA GGCCCTCACA 360  
 GTCCATGCCCT CTCTCCCTGC AGCCCAACCT GCTTCCCGAT CCTTCCCTGA CCCCAGGGGC 420  
 CTCTACCACT TCTGCCTCTA CTGGAAACGA CATGCTGGGA GATTACATCT TCTCTATGGC 480  
 AAGCGTGACT TCTTGCTGAG TGACAAAGCC TCTAGCCTCC TCTGCTTCCA GCACCAGGAG 540  
 GAGAGCCTGG CTCAGGGGCC CCCGCTGTTA GCCACTTCTG TCACTCCTG GTGGAGCCCT 600  
 CAGAACATCA GCCTGCCAGC TGCCGCCAGC TTCACTTCT CTCTCCACAG TCCTCCCCAC 660  
 ACGGCCGCTC ACAATGCCTC GGTGGACATG TGGAGCTCA AAAGGGACCT CCAGCTGCTC 720  
 AGCCAGTTTC TGAAGCATCC CCAGAAGGCC TCAAGGAGGC CCTCGGCTGC CCCCAGGAGC 780  
 CAGCAGTTGC AGAGCCTGGA GTCGAAACTG ACCTCTGTGA GATTATGGG GGACATGGTG 840  
 TCCTTCGAGG AGGACCGGAT CAACGCCACG GTATGGAAGC TCCAGCCAC AGCCGGCCTC 900  
 CAGGACCTGC ACATCCACTC CCGGCAGGAG GAGGAGCAGA GCGAGATCAT GGAGTACTCG 960  
 GTGCTGCTGC CTCGAACACT CTTCAGAGG ACGAAAGGCC GGAGCGGGA GGCTGAGAAG 1020  
 AGACTCCTCC TGGTGGACT CAGCAGCCAA GCCCTGTTC AGGACAAGAA TTCAGCCAA 1080  
 GTCTGTGGTG GCTGTGTGTT GGGGATTGTG GTACAGAAC CCAAGTAGC CAACCTACG 1140  
 GAGCCCGTGG TGCTCACTTT CCAGCACCAG CTACAGCCGA AGAATGTGAC TCTGCAATGT 1200  
 GTGTTCTGGG TTGAAGACCC CACATTGAGC AGCCCGGGGC ATTGGAGCAG TGCTGGGTGT 1260  
 GAGACGCTCA GAGAGAGAAC CCAACATCC TGCTTCTGCA ACCACTTGAC CTACTTTGCA 1320  
 GTGCTGATGG TCTCTCGTGG GAGGTGGAC GCCGTGCACA AGCACTACCT GAGCCTCCTC 1380  
 TCCTACGTGG GCTGTGTGTT CTCTGCCCTG GCCTGCCTTG TCAACATTGC CGCCTACCTC 1440  
 TGCTCCAGGG TGCCCTTGCC GTGCAGGAGG AAACCTCGGG ACTACACCAT CAAGGTGCAC 1500  
 ATGAACCTGC TGCTGGCCGT CTCTCTGCTG GACACGAGCT TCCTGCTCAG CGAGCCGGTG 1560  
 GCCCTGACAG GCTCTGAGGC TGGCTGCCGA GCCAGTGCCA TCTTCTGCA CTCTCCCTG 1620  
 CTCACCTGCC TTCTCTGGAT GGGCCTCGAG GGGTACAACC TCTACCGACT CGTGGTGGAG 1680  
 GTCTTTGGCA CCTATGTCCC TGGCTACCTA CTCAGCTGA GCGCCATGGG CTGGGGCTTC 1740  
 CCCATCTTTC TGGTGAAGCT GGTGGCCCTG GTGGATGTGG ACAACTATGG CCCATCATC 1800  
 TTGGCTGTC ATAGGACTCC AGAGGGCGTC ATCTACCTT CCATGTGCTG GATCCGGGAC 1860  
 TCCTTGGTCA GCTACATCAC CAACCTGGGC CTCTTCAGCC TGCTGTCTT GTTCAACATG 1920  
 GCCATGCTAG CCACCATGGT GGTGCAGATC CTGCGGCTGC GCCCCACAC CCAAAAGTGG 1980  
 TCACATGTGC TGACACTGTC GGGCCTCAGC CTGGTCTTGG GCCTGCCCTG GGCCTTGATC 2040  
 TTCTTCTCT TTGCTTCTGG CACCTTCCAG CTGTCTGCTC TCTACCTTT CAGCATCATC 2100  
 ACCTCCTTCC AAGGCTTCTC CATCTTCATC TGGTACTGGT CCATGCGGCT GCAGGCCCGG 2160  
 GGTGGCCCTC CCCTCTGAA GAGCAACTCA GACTGCGCCA GGCTCCCAT CAGCTCGGGC 2220  
 AGCAGCTGT CTAGCCGATC CTAGGCTCC AGCCCACTG CCAATGTGAT GAAGCAGAGA 2280  
 TGGGCGCTG CTGAGGCTG CCTGTGGCCC CCGAGCCAGG CCGAGCCCA GGCAGTCTG 2340  
 CCGCAGACTT TGGAAAGCCC AAGSACCATG GAGAGATGGG CCGTGGCAT GGTGAGCGGA 2400  
 CTCGCGGGG TGGGGCTTTT GAATGGCCCT TGGGGACTAG TCGGCTCTCA CTCAGCTCCC 2460  
 ACGGAGACTA GAAATGGGCC GCCATGCTGC CTAGGGTACT GTCCCCACAT CTGTCCCAAC 2520  
 CAGCTGTGAG GCCTGCTCTC TCCTTACAAC CCCTGGGCCC AGCCTCATG CTGGGGGCCA 2580  
 GGCTTGGAT CTGAGGGTGC TGGCACATCC TTAATCTGT GGCCTGCCT GGGACAGAAA 2640  
 TGTGGCTCCA GTTGTCTGT CTCTCGTGGT CACCTGAGG GCACTCTGCA TCCTCTGTCA 2700  
 TTTTAACCTC AGGTGGCACC CAGGGCGAAT GGGGCCAGG GCAGACCTTC AGGGCCAGAG 2760  
 CCTGGCCGA GGAGAGGCC TTTGCCAGGA GCACAGCAG AGCTCGCCTA CCTGTAGGCC 2820  
 G

**A50 Protein sequence**

Gene name: G protein-coupled receptor 56  
 Unigene number: Hs.6527  
 Protein Accession #: NM\_005682.1  
 Signal sequence: 1-26  
 GPS domain: 342-394  
 Pfam domain: 7tm\_2 [400-665]  
 Transmembrane domains: 410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MTPQSLQTT LFLLSLLFLV QGAHGRGHRE DFRPCSQRNQ THRSSLHYKP TPDLRISIEN 60  
 SEEALTVHAP PPAHPASRS PFDPRGLYHF CLYNNRHAGR LHLLYGKRDF LLSKASSLL 120  
 CFQHQEESLA QGPPLLATSV TSWNSPQNIS LPSAASPTFS FHSPPHTAAH NASVDMCELK 180  
 RDLQLLSQFL KHPQKASRRP SAAPASQQLQ SLESKLTSVR FMGDMVSFEE DRINATVWKL 240  
 QPTAGQLDLH IHSRQEEQES EIMEYSVLLP RTLFTQRTKGR SGEAEKRLLL VDFSSQALPQ 300  
 DKNSQVLGE KVLGIVVQNT KVANLTFVTV LTFQHQQLPK NVTLCQCVFWV EDPTLSSPGH 360  
 WSSAGCETVR RETQTSFCFN HLTYFAVLNV SSVEDAVHK HYLSSLVYVG CVVSALACLV 420  
 TIAAYLCRSV PLPCRRKPRD YTIKVMNLL LAVFLLDTSF LLSEPVALTG SEAGCRASAI 480  
 FLHFSLLTCL SWMGLGYNL YRLVVEVFGT YYPGYLLKLS AMGWGFPFPL VTLVALVDVD 540  
 NYGPIILAVH RTEPGVIYPS MCWIRDSLVN YITNLGLPSL VFLFNMAMLA TMVQIILRLR 600  
 PHTQKWSHVL TLLGLSLVLG LPWALIFFSF ASGTFQLVVL YLFSIITSFQ GFLIFIWYWS 660  
 MRLQARGGPS PLKNSDCAR LPISSGSTSS SRI

**A51 DNA SEQUENCE**

Gene name: Hypothetical protein FLJ20063  
 Unigene number: Hs.5940  
 Probeset Accession #: AA053660  
 Nucleic Acid Accession #: AA053660  
 Coding sequence: 218-1360 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CCCCCTGAC TTTGTACAGC TACTTCACTG CTTCCTCCCA ATTAGTACAC ATAGTTCCTC 60

5  
10  
15  
20  
25  
30  
35  
40  
45

CACAATTCCT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCCTCCA CAATTCCTAT 120  
 ACCTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAT TCATTAGCTA CCTCTGACAT 180  
 AATCACCGCT TCATCTCCAA ATGATGGATT AATCACAATG GTTCCTCTG AAACACAAAG 240  
 TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGCCTC CCACTGGCAC 300  
 CGCTTTATTG GAGACCAGCA CCCTAAACAG CACAGGTCCC AGCAATCCTT GCCAAGATGA 360  
 TCCCTGTGCA GATAATTGCT TATGTGTTAA GCTGCATAAT ACAAGTTTTT GCCTGTGTTT 420  
 AGAAGGGTAT TACTACAAC CTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT 480  
 TTCAGTGACA GTATCAGAAA CATTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA 540  
 CTGTCATAGT GAAATTACTA GCTTGTTTAA AGATGTATTT GGCACATCTG TTTATGGACA 600  
 GACTGTAATT CTACTGTAA GCACATCTCT GTCCACAAGA TCTGAAATGC GTGCTGATGA 660  
 CAAGTTTGTG GATGTAAACA TAGTAACAAT TTTGGCAGAA ACCACAAGTG ACAATGAGAA 720  
 GACTGTGACT GAGAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA 780  
 TGATTTGACC CTTCGGTGTG ATTATTATGG CTGTAACCAG ACTGCGGATG ACTGCCTCAA 840  
 TGGTTTAGCA TGGATGTGCA AATCTGACCT GCAAGGGCCT AACCCACAGA GCCCTTTCTG 900  
 CGTTGCTTCC AGTCTCAAGT GTCTCTGATG CTGCAACGCA CAGCACAAAG AATGCTTAAT 960  
 AAAGAAGAGT GGTGGGGGCC CTGAGTGTGC GTGCGTGCCC GGCTACCAGG AAGATGCTAA 1020  
 TGGGAAGTGC CAAAAGGTGTG CATTGGGCTA CAGTGGACTC GACTGTAAAG ACAAAATTTCA 1080  
 GCTGATGCTC ACTATTGTGG GCACCATGCG TGGCATTGTC ATTCTCAGCA TGATAATTGC 1140  
 ATTGATTGTC ACAGCAAGAT CAAATAACAA AACGAAGCAT ATTGAAGAAG AGAACTTGAT 1200  
 TGACGAAGAC TTTCAAAATC TAAAAGTGGG GTGACAGGCT TCACCAATC TTGGAGCAGA 1260  
 AGGGAGGCTC TTTCCTAAGG TCAGGATAAC GGCTCCAGG GACAGCCAGA TGCAAAATCC 1320  
 CTATTCAAGA CACAGCAGCA TGCCCGGCCG TGACTATTAG AATCATAAGA ATGTGGAACC 1380  
 CGCCATGGCC CCAATCCCAAT GTACAAGCTA TTATTTAGAG TGTTTAGAAA GACTGATGGA 1440  
 GAAGTGAGCA CCAATAAAGA TCTGGCCTCC GGGGTTTTTC TTCCATCTGA CATCTGCCAG 1500  
 CCTCTCTGAA TGGAAAGTGT GAATGTTTGC AAGGAATCCA GCTCACTTGC TAAATAAGAA 1560  
 TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGTG AGAGAGGTGG TTTTCTTCAA 1620  
 TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTCTTCT TAATCTTTT CCTGGTAGGG 1680  
 CAACAGAAC CTATTCCTAAT CTAGAGGAAA GCTCCCGCAG ATTGCTTGCT CTTGGGCAAA 1740  
 CATTGCTCTT GAGTTAAGTG ACCTAATCC CCTGGGAGAC ATACGCATCA ACTGTGGAGG 1800  
 TCCGAGGGGA TGAGAAGGGA TACCACCAT CTTCAGGGG TCACAAGCTC ACTCTCTGAC 1860  
 AAGTCAGAT AGGGACACTG CTCTATCCC TCCAATGGAG AGATTCTGGC AACCTTTGAA 1920  
 CAGCCGAGAG CTGCAACCT AGCCTCACCC AAGAAGACTG GAAAGAGACA TATCTCTCAG 1980  
 CTTTTTCAGG AGGCGTGCTC GGAATCCAG GAACTTTTG ATGCTAATTA GAAGGCCTGG 2040  
 ACTAAAAATG TCCACTATGG GGTGCACTCT ACAGTTTTTG AAATGCTAGG AGGCAGAGG 2100  
 GGCAGAGAGT AAAAACAATG ACCTGGTAGA AGGAAGAGAG GCAAAGGAAA CTGGGTGGGG 2160  
 AGGATCAATT AGAGAGGAGG CACCTGGGAT CCACCTTCTT CCTTAGGTCC CCTCCTCAT 2220  
 CAGCAAGGGA GCACCTCTCT AATCATGCCC TCCGGAAGAC TGGCTGGGAG AAGGTTTAAA 2280  
 AACAAAAATG CCAAGGATTA GAGCCTTAGG TCAGTTTGAA ATTGGAGACA AACTGTCTGG 2340  
 CAAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCC GTCCAGCCTC GGGGTGTAGG 2400  
 TTTCTGAGT GTGCCATTGG GGCCTCAGCC TTCTCTGGTG ACAGAGGCTC AGCTGTGGCC 2460  
 ACCAACACAC ACACAACAC ACACAACAA GGGGGCAACC ACATCCAGTA 2520  
 CAAGCTTTTA CAAATGTTAT TAGTGTCTT TTTTATTCT AATGCCCTGT CCTCTAAAA 2580  
 GTTATTATAT TTGTTATAT TATTGTCTT TGACTGTAA TTGTGAATGG TAATGCAATA 2640  
 AAGTGCCITT GTTAGATGTT GAAAAAATA AAAAAAATA AAAAAAATA A

**A52 Protein sequence:**

Gene name: Hypothetical protein FLJ20063  
 Unigene number: Hs.5940  
 Probeset Accession #: AA053660  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 289-311  
 EGF domain: 45-74  
 SEA domain: 80-196  
 Cellular Localization: plasma membrane

60  
65

1 11 21 31 41 51  
 MVPSETQSNM EMSPTTEDNQ SSGPPTGTAL LETSTLNSTG PSNPCQDDPC ADNSLCVKLH 60  
 NTSFCLCLEG YYNSSTCKK GKVPFGKISV TVSETFDPEE KHSMAVQDLH SEITSLFKDV 120  
 FGTSVYQQT VILVSTSLSP RSEMRADDKF VDVITVITLA ETTSNDEKTV TEKINKAIRS 180  
 SSSNPLNYDL TLRCDYYGDN QTADDCLNGL ACDCSKDLQR PNPQSPFCVA SSLKCPDACH 240  
 AQHKQCLIKK SSGAPEACV PGYQEDANGN CQKCAFYSG LDCIKDKFQLI LTIIVGTIAGI 300  
 VILSMIIALI VTARSNNKTK HIEEENLIDE DFQNLKLRST GFTNLGAEGS VFPKVRITAS 360  
 RDSQMNPYS RHSSMPRPDY

**A53 DNA SEQUENCE**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80

1 11 21 31 41 51  
 ACCGGGCACC GGACGGCTCG GGTACTTTCTG TTCCTAATTA GGTCTATGCC GTGTGAGCCA 60  
 GGAAAGGGCT GTTGTATGCG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGGGGA GCGGATGTC 180  
 AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240

5 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTGTC ACCAGATGCA 300  
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAGAT ACAGATGTGC CTCACTCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGSTGTT CACAGCTGCT TCGTGGAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAAAATG TGCCTGTGCC CAATGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 10 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGGT TACCTTGACG TGCACAGCCT GTGGTCTATG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTCAGTTCC AGGGCTACCA CCGTGTGCGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGATC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 15 CTAGTTTCCC TGTGTGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200  
 GATGGAAGAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTGCG TGAACACAGC GGCCGTCCCT TTGATTTCGA ACAAGATCTG CAACCAAGG 1320  
 20 GACGTGTAGC GTGGCATCAT CTCCTCTGCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCCG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCGGTG TCACCTCCTT CTTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 25 AACTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCG AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTGG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800  
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCTGTGTTCA AGCGATTCTC 1860  
 30 TTGCTATGAG TGTCCAGTGA GCTGGGACCA CAGGTGCCCG CCACCAACCC CACTAATTT 1920  
 TTGATTTTTT AGTAGAGACA GGGTTTCACC ATGTTGCCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCTCTGT TCAGCTCTCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040  
 ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGCT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160  
 35 ACGAGATAAG CAGTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACAGCCCC AGAAGTGACG AACTGCAGTC ACTGCAGTTC TCTATCTCTA GGGACCAGAA 2280  
 CCAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCTTAT TTTCATGATT TCTTTGTAGC ATTGTGTGCT TGACGTATTA 2400  
 TTGCTCTTGG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAAAAA

40 A54 Protein sequence:  
 Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 45 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

50  
 1 11 21 31 41 51  
 | | | | |  
 MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLPLKFFP IIVIGIIALI 60  
 55 LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120  
 TAASWKTMCs DDWKHYANV ACAQLGFPSY VSSDNLRVSS LGGQFREEFV SIDHLLPDDK 180  
 VTALHHSVYV REBCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240  
 LCGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSILVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGVKVCWT SGWGATEDGA GDASPVINHA 360  
 60 AVPLISNLIK NHRDVYGGII SPSMLCAGYL TGGVDSQQED SGGPLVCQER RLWLVLGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

65 A55 DNA SEQUENCE  
 Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Probeset Accession #: AA215333  
 Nucleic Acid Accession #: NM\_014373  
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51  
 | | | | |  
 GTGGCCTCGA GGTGGTGGCA GGGCCGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG 60  
 GCTCCCGAG GCAGGTTCCG CTGGAAGGAA CCGCTCTCGC TTGCTCTAC ACTTGCGCAA 120  
 75 ATGCTCTCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180  
 AAATAACATA ATTGAAGGCA GTAAAGTGTA AATTAATAG GAAGATCATC AGTCAAGGAA 240  
 GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTATC ATGTGTATT CAGCAGTCT 300  
 TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAACTGCTC TTTTCAGTAC 360  
 CAGTTACGTC AAACAAACCA GCGCCCTAGAC GTTAACATAT TGCTATTCTT GATCATACTT 420  
 80 GGGAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAAT 480  
 TTTATGGAAT ATTTTGTGAT TTCACTAGCA TTCGTGATC TTTTACTTTT GGTAAACATT 540  
 TCCATTATAT TGTATTTCAG GGATTTTGT TTTTAAAGCA TTAGGTTTAC TAAATACCAC 600  
 ATCTGCCTAT TTACTCAAAAT TATTTCCTTT ACTTATGGCT TTTTGATTA TCCAGTTTTC 660  
 CTGACAGCTT GTATAGATTA TTGCCTGAAT TTCTCTAAAA CAACCAAGCT TTCAATTAAAG 720  
 TGTCAAAAT TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTCACT CCTTGCTTAT 780

5 GTTTTGGGAG ACCCAGCCAT CTACCAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840  
 TGTCTTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA 900  
 TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960  
 ACTTCCTATA TGAATGAAAC TATCTTATAT TTTCTTTT CATCCCACTC CAGTTATACT 1020  
 GTGAGATCTA AAAAAATATT CTATCCAAAG CTCATTGTCT GTTTTCTCAG TACCTGGTTA 1080  
 CCATTGTAC TACTTCAGGT AATCATIGTT TTACTTAAAG TTCAGATTCC AGCATATATT 1140  
 GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTT TCATTGCTAC AGTGATTTGG 1200  
 TTTAATTGTC ACAAGCTTAA TTTAAAGAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260  
 10 TGAAGTGCT GCTTCATTCC ACTTACAATT CCTAATCTTG AGCAAATTGA AAAGCCTATA 1320  
 TCAATAATGA TTGTTAATA TTATTAATTA AAAGTTACAG CTGTCATAAG ATCATAATTT 1380  
 TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACATAAAC AACTTTTGCC 1440  
 CCTGACTGAC TAGCATTCCA GAATGTGTCT TTTGAAGGGC TATACCAAGT ATTAATAGT 1500  
 GTTTTATTTT AAAAAACAAA TAATTCCAAG AAGTTTTTAT AGTTATTCAG GGACACTATA 1560  
 15 TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT 1620  
 GATGTTTGTG TTAATCAAAA AACTACTGG ATGCAAACTG TTATGTAAT CTGAGATTTC 1680  
 ACTGACAACT TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAT GTAAGCAAGA 1740  
 AAAAAAAA

20 A56 Protein sequence  
 Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Protein Accession #: NP\_055188  
 Signal sequence: none found  
 25 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297  
 Cellular Localization: plasma membrane

30 1 11 21 31 41 51  
 | | | | |  
 MTALSSENC VQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRKNT CQNFMEYFCI 60  
 SLAFVLLLL VNSIILYFR DFVLLSIRFT KYHICLFTQI ISFTYGLHY PVFLTACIDY 120  
 CLNFSKTKL SFKQCKLFYF FTVILINISV LAYVLGDPAI YQSLKAQNAV SRHCFYVSI 180  
 QSYWLSFFHV MILEVARIIT WEEVTTLVQA IRTSYMMNET ILYPFSSHS SYTVRSKKIF 240  
 35 LSKLIVCFLS TWLPFVLLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300  
 LKDIGLPLDP FVNWKCCFIP LTIPNLEQIE KPISIMIC

40 A57 DNA SEQUENCE  
 Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 | | | | |  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 50 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCGGC 180  
 CTGGGCGAGA GCGAGGCCAG CGCGACTTT GGGGCTGCAG GGAGCCCCCG CCACTTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GCGTCGAGCC 300  
 TGTGCGAGCG GGGCGCTGCC CCGTCCCTCC TCGGGGCCCC CCGTCCCTGC CTGACGTGCC 360  
 55 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGC AGGTGACGCA GAAGAGTGAG CGCATCAAGC AGCTGGAGCA GGAGAAGTGG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCGCTGAGCC AGCAGGAGCG GGGACCTCTG 540  
 GATTCCACTC TCATCTAGTC CTGTGGGCCG GCGTGGGCCC CCAGGCGCAG CCTGGCACTC 600  
 AGCCCTTCGA GGGTGGGGCG CCGATGCGAC CCACCTCTC TGGCTGGAGA CCCCAGGAG 660  
 60 GCGCAGGCAC AGTCCCGGAG TGGGGCGCTT CCGCGCGCCC TTGCCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGAG CTACTACTGG CCGCTGTGAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCCAGCGG TGCCGCGCTG 900  
 GGTCCCATCT TCAGGGAAG GCATGCCCA CGCCAGGCTG CACTTCCAC AACGGGCAGC 960  
 65 AGAGGGCGCG GGGCGGCTCC GACGCGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGAGC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTCGCC TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGCCAAAG CTGAGGACCC CTGGCTGAGC CGGATCGGCA GCGCGGGTGG GCGAGAGCTT 1200  
 GGCTGTCATG TGCTCTCCAC AGACCTGGG GTGATGGCCT TCCCGCTCTT GCGCGGGAGC 1260  
 70 TTGCCCCACG TTGAGTCCCA CACACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCAGTCA TAGGCAAAAG CTGTTTCCCC CGACTCAGGA TTTCAGAGGC 1380  
 CTGGGGTCTT GCTCAGCCCC CTTTGTCTCT ACGCCAGGCC TGTCGCCAGG TTTGAGCTGG 1440  
 GAGAGGGCAC CTCCTCAGC CAAGGAAAAA GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAGTCCC CTGTGGGTGT ACTCCCTCAG CCGCTGCCCA GCGCCACTCC CGCTGGTGTCT 1560  
 75 GGAGTACGCA CTGGTGGGGG GGGCTGTCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620  
 GAACAGGGGG CAGGCGAACA GCATCGATGG GTTCTGCAGC CAGGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGGCGAG GGCCTCCGAT GCGGGGTGAG TGGCTGGGGG GCGCAGGGCC 1740  
 CCGATGCGGG GGTGAGTGGG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCATTTGGT 1800  
 ACATGTCCC ACAGGCAACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860  
 80 CCTTCCGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGCAGG GTGTGCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980  
 GCGCTCTTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCGCTG 2040  
 ACCTCTCGGG CAGGAAGAGG TGCAGTCTCT GAGGGCTGTG GCGCCACAGC CCCAGCACCC 2100  
 AGGTGAGTGC CAGCGCAGT GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160  
 GCGTGGGGTC TGCCACCCAG GCGCTCCCCA CGTCTGCCCT TGAGGGTGCC TGCCATGCCC 2220

5 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280  
 GGTGACTTCA TCAGGAGACC GCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340  
 GAGACAGGCT GGACCTCCG GAAAAACTGC CTTTCAGCCT TGGTGTCCG TGCAAGGTGA 2400  
 AAAGAAATAG GTCTCCCGAG TTACAGCTT GAAATCAGGC TAGTGAGTGG CCTTGAGAC 2460  
 CACGAGGGGA GAATTTAAAG GCCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520  
 GCAGACCTTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580  
 GAGCAGCGTC CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAAGT ACATACAGT 2640  
 GCGTGACAC TGATGATACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700  
 10 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760  
 TTTTGTGTTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGGTTCAAGC 2820  
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAAAAAAAG AAAAAGAAAG AAAAAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 15 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTGTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A58 DNA sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 20 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGGTAGAAG TGAAGTACTT 60  
 TTTTATTGTC AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120  
 CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCCGGTGGT GCGGCCCTCT CCCAGGAGAG 180  
 30 ACAAAACAGG GTCCACAGTG GCAGCCGCGC CCGGGCGGCC CCTCTGTGA TCCCGTAGCG 240  
 CCCCTGGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCGCGGGCAC CGAGCGCTGG 300  
 TCGCCGCTCT CTCTCCGTTA TATCAACATG CCCCCTTTCC TGTGCTGGA GCGCGTCTGT 360  
 GTTTCTCTGT TTTCCAGAGT GCCCCATCTC CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420  
 GAAACCATCG GGAAGATTCG AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480  
 35 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAGG GGAGCTTTGA AAGGTCCAAG 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600  
 GCATTCCAGT TCAGTTCCAG TCCTCATCTG GAATTCCTCT TGGATTCTAT TTCAACCCAA 660  
 CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAAG GAGGGCGCAC GGAGACGGAA 720  
 CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCTCGGAG GCAGAAATGC TTCTGTGCC 780  
 40 CAGATCTCTA TCATGTCAC TGATGGGAAG TCCAGGGGGG ATGTGGCACT GCATCCAAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900  
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGG TGCTGTGGG TGAGCAGGTG 960  
 GAGGATGCCA CCAACGGGCT CTTCAGCACC CTCAGCAGCT CGGCATCTG CTCAGCGGCC 1020  
 ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080  
 45 GAGTTGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GAGCCCTTGC GGTGCTGGCT 1140  
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGTC CACTGTCTAC 1200  
 AGGACCACTC GCGCAGGCCCT CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260  
 CCAGAAAGGCT TGGACGGCTA CCAATGCCCT TGCCCGCTGG CCTTGGAGGG GAGGGCTAAC 1320  
 TGTGCCCTGA ASCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCTGCTT GGACAGCTCT 1380  
 50 GCGGGACCCA CTCTGGAAGG CTTCTGCGG GCCAAGTCT TCGTGAAGCG GTTGTGCGG 1440  
 GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500  
 CTGGTGGCGG TCGCTGTGGG GAGTACCAG GATGTGCTG ACCTGGTCTG GAGCCTCGAT 1560  
 GGCATTCCCT TCCGTGTGGG CCCCACCTG ACGGGCAGTG CCTTGGGCA GCGCGCAGAG 1620  
 CGTGGCTTCG GAGAGCCGAC CAGGACAGGC CAGGACCGGC CAGCTAGAGT GGTGTTTTTG 1680  
 55 CTCACCTAGT CACTGTCGGA GGATGAGGTT GCGGGCCGAG CGGTGACGC AAGGGGCGGA 1740  
 GAGCTGTCTC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800  
 GCGAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1860  
 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGGT GCGGACACA AGCCCTGGAC 1920  
 CTGCTCTTCA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980  
 60 AGCTTTGTGA GAAGCTGTGC CTTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCG 2040  
 CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGG TGGACACCAA ACCCAACCGG 2100  
 GCTGCGATG TCGCGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGCG 2160  
 ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTCTGT 2220  
 GTCCCAAGAG CTGTGTTGGT GCTCAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCT 2280  
 65 GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGCGTGGG GCTGTCTTA 2340  
 AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CCGGATTCCC TGATCCACGT GGCAGCTTAC 2400  
 GCGGACCTGC GGTACCAACA GGAAGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460  
 CCAGTCAACC TCTGCAACC CAGCCGCTGC ATGAATGAGG GCAGCTGCGT CTGCAAGAT 2520  
 GGGAGCTACC GCTGCAAGTG TCGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580  
 70 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GATGAGATTG TTGAGACGCC CCGTAGGCAC 2640  
 ATGGCTCCCG TGCAAGAGGG CAGCAGCGGT ACCCTCCCA GCAACTACAG AGAAGGCGCTG 2700  
 GGCATCTGAA TGGTGCCTAG CTTCTGGAAT GTCTGTGCC CAGGTCTCTA GAATGTCTGC 2760  
 TTCCGCGCGT GCGCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 75 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTTGAAAGTT 2880  
 TTGATGTGTA AGTAATAACC CACTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940  
 CTGCCACCTT TCCTTTGAGG ATAAACAAGG GGTCTGAAG ACTTAAATTT AGCGGCTCTGA 3000  
 CGTTCCCTTG CACACAATCA ATGCTGCGCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060  
 AGGCTTTTAC TAGAGCATCC TTTGAGCGGC GAAGGCCACG GCCTTTCAAG ATGGAAGCA 3120  
 80 CAGCTTTTTC CACTTCCCCA GAGACATTCT GSATGCATTT GCATTGAGTC TGAAGGGGG 3180  
 CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAGA GACTTGGAAA 3240  
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300  
 TGTGATGGG CCGAGTCTG GAGGGCCAG TAAATCGTT CTGAGTCGTG AGCAGTGTCC 3360  
 ACCTGAAGG TCTTC

A59 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLLEAV CVLFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
    SVKGGSFERS KHFATVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
    MVFKGGRTE ELALKYLLHR GLPGGRNASV PQILIVTDG KSQGDVALPS KQLKERGVTV 180
    FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
20  SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEK RVDLLFLDLS SAGTTLDGFL 360
    RAKVVFVKRFV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIFPRGGPT 420
    LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
    EAVRAELEEI TGSPKHYVMVY SDPQDLFNQI PELQGLKCSR QRPGCRTQAL DLVFMLDTSA 540
    SVGPENFAQM QSPVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
25  APYLGVGSGA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLNRNGI 660
    SVLVVGVGVFV LSEGLRRLAG PRDSLHVA AADLRVHQDV LIENLCGEAK QPVNLCKPSP 720
    CMNEGSCVLIQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
    RTPPSNYREG LGTEMVPTFW NVCAQGP
  
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 ProbeSet Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTACAGG ATCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
    AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGG CGAGATCAT CATTTGTGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGAAGGAGAG 240
    CTGGACTGTC CTTTGGGGGA GGAAGGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
45  GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACTGTGC AGGTGCTGGA CTCGGCCACA 360
    GGAACCTGGT TCTCTGCTGT TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
    GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACCTCAAGT 540
    GGGCCCTGTC CTTACAGGCTC CTTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
50  AAGACCCCCC GTTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCCAGT AGCAAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CACTGGGTC 720
    CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
    GGCTCAGACA AACTGGGCAG CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
    TTCAACCCCA TCTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
55  ACTTCTCTCA GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
    GCCACCCAC TCTGATCAT TGGATGGGGC TTTCAGAAAG AGAATGGAGG GAAGATGTCT 1020
    GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
    GCGTACCAAG GGAAGATCAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
    GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
60  GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTA
  
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 ProbeSet Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

```

1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPITIAL LSLASIIIVV VLIRVILDKY 60
    YFLQGQPLHF IPRKQLCDGE LDCPLGEDEB HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120
    GNWFSACFDN FEALAEATAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELRMENSS 180
    GPCLSGSLVS LHLACGKSL KTRPVVGEE ASVDSWPVQV SIQYDKQHV GGSILDFHWV 240
    LTAAHCFRKH TDVFNWKVRA GSKDLGSPFS LAVAKIIIE FNPMPKOND IALAKLQFPL 300
    TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
    AYQGEVTEKM NCAIGPEGGV DTCQGDGGGP LMVQSDQWHV VGVISWGYGC GGPSTPGVYT 420
    KVSAYLNIWY NVWKAEL
  
```



A62 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

```

10      1      11      21      31      41      51
      |      |      |      |      |      |
      CCAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
      CTGAGATCCT TGCCTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
15      CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
      AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
      AAGCTGAGGA ACTGCTCTGA TGCCGAGCTC GAGTGTCACT CTTACGGAAG CGGAGCCAC 300
      CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
      CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420
20      TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
      AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540
      AACAGCGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
      AACTCCTGCA CCAGCCCGCT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
      TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720
25      GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTCTAGCTC TAAATGTTTG 780
      CCGCGCCATC CCTTTCCACA GTATCCTTCT TCCTCCTCCT CCTGTCTCTG GCTGTCTCGA 840
      GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
      AAAGATTTGA AGACAGAAGG AAGAAACTCA GGAGTAAGCT TCTAGACCCC TTCAGTCTCT 960
      ACACCTTCTC GCCCTCTCTC CATTCCTGTC ACCCCACCCC AGCCACTCAA CTCTGCTTGG 1020
30      TTTTTCCTTT GGCCTATAGG AGGTTTACCA GTAGAATCCT TGCTAGGTGG ATGTGGGCCA 1080
      TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
  
```

A63 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

```

45      1      11      21      31      41      51
      |      |      |      |      |      |
      MASRMRLLLL LLCLAKTGV LGDIIMRPSC APGNFYHKSN CYGYFRKLRN WSDAELECCS 60
      YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG 120
      KSMGGKHKCA EMSNNNFLT WSSNECNKRQ HFLCKYRP
  
```

A64 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

```

60      1      11      21      31      41      51
      |      |      |      |      |      |
      GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
      TCCTCTGTGG ACCTCTGCGG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
      CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGAGG GCGGAGGGCG 180
      CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
      CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGGG GAATGGCGAG ACAGTCCAGG 300
65      AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCATCCAAA CGTATCTTAC 360
      GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
      CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
      ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTGGCT GTAGAGAAGG 540
      AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
70      TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
      TCATCGTGAC CGACCAAGAT GACCAACAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
      GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
      ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
      AGGACCCACA CGACTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
75      CCACTGGCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
      TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
      ACAATGCTCC CATGTTTGAC CCCGAGAAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080
      GCCATGAGGT GCAGAGGCTG ACGGTCAGT ATCTGGAGGC CCCCACTCA CCAGCGTGGC 1140
      GTGCCACCTA CCTTATCATG GGCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
80      CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGSGTTT GGATTTTGAG GCCAAAAACC 1260
      AGCACACCTA GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
      CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACTGTG TTTGTCCAC 1380
      CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
      CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCTCT AGAGACCCAG 1500
  
```

CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCCACCACT GGCACGGGAA CCTTCTGCTT AACACTGATT GATGTCAAAG 1680  
 ACCATGGCCC AGTCCCTGAG CCCGTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740  
 ACCTGTGTA CATCAGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTC CAGGCCAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGGAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCTGTGCTCT GCTGTCTCTC CTGCTGGTGC TGCTTTTGT GGTGAGAAAG AAGCGGAAGA 2100  
 TCAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGG TGGGGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTAACGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGTAA CACAGACCCC ACAGCCCGC CCTACGACAC CCTCTGGTG TTCGACTATG 2400  
 AGGGCAGCG CTCGACGCG GGTCCCTGA GCTCCCTCAC CTCCCTCCGC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAGAAGCTG GCAGACATGT 2520  
 ACGTGGCGG GGAGGACGAC TAGGGCGCCT GCCTGCAGGG CTGGGGACCA AACCTCAGGC 2580  
 CACAGAGCAT CTCCAAGGG TCTCAGTTC CCTCTCAGCT GAGGACTTGG GAGCTTGTCA 2640  
 GGAAGTGGC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTAG AGTGGTTGCT 2700  
 TCCTTAGCTT TTAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC AGGTTGCGCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 TGCTCAACCC TGTGTCTCGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCTGGT GCAACTTAAT TTTTITTTT AATGCTATCT 2940  
 TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCAGCA GCTGCTGGGC CCACTGGCCG 3000  
 TCTGTCATT CTGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTT CTGTGCGT TGCTATAGAT 3120  
 GAAGGTGAG GACAATCGTG TATATGTACT AGAAGTTTTT TATTAAGAA A

**A65 Protein sequence:**  
 Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 MGLPRGPLAS LLLLQVCNLQ CAASEPCRAV FREAEVTL EA GGAEQEPGQA LGKVMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDV VAPISVPENG 120  
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGNLLN KPLDREEIAK 180  
 YELFGHAYSE NGASVEDPMN ISIIVTDQND HKPKFTQDPT RGSVLEGLP GTSVMQVTAT 240  
 DEEDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TMDGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAVPEN AVGHEVQRLT VTDLDAPNSP 360  
 AWRATYLMG GDDGDHFTIT THPESNQGL TTRKGLDPEA RNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGNLAMP DSGQVTAVGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLD 540  
 VNDHGFVPEP RQITICNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKFEL KQTYDVHLIS LSDHGNKEQL TVIRATVCD C HGHVETCPGP WKGGFIFVL 660  
 GAVLALLFL LVLLLVRK RKIKEPLLP EDDTRDNVY YGEEGGSEED QDYDITQLHR 720  
 GLEAREPVVL RNDVAPTIIP TMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDITLHV 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKCLA DMYGGEEDD

**A66 DNA SEQUENCE**  
 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGATTCTCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCTCCAGC CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTCTAGTCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCC TATTATGCTG CTCTCGGCTT CTGCACTCAT CAGTGTTTTA 240  
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
 GCCTTTGTTC AGGAATATCG TTCAGAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360  
 CCAGATGCC ATTGTGTGGG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420  
 CCAGGTGATA CAGTTTGCCT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTIT 480  
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTT 540  
 AAGGTGACAG CTCTCAGCG AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTTCAT TGGAACAGGA 660  
 GAAATTTCTG AATTTGGGGA GGTTTTAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTT CTGTGTATA 780  
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAA ATATCCTGGA AATGTTTACT 840

5  
 10  
 15  
 20  
 25  
 30

```

ATTAGTGTA  GTTTGGCTGT  AGCAGCAATT  CCTGAAGGTC  TCCCCATTGT  GGTACAGTGT  900
ACGCTAGCTC  TTGGTGTAT  GAGAAATGGT  AAGAAAAGGG  CCATTGTGAA  AAAGCTGCCT  960
ATTGTTGAAA  CTCTGGGCTG  CTGTAATGTG  ATTTGTTTCT  ATAAACTGG  AACACTGACG  1020
AAGAAATGAAA  TGAATGTTAC  TCACATATTT  ACTTCAGATG  GTCTGCATGC  TGAGGTTACT  1080
GGAGTTGGCT  ATAATCAATT  TGGGGAAGTG  ATTGTTGATG  GTGATGTTGT  TCATGGATTG  1140
TATAACCCAG  CTGTTAGCAG  AATTGTTGAG  GCGGGCTGTG  TGTGCAATGA  TGCTGTAATT  1200
AGAAACAATA  CTCTAATGGG  GAAGCCAACA  GAAGGGGCTC  TAATTGCTCT  TGCAATGAAG  1260
ATGGGCTTGT  ATGGACTTCA  ACAAGACTAC  ATCAGAAAAG  CTGAATACCC  TTTTAGCTCT  1320
GAGCAAAAGT  GAGTGGCTGT  TAAGTGTGTA  CACCGAACAC  AGCAGGACAG  ACCAGAGATT  1380
TGTTTATGTA  AAGGTGCTTA  CGAACAAAGT  ATTAAGTACT  GTACTACATA  CCAGAGCAAA  1440
GGGCAGACCT  TGACACTTAC  TCAGCAGCAG  AGAGATGTGT  ACCAACCAAG  GAAGGCAAGC  1500
ATGGGCTCAG  GGGGACTCAG  AGTCTTGCT  TTGGCTTCTG  GTCCGTAAGT  GGGACAGCTG  1560
ACATTTCTTG  GCTTGGTGGG  AATCATTTAT  CCACCTAGAA  CTGGTGTGAA  AGAAGCTGTT  1620
ACAACACTCA  TTGCCTCAGG  AGTATCAATA  AAAATGATTA  CTGGAGATT  ACAGGAGACT  1680
GCAGTTGCAA  TCGCCAGTCG  TCTGGGATTG  TATTCACAAA  CTTCCAGCT  AGTCTCAGGA  1740
GAAGAAATAG  ATGCAATGGA  TGTTCAGCAG  CTTTCACAAA  TAGTACCAAA  GGTTCAGTA  1800
TTTTACAGAG  CTAGCCCAAG  GCACAAGATG  AAAATTATTA  AGTCGCTACA  GAAGAAGCGT  1860
TCAGTTGTAG  CCATGACAGG  AGATGGAGTA  AATGATGCAG  TTGCTCTGAA  GGCTGCAGAC  1920
ATTGGAGTTG  CGATGGGCCA  GACTGGGTACA  GATGTTTGCA  AAGAGGCAGC  AGACATGATC  1980
CTAGTGGATG  ATGATTTTCA  AACCATAATG  TCTGCAATCG  AAGAGGGTAA  AGGGATTAT  2040
AATAACATTA  AAAATTTCTG  TAGATTCCAG  CTGAGCACGA  GTATAGCAGC  ATTAACITTA  2100
ATCTCATTTG  CTACATTAA  GAACCTTCTC  AATCCTCTCA  ATGCCATGCA  GATTTTGTGG  2160
ATCAATATTA  TTATGGATGG  ACCCCAGCT  CAGAGCCTTG  GAGTAGAACC  AGTGGATAAA  2220
GATGTCATT  GATAACCTCC  TCGCAACTGG  AAAGACAGCA  TTTTGACTAA  AAACTTGATA  2280
CTTAAATAT  TTGTTTCTAT  AATAATCATT  GTTTGTGGGA  CTTGTTTGT  CTTCTGGCGT  2340
GAGCTACGAG  TCAATGTGAT  TACACCTCGA  GACACAACAA  TGACCTTCAC  ATGCTTTGTG  2400
TTTTTGACA  TGTTCATGTC  ACTAAGTTCC  AGATCCCAGA  CCAAGTCTGT  GTTTGAGATT  2460
GGACTCTGCA  GTAATAGAA  GTTTTGCTAT  GCAGTTCTTG  GATCCCATCAT  GGGACAATTA  2520
CTAGTTATTT  ACTTCTCTCC  GCTTCAGAAG  GTTTTTCAGA  CTGAGAGCCT  AAGCATACTG  2580
GATCTGTGT  TTCTTTTGGG  TCTCACCTCA  TCAGTGTGCA  TAGTGGCAGA  AATTATAAAG  2640
AAGTTTGAAA  GGAGCAGGGA  AAAGATCCAG  AAGCATGTTA  GTTCGACATC  ATCATCTTTT  2700
CTTGAAGTAT  GA
  
```

35  
 40  
 45

**A67 Protein sequence:**  
 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

45  
 50  
 55  
 60

```

1      11      21      31      41      51
|      |      |      |      |      |
MIPVLTSKKA  SEFPVSEVAS  ILQADLQNGL  NKCEVSHERRA  FHGWNEFDIS  EDEPLMKKYI  60
SQFKNPLIML  LLASAVISVL  MHQFDDAVSI  TVAILIVVTV  APVQYRSEK  SLEELSKLVP  120
PECHCVREK  LEHTLARDLV  PGDTVCLSVG  DRVPADLRLE  EAVDLSDIES  SLTGETTPCS  180
KVTPAQPAAT  NGDLASRSNI  AFMTGLVRGC  KAGGVVIGTG  ENSEFGEVFK  MMQAEBAEPT  240
PLOKSMDLIG  KQLSFYSFPI  IGIIMLVGNL  LGRDILEMPT  ISVSLAVAAI  PEGPLPIVTV  300
TLALGVMRMV  KRAIVKGLP  IVEVLGCCNV  ICSDKTGTLT  KNEMTVTHIF  TSDGLHAEVT  360
GVGVNQFGEV  IVDGVVHGF  YNPAVSRIE  AGVCNDVAI  RNNTLMGKPT  EGALIALAMK  420
MGLDGLQQDY  IRKAEYFPSS  BQKMAVKCV  HRTQDRPEI  CFMKGAYEQV  IKYCTTYQSK  480
GQTLTLTQQ  RDVYVQEKAR  MGSAGLEVLA  LASGPELGQL  TFLGLVGIID  PPRTGVKEAV  540
TTLIASGVS  KMITGDSQET  AVAIALSLGL  YSKTSQSVSG  EIDAMDVQQ  LSQIVPKVAV  600
PYRASPRHRM  KIKSLQKNG  SVVAMTGDGV  NDAVALKAAD  IGVAMQGTGT  DVCKEAADMI  660
LVDDDFQTIM  SAIEEGKGIY  NNKKNFVRPQ  LSTSIATLTL  ISLATLMNFP  NPLNAMQILW  720
INIIMDGPPA  QSLGVEFVVK  DVIRKPPRNW  KDSILTENLI  LKILVSSIII  VCGTLFPVFW  780
ELRENVITPR  DTTMTFTCFV  FFDMMFNALSS  RSQTSKVFEI  GLCSNRMFCY  AVLGSIMGQL  840
LVYIFPPLQK  VFQTESLSIL  DLLFLLGLTS  SVCIVAEIIE  KVERSREKIQ  KXVSSTSSSF  900
LEV
  
```

65  
 70

**A68 DNA SEQUENCE**  
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

75  
 80

```

1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG  GGGCCCGTCT  GCAGCAAGTG  ACCGACGGCC  GGGACGGCCG  CCTGCCCCCT  60
CTGCCACCTG  GGGCGGTGCG  GGCCCGGAGC  CGGAGGCCCG  GGTAGCGCGT  AGAGCCGGCG  120
CGATGCACGT  GCGCTCACCTG  CGAGCTGCGG  CGCGCACAG  CTTCGTGGCG  CTTCTGGGCG  180
CCCTGTTCTT  GCTGCGCTCC  GCCCTGGCCG  ACTTCAGCCT  GGACAAACAG  GTGCACTCGA  240
GCTTCATCCA  CGGCGGCTCC  CGCAGCCAGG  AGCGGCGGGA  GATGCAGCGC  GAGATCCTCT  300
CGATTTTGGG  CTTGCCCCAC  CGCCCGCGCC  CGCACTTCCA  GGGCAAGCAC  AACTCGGCAC  360
CCATGTTTAT  CTGGGACCTG  TACAACGCCA  TGGCGGTGGA  GGAGGGCGGC  GGGCCCGGCG  420
GCCAGGGCTT  CTTCTACCCC  TACAAGGCGG  TCTTCAGTAC  CCAGGGCCCC  CTTCTGGCCA  480
GCCTGCAAGA  TAGCCATTTC  CTCACGACG  CCGACATGGT  CATGAGCTTC  GTCAACCTCG  540
TGAACATGA  CAAGGAATTC  TTCCACCCAC  GCTACCACCA  TCGAGAGTTC  CGGTTTGATC  600
TTTCCAAGAT  CCCAGAAGGG  GAAGCTGCA  CGCGAGCGCA  ATTCGGGATC  TACAAGGACT  660
  
```

5  
10  
15  
20

```

ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG 780
AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACAGCAAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT GGCCTCGACG CTCTCGGTGG AGAOGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCGTATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
TCCTCAAGGC CACGAGGTTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AACACAGCGCA 1020
GCCAGAACCG CTCGAAGACG CCCAAGAACCC AGGAAGCCCT CCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCCGCC TACTACTGTG 1200
AGGGGGAGTG TGCTTCCCT CTGAATCTCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
AGACGCTGGT CCACCTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCAGAA TTCAGACCCT 1440
TTGGGGCCAA GTTTTCTCG ATCTCTCATT GCTGCGCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCTTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC ACACCTATGG TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCCTACAAGC TGTGACGGCA AAACCTAGCA GGAAAAAACA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTTGGT GGGGAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGGCG CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAGC AATGAATG

```

25  
30

A69 Protein sequence:  
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195  
Probeset Accession #: BE616633  
Protein Accession #: NP\_001710.1  
Signal sequence: 1-30  
Pfam domains: TGFb\_propeptide [37-281]  
Transmembrane domains: none found  
Cellular Localization: secreted

35  
40  
45

```

1 11 21 31 41 51
MHVRSIRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQRREILS 60
ILGLPHRPRP HLQGHKHSNP MFMLDLYNAM AVEEGGGPGG QGFSYFYKAV FSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHRFRFDL SKIPGEAVT AAEFRYKYDY 180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVEDITA TSNHVVNPR 240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
QNRSTPFKNQ EALRMANVAE NSSSDORQAC KKEHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
GECAPPLNSY MNATNHAIVQ TLVHFNPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
RNMVVRACGC H

```

Cervical

50

A70 DNA sequence  
Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTCCGGAGA CCGCGGCGCT 60
GAGGACGCGG GAGCCGGGAG CGCAOGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
CATAACCAAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
AATGGAAAGG CCAGAAAGA GGAATGGTAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTGTG GGTCACTTCT 480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGGGG ACATCCCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
CTGCCCTCCA TGAAAACAG AGATTTTGTG GATGGACCTA TACACCAAGG GGCTTTACTT 660
ATATCTGTGA CTGCTGTAG TTTGCTCTTG GTCTTATCA TATTATTTTG TTAATTCCGG 720
TATAAAGAC AAGAAACCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCCTCC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900
ATTGGAAGG GTGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGTGAGCT 960
GTGAAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080
GGGTCCCTGA CCAAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
TATCTGAAGT CCAACACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGCT 1200
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
CATCGAGATC TGAAGAATAA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
ACTCGAGTGT GCACCAACCG CTATATGCCCT CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TGTGTGTCAT CAGAAGTTA 1620

```

5 CGCCCTCAT TCCAAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740  
 ACACCTGCCA AATGTCTAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800  
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAAGC CTGAACATC GTCTGCTTC CCAGTGGGTT CAGACCTCAC 1920  
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTTGTG GCGGAGAAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

#### 10 A71 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51  
 | | | | | |  
 MLLRSAGKLN VGTKKEDGES TAPTTPRKVL RCKCHHCPPE DSVNNICSTD GYCFTMIEED 60  
 DSGLPVVTSQ CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120  
 25 GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQETPRYS IGLEQDETYI PPGESLRDLI 180  
 EQSSSSSGSGS GLPLLVQRTI AKQIQMVKQI GKRGYGEVMM GKWRGEKVAV KVFFTTTEAS 240  
 WPRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQKGPAIAH RDLKSKNILV KKNGTCCIAAD LGLAVKFISD 360  
 TNEVDIPNT RVGTIKRYMFP EVLDESINRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420  
 30 EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS 480  
 RLTLARVKKT LAKMSESQDI KL

#### Bladder

##### A72 DNA SEQUENCE

35 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 | | | | | |  
 ATGTTACAGG ATCTTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60  
 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120  
 45 CTGAGCTCGG CGAGTATCAT CATTTGTGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180  
 TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240  
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300  
 GCGATGGCAG TCCGCTCTTC CAAGGACCGA TCCCACTGTC AGGTGCTGGA CTCGGCCACA 360  
 50 GGGAACTGGT TCTCTGCTTG TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCTGTG 420  
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480  
 GATCTGGATG TTGTTGAART CACAGAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540  
 GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600  
 AAGACCCCTC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660  
 55 AGCATCCAGT ACAGACAAAC GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACCTGGTC 720  
 CTCACGGCAG CCCACTGCTT CAGGAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780  
 GGCTCAGACA AACTGGGCGC CTTCCATCC CTGGCTGTGG CCAAGATCAT CATATTGAA 840  
 TTCACCCCA TGTACCCCAA AGACAATGAC ATGCCCTTCA TGAAGCTGCA GTTCCACTC 900  
 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960  
 60 GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020  
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGTGTCAA TGCAGACGAT 1080  
 GCGTACCAGG GGAAGTCAC CGAGAAGATG ATGTGTGAGC GCATCCCGGA AGGGGGTGTG 1140  
 GACACCTGCC AGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200  
 GTGGGATCAG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260  
 65 AAGGTCTCAG CTTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

#### A73 Protein sequence:

70 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 75 LDLa domain: 54-94  
 Tryp\_SpC domain: 204-429  
 Cellular Localization: plasma membrane/ER

80 1 11 21 31 41 51  
 | | | | | |  
 MLQDPDSQIP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60  
 YFLOGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPPEGP AVAVRLSKDR STLQVLDSAT 120

GNWFSACFDN FTEALAEAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180  
 GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWPNQV SIQYDKQHC GGSILDPHV 240  
 LTAHCFRKH TDVFNWVRRA GSDKLGSPFS LAVAKIIIE FNPMPKDN IALMLQFPL 300  
 TFSGTVPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASQV IDSTRCNADD 360  
 AYQGEVTEKM MCAGIPEGGV DTCQGDSSGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420  
 KVSAYLWYIY NVWKAEI

## A74 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]

Unigene number: Hs.19322

Probeset Accession #: AA088458

Nucleic Acid Accession #: AA088458

Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GGGACTGGTA CCAGCAGCAG CTGCAACAGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCGACITTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCGGGGCCCC CTGCGCTGC CCTGACGTCC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480  
 GGCTCTATTA ACAGCTGTT TGAGGCCGCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC 600  
 AGCCCTTCGA GGGTGGGCGC CCCATGCGAC CCACCTCTCT TGGCTGGAGA CCCCCGGCAG 660  
 GCCCAGGCAC GGTCTCGGAG TGGGCGCCTT CCTGCCGCCC TTGCCAGATG GGCTCCCGAG 720  
 GCGTGGCCCC GGTCTGGTCC CGCACCGAGC GCTTGACTCC GTTTGGGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGAG CTACTACTGG CGCTGTCTAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCCAGCGG TGCCGCCCTG 900  
 GGTCCCATCT TCAGGGAAGG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GTGGCTGCTG TGGCTGGGGA GCCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGCCAAAG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 GGCCTGCATG TGCTCTCCAC AGACCTTGGG GTGATGGCTT TCCCGCTCTT GGCGGGAGG 1260  
 TTGCTCGGAG CCGAGCTCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGCCCCCA 1320  
 GACAGCTCCC AGGCACGTCA TAGGCAAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380  
 CTGGGCTCTC GCTCACCCCC CTTTGTCTCT ACGCCAGCCG TGTCCCGAGG TTTGAGTGG 1440  
 GAGAGGCCAC CTCCTCTAGC CAAGGAAAGC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAGGTCCC CTGGGTGTGC ACTCCCTCAG CCGCTGCCCA GGCCTCACTC CGCTGGTGCT 1560  
 GGAGTACGCA CTGGTGGGGG GGCCTGTGCT AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620  
 RAACAGGGG CAGCGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGGCGAG GGCCTCCGAT GCGGGGTGAG TGCCTGGGGG GCGCAGGGCC 1740  
 CCGGATGCGG GGTCACTGCG TGGGGGGGCG AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800  
 ACATGTGCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCC GGCAGGCAGC GTGGCACTC 1860  
 CCTTCCGGAG CCGAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980  
 CGCTCTCTAC CTTGAAGATG GAGTGGGCT TCCAGGGGA CATAAGGATG TCAGGCGCTG 2040  
 ACCTCTCTGG CAGGAAAGGG TGCAGGTCTCT GAGGGCTCTG GCCCCACAGC CCCAGCACCC 2100  
 AGGTGAGTGC CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGTCAGCA 2160  
 GGCCTGGGTC TGCCACCCAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCC 2220  
 TGGGGATCCA TGCGATCTTT ACTGGAATGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280  
 GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340  
 GAGACAGGCT GGCACCTCCG GAAAAACTGC CTTTCAGCCT TGGTGTTCGG TGCAAGGTGA 2400  
 AAAGAAATAG GTCTCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460  
 CACGAGGGGA GAATTTAAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGBC AGAGGCACAT 2520  
 GCAGACCTCG CCGTGGAGCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580  
 GAGCAGGCTC CCGGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACAGT 2640  
 GCGTGACAC TGTGATGACA CCCGAAATG TCTCAGGATG TTGAAATGTG TCCITGGGGG 2700  
 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760  
 TTTTGTGTTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGGTTCAGC 2820  
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAAAAAA AAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAACAC CACAGGAAA CAATACACTA TGAGACCCAG CAGAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

## A75 DNA SEQUENCE

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor

Unigene number: Hs.227948

Probeset Accession #: AB035089

Nucleic Acid Accession #: AB035089

Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60  
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAGAAGG 120  
 CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGCAGAGGGT TAGATTGGT 180  
 TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTGG CAGAGTAGGA 240

	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACGTG	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTCG	TTTTCAAACC	TACTGGAGT	TGTTTCCCT	CATGAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTGTCTCTG	AGGTTGTTC	ATGTATACAT	ATCTATATCT	420
5	GTAGACAGAA	TCCITGGGAA	TACAGTAATT	GACATATATT	CTGTTATTG	ATGCTTGAAA	480
	AATCTCTCC	ACTAACCACT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGI	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACTTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GGTCAGGAA	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATTA	660
	GTARTGACAG	GATATTTCTT	GAAGGTGTAA	TTTCCCATTG	AGGATTTGTT	TTTAATTTCT	720
10	GGATTCCTGG	AGCCAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTGGGAA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCCITT	CTAGCCTGTC	TATCAGATGC	900
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCATT	TGAATCTATC	960
	CAAGCTTTCT	CTAATTTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCTTAAAG	1020
15	TTCAACCTTC	AGGGCAAAAC	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATTTCTCT	1080
	CCATAGATTG	GTCCCTCTGA	ACCCCGGTTT	GTCTCAGCTT	GTTATCCTGT	TTTTTTCTTC	1140
	CTCCATATCC	CAGGATGAGC	TTGTTGCTTC	TGTCCTATGA	GACATTAGAT	TCCTTTCTTT	1200
	TGGTACCCGA	GTAATCCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGG	TCTTATAGCG	1260
	CTGGATGCGAG	ACTCAGCTGA	GAAGACCAAT	ATTCATTTTT	GGATTTCTTT	ATCTCAGATA	1320
20	TTTCTCTTTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTATG	TCCATCAACG	CCCCATTAGT	1380
	CTATTCCCGG	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTGAGA	GACTCAAAAC	1440
	ATATATATG	TACACAGGAA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAAT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTCAG	1560
	CCTATGTGTT	TCTGGCAGCT	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTT	ATGTGCTGAG	1620
25	AAAACAAACT	CACGGCTGGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TGGGGAGAAA	1680
	TGTGGAGAAA	TGAGAACTCT	ATTCAAGGTC	GGTTGGAATG	CACACTGTGT	CAGAAATCTA	1740
	TGAGAGAGCT	TCTGGCATTT	CCTCAAAATG	TTAACCTGGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCATTTCAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAGAGCT	ACAACATCAT	TATTCATAAT	AGTAAAAGGA	TGGAAACAAC	ACAAATGTCC	1920
30	ATCAACTTAT	GAATTAAGAA	AATCTGGTCT	ATTCTATGAA	TGGAATATTA	TTGACACCAA	1980
	AAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAAGAGCT	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGA	2100
	ATAGGCAAT	CCATAGAAAC	AGGAGGTAGA	TTCTTGGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
	AGAATGAAGT	ACAAGATTTC	TTTTGGAGGT	AGTGAAATTG	TTGTGGAATG	AGATCATGAT	2220
35	GATGATAGCA	CAACTTTTGG	AATATAATAA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280
	TATATAAAT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTCAGGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAG	2400
	ATTCTTCAGA	TTACAAGATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
	AAACAGAAAG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
40	CTTCATTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
	GCTCTTCTCA	GTGTGAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATAGCT	GAGACTGGCA	AGAAAAAGAG	GTTTAATTGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCCT	CAGAATCACA	GTAGGAGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760
	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGGATCT	CCTGAGGCTT	2820
45	ATTAACATAT	ATGAGAAATG	CACAAGAAAG	ACCCGCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCCTC	CAATAACATG	TGGAATTTCT	GGTAGATACA	ATTCAAGTTG	AGATTTGGGT	2940
	GGGAACAGAG	CAAAACCAT	TCACCTCAGC	AGGCAGATAA	CTTCTCACT	GAGCCTATGC	3000
	AACAGAAAC	CATCTGGGAT	GGTTGTAAGG	GGCACAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAGAGCTGAG	CATCTCAGGAG	AAGGCAATAG	AATCCTATTC	TCCATAGTAT	GCTATAAGAT	3120
50	ACTGAAGTAC	ACTTCTTTC	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCTTGTGTA	3180
	TACAGAAAA	TTACTTAAGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAG	CTTTTATGTT	CTTTGGTATT	CGAAGTATGC	CTAAAAGACA	ATGCAAAATC	3300
	CAAGAAAGA	ATGTTGGGGT	TTTTGTTTGT	TTGGTTTGTG	TTTTGTTTGA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTTCT	AACCTATTCT	3420
55	CAATGGGCAAT	AGAAAGGCAC	CTACATGTAT	TTACATGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAGAAAG	AGGTACAAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTCTATA	ATTTTTCAT	TCATAAGGT	GAGTGTATGC	CCGCTTGTGA	AATCTGAAGT	3600
	TGAGTAACCT	CAATACTTAA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	CCCCACCTCT	GCTTCTCTTA	3720
60	GGAAACACAG	TAAAGAGCTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAAAT	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAAT	CTCCTGCATT	CTGCTGATTT	ATATTTTACT	3840
	TATTTCTGCA	GAGCAAAAT	AAAATACCTA	TTTCATCTGA	TTTGTCTTTT	ATCTAAATTT	3900
	CTTAGTTCCA	AGTAAACCAA	GGCACTTTTA	GGAAACACGA	GGGAGAGTGC	CTTGACGCCA	3960
	GAGAGTCTTG	AAGGAGATGT	CAGGGACGCA	TCCTAACAGC	TGGTTGATG	TGATCCACAG	4020
65	AGGTCTCTTG	TAGCATTTCA	TTGTAAGGCC	ATCCTAACCTA	GCTTAGTGT	AAACAGCAAT	4080
	GAAAGAAAGA	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTGG	4140
	TAAGCCTTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTT	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCATT	CCATTTATTA	AAGTCAATCT	GACAGGAATC	4320
70	TGATGCTTTT	CCAGGAGTTC	CAGATCACAT	CGAGTTCAAC	ATGAATTCAC	TCAAGTGAAGC	4380
	CAACACCAAG	TTATGTTTGG	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAACACAT	4440
	CTTCTATTCC	CTTATTCAGCA	TCACATCAGC	ATTAGGGATG	GTCCTCTTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTCAG	4560
	TTTTTCTCTG	GTTCCGTGGG	CTAGCAGCGA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
75	AGCACAGGGG	GCTGTGCGAG	AATTCCCAT	ACTGTGAGAC	CAGTACTTAA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTGTGC	CCGCTTCATG	TCTCTTCCAG	GTTCTTCACT	TGATCAAGT	4740
	CACAGAGAAC	TACAGAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CAGCTGATTT	4800
	CAGCTTTAGA	TCCCTGAACA	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACTAAGAAA	4860
	AGGCCAGTTT	TAGGGAAAAAT	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
80	TTATGGGCAC	ATAATTTATTA	TTCTCTATTT	CTGCGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGGTTCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTTCTTAC	5040
	AAATGATGAA	TAAAGACGAG	ACACAACTGC	TGGGAGTCCC	AGTGACCTCA	TCCCAGAAAA	5100
	CTAAGGGTAA	GAATAAATCT	GACTCAATAC	ATGCAATATC	ATGCAATATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAAGTCAAT	AATAAATGTT	ATTATTTATTA	TAAAGTAGCT	ATAAATATAC	5220
	TAATCATAAAT	AATGTGAAAA	TAATTTAATT	TTCAATTGAGT	CATTAAATGAG	ATTCAGAGGA	5280

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

ATAAGCACAA GTCCAAAGTAT ATTTTGGAAA ATGATTGCTA TGGAAATATAT TGGTTTAGAG 5340  
 CCTTAATAGT GCAAAAATGCT TTGCTGGAAG GTAGAAAGTT CTAGATTATA ACAGGCTTAG 5400  
 GTTCAAAACCT TGGCACTTCT AATTATATGTC TCTATAAACA GGGTTTTTTT CCCCAATTCTC 5460  
 TGAGCTTTCT TGTGTTTCATC TGAATTGAAC TAAAGACTTA GAGTTACCCA TGTAAAGTCC 5520  
 TTAGCCATGG ACCTGGCATA CACTCTTCTT ACGTGCAGAG AATGACCATC ATGAGGAAAG 5580  
 AGCCACAGAT CAGTCAATGT GTCTACAAG ATAATAGCAC CAACAGGTAT AACAGGGCTT 5640  
 CCTGGCATAA TCTATTTAAA ATATCCAACC TTCAACATAC TCGTATCCTT GATGACTGTT 5700  
 AGAAGTGAAA TATGGTCCTT GCCATAAAGG AGCTGAGAGT TTAACCTGGG AGCTAAACCT 5760  
 AACCCCTTAA ACCAACAAAG AGAAAATCTA CTGGTAGACA GCGCTGCATC TTTAGTTTCA 5820  
 AAGAGAAAAG ATTGCAGTAC GTTAGAGCAA GAAGAAATTT CTGGAAGAAG TCAAAATATA 5880  
 GGTGGATTCT GAAGGGTATT TGAGGTGAAA TACACCAATT ATCAGGGAAT AACATCAAAG 5940  
 GTCCTCAATG AGACTACCAG CATTAGGGA CTGATCTAAC AGACTTAGCA TGGSTTTAGT 6000  
 ATTTACATTG ATACAGCAAT TGAATGATCT CCTTTTTTGA TGTTTGAAGG TTGATAGGTC 6060  
 AGGAAATGTT CATCAACAGT TTCAAAAGCT TCTGACTGAA TTCAACAAAT CCACTGATGC 6120  
 ATATGAGCTG AAGATCGCCA ACAAGCTCTT CGGAGAAAAG ACGTATCAAT TTTTACAGGT 6180  
 AATTTACCTT GGCCTACCCA CATTTTCTT GCATCCTGAT GTCTGTGTCT CTGAGTGGCC 6240  
 AAATGGAAGA AAGCAAGGCA GATGAGCCTG GCCGACCCAG GTGGAGAGCA TTTACTCAGA 6300  
 GTGCAATAGC TCCATTTCCA CAACCTCTCC CCACTGGAGT GTCCAGAGCC CCAACGATAC 6360  
 ATCACTGAAG TGTGATTATA GGGATAATCT TGTGATAAAA GAGGAGGTG TGTAAATAGAG 6420  
 TGAGTAAGAG TAAATAGTAA TAAGATACCA TCGATAAAT GGCATGATC CAGTACACATA 6480  
 CGATACATCT TGGTGGGAAA TGTATGACTA ATGGGATATT ATTGAATGAG GCAGGCTTGG 6540  
 GTGAGTTTCT GAGAATAGTT GAGGAAGTAC CAGGAAATAT TGAATGCACA GAGTGAAGA 6600  
 CAAAAACAAA GATCAGAAAC ATCATGGTTA AAATTACTGG AGAGAAGTCT GAGAAGCAAT 6660  
 GAATCTCTTT CAGGGAAGCC TGCTCTGCAG TTTGCAAAAC ACAGCCTCTT CTGCTTCTGC 6720  
 CTTTTGCCAA GATGATATTG ACCTTCAGTG ACCTCTTCTT TGTGCCAGCC CACATTCCCC 6780  
 TTTTGCATGT CTTACATGAC ACCTGTATAA AAATATCCAT GGACAGGAGA TACTGCATCT 6840  
 ATTCAGGCTC TGGATTGAGC TTACTGTTGT TACAATAAAG TAAGTTTGGT AATATATAGT 6900  
 TACATAAATT ACTCTCAATT CCTACTTCTT CCTTCATATC TCAAGGAAT ATTAGATGC 6960  
 CATCAAGAAA TTTTACCAGA CCAAGTGGGA ATCTACTGAT TTTGCAAAAT CTCCAGAAGA 7020  
 AAGTCGAAGG AAGATTAATC CCTGGGTGGA AAGTCAACAG AATGGTAGGA GAGCCACCCA 7080  
 TTATAGAAGC ACCTTTGAGA AACCTATGCC AGTGAGCCTT GTGCTTGACA CTGCATGGGG 7140  
 GAACAGGTGT GGGGATTGAG ATGGGTTTGC AGGGAGGGCT GAACAGGGCA CTCAGATGA 7200  
 AGGATTTGTC CAAATGAATA TGAAGAGAGC CTAGGGGAGC CAAGGAGGAA ATCAGAGGAA 7260  
 GCCAATTAGA TGGAAACACA TCTGGAGAAT TATTTGCTTA TGGCCCTGCA TGACAATAGC 7320  
 TTTGTGATCT CCCGTCTCC GCTCAGACCT ATTTTGAGAT CATATCCTTT ACTTTAAATC 7380  
 AGACTCAAT TTTTATGATG AATATTAAT AGAAAACATT AGAAAGCGTC TCTCGTCTCC 7440  
 TTTACTAATT GGGAAACAAG CAGCTCTCTG GTAAATCACC CTTTGTCTCT TGAGCTGAG 7500  
 CTGCCCTGAT CACATCTGTA GCCAATGTGT TCTGCAGGGA TTATCAGAGC TCTCTTCCCC 7560  
 ATCAAGGGCA AAGAGCTTGA CAAAGTCTCC ATTTACAGA CATCTTCTT ACCTCCACCC 7620  
 TCTCATTTCA GGGCAAACTT ACAGCAACTC AACATGAGAG TGAATAGGAA GATACCCCGG 7680  
 GAAGTAGTGT CTGACAGCAC AGGACATGCG TTTCATATTA CAGAGCTCAA GTCACTCATC 7740  
 CTAAATGCA ATCAGGGCCT CCTTCTCTG AATGGGGACC CCGTAGTTAA AAAAAATAA 7800  
 AAGTAGGAAG AGGAGGAGAG GAGAAAGGAA AGACATATGT TGGAAAGATA GACAAAATCA 7860  
 GTTTATCAGT ATTTCCAAAT AGATGATTGG AGACATTCAT ACACAGAGAA CGTGAACTCC 7920  
 TTCTCTATCA CAAGAAGTGA TGCTCCTATC AAGGGTAACT TTATACGACT GGAGCCTTGA 7980  
 AGAAAGCTGC ATCTGTGTA CCACTGGTCA GTGAGTCTAA CAATTCAAAG ATCAAAGTCA 8040  
 GTGAGTCTCA AGCAGGGATT TGGGTCAATA ATTAACGATC AGTCACGAAC ATTTGCAAG 8100  
 CATCTTCCAG ACNAGCCATT TGTAGCTTGT GTAAAGACT CTTTATTCTT TTCCCTTGCA 8160  
 GAAAAAATTA AAAAACTATT TCCTGATGGG ACTATTGGCA ATGATAAGAC ACTGTTCTT 8220  
 GTGAAGCAAA TCTATTTCAA AGGGCAGTGG GAGAATAAAT TAAAAAAGA AAACAATAAA 8280  
 GAGGAAAAAT TTTGGGCAAA CAGGTATTG TCTATATTTT ATTTATATAG TGAATATGT 8340  
 TAATACATGG AATGTTAAAC ATTTCTGATG GAATGTAACA TGATAAGTAA AAAATAAAAA 8400  
 TTGTTTATGT CTGTTATTAT GTTGTTTTAC TCTTATAACT TTATTAGTT AGGAATACCT 8460  
 GAAAAAATTA AAAAACTATT TCCTGATGGG ACTATTGGCA ATGATAAGAC ACTGTTCTT 8520  
 TGTTGCTATC TCAATATAT TATCTTTTTT GTCTTGTGTT TCAGTGTTA TTTGTTGGAC 8580  
 ACATTGATT ATTGCAAGT ACATACAAAT CTGTACAGAT GATGAGGCAA TACAATCTCT 8640  
 TTAATTTTGC CTGCTGGAG GATGTACAGG CCAAGGTCCT GGAATACCA TACAAAGGCA 8700  
 AAGATCTAAG CATGATTCTG CTGCTGCCAA ATGAAATCGA TGGTCTGCAG AAGGTAAGAA 8760  
 CTGCACTCA CAATCTTCTC TTCTACTGCC GGACATTTT CCAAGATGA CAAGTTTAAA 8820  
 CAAGGTAAAA GCTTATGACC GAGTTCCTC AAAATGATGA AAAATTCTAA ATGAGGAATG 8880  
 ATGACTCACC TCTATATTAC AAATATTGA GCATAGGGCC TGACACAAAC TGAAGGCTTA 8940  
 GTTTTGTGTT GTTTGTTTGT TTTTATTATT ATTATTATA TACTTTAAGC TTTAGGGTAC 9000  
 ATGTGACAAA TGTGCAGGTT AGTTACATAT GTATACATGT GCCAGCTGG TGTGCTGCAC 9060  
 CCATTAACT ATCATTTAGC GTTAGGTATA TCTCCTAATG CTATCCCTCC CCCCTCCCC 9120  
 CACCCCAACA CAGTCTCTAG AGTGTGATGT TACCTTCTG TGTCCAAGTG TTCTCAITGT 9180  
 TCAATTCCCA TCTATGATT AATTCCATCT ATGGCTTAGT TAATGATTAA TTTATTAGAG 9240  
 TTACATGCAT TGGATATCAA TTTGATGATA TTATTATGCA GCAATTTAAA CTGACTGGG 9300  
 AGAAATATAT ACCAATGTGA GGAAGTTTA CAAATAGGCC GAGTAGAAAA GGAATACAA 9360  
 ATTTAGGAAT TTAGGGAATT ACAATTTAAT AATTGCAATG TGTACTAAAT AATGTATACA 9420  
 GAAAAATATG ATGAGCCTAT TAAAAATTGA CACATGTAGT AGGCTGTTGG CACAAGAAAT 9480  
 AGTGATACAT ACAGTTTCAAT GTGTACAAAA TAATGTAATC ATATTTTACA TGTGTATCAT 9540  
 ACAGTTGTAT ACATACATAT GTACACATAT ACATATACGT AAAACATGA TTCTGTTTTT 9600  
 ACATACATGT ATATACATAT ACATATATA CCCAATGTAT TTATATATC AGGACTCATA 9660  
 TTTTACCTAT TAGAATAATA ATGTCTATTA AAGTGAACTC TCTGTATTTC ACTTTATTG 9720  
 CCAAAAATAT GAATCTCCAC ATAGTCAATT CATTGTTAAG GTGTATTAGA GATCGACAGT 9780  
 TAGTCAATC AGTTTCTTTT TTCCATTTGT ATAGCTTGAA GAGAACTCA CTGCTGAGAA 9840  
 ATTTGATGAA TGGACAAGTT TGCAGAATAT GAGAGAGACA TGTGTGATG TACACTTACC 9900  
 TCGGTTCAAA ATGGAAGAGA GCTATGACCT CAAGGACACG TTGAGAACCA TGGGAATGGT 9960  
 GAATATCTTC AATGGGAGAT CAGACCTCTC AGGCATGACC TGGAGCCACG GTCTCTCAGT 10020  
 ATCTAAAGCT CTACACAAGG CCTTTGTGGA GGTCACTGAG GAGGAGTGG AAGCTGCAGC 10080  
 TGCCACCGCT GTAGTAGTAG TCGAATTATC ATCTCCTTCA ACTAATGAAG AGTTCTGTTG 10140  
 TAATCACCCCT TTCCTATTCT TCATAAGGCA AAATAAGACC AACAGCATCC TCTTCTATGG 10200  
 CAGATTCTCA TCCCATAGA TGCAATTAGT CTGTCACCTC ATTTAGAAAA TGTTCACTTA 10260  
 GAGGTGTTCT GGTAAACTGA TTGCTGGCAA CAACAGATTC TCTTGGCTCA TATTTCTTTT 10320



5 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTGA ATGATTAAAA TAGCATGCCT 10380  
 TTCTCTCTTT CTCTTAATAA GCCACATAT AAATGTACTT TCCTTCCAG AAAAATTCC 10440  
 CTTGAGGAAA AATGTCCAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTGAA 10500  
 ATATAATTCT GTTCTTGACC TGTTTAAAT GAACCAACC AAATCATACT TTCTCTTCA 10560  
 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620  
 GTTTCTAAT TTTGTGATTC TATAAACAC ATCATCAATA AAATAATGAC ATAAATCAT 10680  
 TTTTGTCTTA CCGTCTTCT CTCTGGAAAG GGCAAGTGTC CAGTTACACA TAGGAAAGAT 10740  
 AATTAGAGA TATATTAATC ATATATAAAG GAAATTAATA AACAGACTAG TTCATGATGA 10800  
 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACACA TAGGAACTTC 10860  
 10 CTATTTTATG CTAAAGGAT AAGAACTCA TTACAGGCTT TGATGGTGTG TTGTCAAAGA 10920  
 GGGGCATAAA ATTATCATAT CCACATCTAG AAAATACATC TCTGGCTACG CTGATATCAA 10980  
 TGGATCGAG GAAAGAACAG TGTGGTTACC ATATATAAAT TAGGAAATCA TTAGAGTATT 11040  
 GGGAGTGGAA ATGGAGAGAA AGAAGAGGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100  
 AGAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAGAATA TCTTGTCTCT 11160  
 15 GAGAGAAAAA AAGACTTTGG GTTTAAATTT GTACTTGATG AATTAAGGTA CTTTAAATAT 11220  
 TCAAATGGAT IDGLQKLEEK LTAEKLEWT SLQNMRETCV DLHLPRPKME ESYDLKOTLR 11280  
 TGATCTGAAG CTCTAAATTT GTGATATTCA ATATAAATAC TTTAGAGTCA TTGGGATAAA 11340  
 TATGGTAGTT GTAGCTAAAA GCAAAAATAA GATACTAGGG AGAAGGATA AAGTTAGAAG 11400  
 20 AAGAAGAAAT CTAGAATTGA CCTTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460  
 CATTTTATT TTCCAGAAAG TAGCTTTCT TAGGGTTCCA TATTACTCC CATAGATTCT 11520  
 TCCC

25 A76 Protein sequence:  
 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 Unigene number: Hs.227948  
 Probeset Accession #: AB035089  
 Protein Accession #: BAB21525  
 30 Signal sequence: none found  
 Transmembrane domains: none found  
 Serine Proteinase Inhibitor domain: 13-390  
 Cellular Localization: secreted

35 1 11 21 31 41 51  
 MNSLSEANTK FMFDLFQFR KSKENNIFYS PISITSALGM VLLGAKDNTA QQISKVLHFD 60  
 QVTENTTEKA ATYHVDRSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFGK KTYQLQEYL 120  
 40 DAIKKFPQTS VESTDFANAP EESRKKINSW VESQINEKIK NLFPPDGTIGN DTLVLVNAI 180  
 YFKQGWENKF KENATKEEFK WPNKNTYKSV QMMRQYNSEF FALLEEDVQAK VLEIPYKGRD 240  
 LSMIVLLPNE IDGLQKLEEK LTAEKLEWT SLQNMRETCV DLHLPRPKME ESYDLKOTLR 300  
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAATATAVV VVELSSPSTN 360  
 EEFCCNHFFL FFIRQNKTNS ILFYGRFPSP

45 A77 DNA SEQUENCE  
 Gene name: hypothetical protein FLJ13459  
 Unigene number: none found  
 Probeset Accession #: XM\_047266  
 50 Nucleic Acid Accession #: XM\_047266  
 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 60  
 CACCATGCCA GGCCTCTCTA ACCTCTTCAA GTCTGTITTC TCATCTGCAA AACAGAGGTA 120  
 ATAAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTTCAT TCATTGTTAT 180  
 CATAAATCAG GACTAACCTG TCTCCCGTTG GGAGTTTGA ACCTAGACCT CATGTCTTCA 240  
 TGACGTCATC ACTGCCCGAG GCCCAGCTGT GTCCTACAC CAGCCCCAGC TGAAGCATCT 300  
 60 TCTTTTCTG CCGTAGAGA TGGTTACAAT GCCTGGCGTG ATGCATTCTG GCCTTCGAG 360  
 ATCCTGGCGG GCGTGTGCCA ACGCTGTGGC CTCCTGCCCC CTGAATACCG AGCCGGTGCT 420  
 TCAAGGTGG GCAGCAAGT CTTCTGACA CCACCGGAGA CCCTGCCCCC AGGGATCTCT 480  
 TCACATGTGG ATTGACATCT TTTCTCAAGA TGTGCTGCT CCACCCCCAG TTGACATCAA 540  
 GCCTCGCGAG CCAATCAGCT ATGAGCTCAG AGTTGTCTAT TGGAAACAGG AGGATGTGGT 600  
 65 TCTGGATGAC GAGAATCCAC TCACCGGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660  
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGAGCTT CACTTCAACT CCCTGACTGG 720  
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTTGAC TACCTGCCCA CGGAGCGGGA 780  
 GGTGAGCGTG TGGCGCAGGT CTGGACCTTT TGCCCTGGAG GAGGCGGAGT TCCGGCAGCC 840  
 TGCAGTGTCT GTCCTGCAGG TCTGGGACTA TGACCGCATC TCTGCCAATG ACTTCTCTTG 900  
 70 ATCCTGGGAG TTGCAGCTAC CAGACATGGT GCCTGGGGCC CGGGGCCCGG AGCTCTGCTC 960  
 TGTGCAGCTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTGGCT GCCCGCGCT 1020  
 GAGGGGCTG TGGCCGGTAG TGAAGCTGAA GGAGCGAGAG GACGTGGAGC GGGAGGCGCA 1080  
 GGAGGCTCAG GCTGGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCCAGAAGA 1140  
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCTC ACGGGCAAGG TGGAGGCGA 1200  
 75 GTTTGAGCTG CTGACTGTGG AGGAGGCGGA GAAACCGCCA GTGGGAAGG GCGGAGGCA 1260  
 GCCAGAGCCT CTGAGAAAC CCAGCCGCC CAAAACTTCC TTCAACTGGT TTGTGAACCC 1320  
 GCTGAAGACT TTTGTCTCT TCACTGGCG CCGGTACTGG CGCACCTCTG TGCTGCTGCT 1380  
 ACTGGTCTG CTACCGTCT TCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG 1440  
 CCAGGTCATC TCCGTCCTCC TCCACAAGTG ACTCTCGTG ACCTTGACA CTCACCCAGG 1500  
 80 GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTCTCTA CCCATGTGAG CTACCCAGG 1560  
 GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG

A78 Protein sequence:  
 Gene name: hypothetical protein FLJ13459

Unigene number: none found  
 Probeset Accession #: XM\_047266  
 Protein Accession #: XP\_047266  
 Signal sequence: none found  
 Transmembrane domains: 291-313  
 C2 domain: 27-86  
 Cellular Localization: plasma membrane / ER

10 1 11 21 31 41 51  
 | | | | |  
 MWIDIFPDQV PAPPVPDIKP RQPISEYELRV VINWTEDEVVL DDENPLTGEM SSDIYVKSUV 60  
 KGLEHDKQET DVHFNSTLGE GNFNWRPFVR FDYLPTEREV SVWRRSGPFA LEEAEFRQPA 120  
 VLVLQVWDYD RISANFLGS LELQLPDMVR GARGPELCSV QLARNAGAPR CNLPRCRLR 180  
 15 GNVVVKLKE AEDVEREAOE AQAGKKGRKQ RRRKGRPEDL EFTDMGQNVY ILTGKVEAEF 240  
 ELLTVEEAEK RPKVGKGRKQ EPLEKPSRPK TSFNWFWNPL KTFVFFIWR RYRTLVLLLL 300  
 VLLTVFLLV FYTIPGQISQ VIFRPLHK

20 A79 DNA SEQUENCE  
 Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Nucleic Acid Accession #: AL137708  
 25 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51  
 | | | | |  
 GGCAITGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60  
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGCT CCCTTCTGT CTGTCTCCTT GCTCTGCCCC 120  
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180  
 ATGGCCTGGG CTGGGCCCTT GAGGCAGGCG TGACTTGGAC ATGGCAAGAG GGGTCCGAGG 240  
 CTCTTGTGGG CAAGCAGGGG GAGGCGCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300  
 35 CTGCTCTCTG GAGCGGTGGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCTG 360  
 GGGTCAACGT AGGCCCATG TAGCACCTCG GTTCCCTGCG CTGTAGGTGA CAGGAGCCAG 420  
 CCCAGCCAGG TGTGCTCCTT CCCAGGCCCG TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480  
 CGCCCGCCCC ACCTTCTCTT CCACCCACAT GCCAAGGGGT GGCCAGGCAG GCAGGTGGAC 540  
 GAGTCCAGCG AGCGGCTGAG TCAGTGTGTG TGGAAATGTC TGGCCGCTCC CAGCTGCACC 600  
 40 CTGCCCCTAC CTGCCACCACT CTACACCTCA TCCTCAGGCG CTGCGGCCCT GAGCCCCCTG 660  
 CAGGAATGCA CCTTTAGCCC AGGCCCTGCT AGTGAGCTCC GCCAGACGCT AGCCCTGCTC 720  
 CTCCCGCCAT GACCCCTGAG ACCCCCTCTG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC 780  
 ATGCTCCACC TGATGAGCTG GCAAAACCAT GTGGGCCCCA GCTGTGTGTC GTGCTGGGGT 840  
 45 AGAGGCAAGG AAGTGAATGG ACCGCAGAGA TGAGACCCCG AGGGATGAGA TGGGACCCCG 900  
 AGGCAGGGCC CAGGGTCCAG GGCACAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCTCTG 960  
 TGGAGACGCG ATCCTACAGT GGGGCGAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020  
 AGGCTGCCCA GGCCTGCTCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080  
 GCTGGGCTTG GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCTCTC CTCCCTTCAG 1140  
 50 CTTCCTGCTG CACAGAACCCT TGGCCCTGCG CCACCCCGTG CTGCCCTCTT GCCTTGGCAG 1200  
 ACCCAGCACT GGCTGTGCTT AGTCAGATGG GGTAGCGGGC AGGGGCCCGA GGGGCCACCC 1260  
 TCCAGCTGTA CCGCAGCTCC TGGGCCGCTT CTCCAAACC AGCAGGGTAG AAAGATGGGG 1320  
 CACCCACCACT TCTCTCCAGT TGCCTCCGGC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380  
 ATTCCAGACC TTGTGCGCGG GACCCCTGTG GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440  
 55 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500  
 CCAGGCCCCC GCTGGGCTCT CATTGCCGCG GCCCTTGGCG CGGGCGTCTT CTCTGCTCTC 1560  
 TGCCCTCTCT GTGCTGCTCT CTGCTGCTGC CGCCGCCACA GGAAGAAGCG CAGGGACAAG 1620  
 GAGTCTGTGG GTCTGGGCGG TGCCCGCGCG ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680  
 TCCTTGCTCA CTAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740  
 60 GGCAGTCA GCGCCAGGGA TGGTTTAAAC CCAACAGAGG CAGGGCGTTG AGGACCTTCC 1800  
 TGGCAGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT 1860  
 GGGCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920  
 TTTGGGTGGG TTTGGCCGCT CTCACAGAGC GAAGCCGACG ATTTGTGCTT GTTGGGTGGC 1980  
 CTGGCTTGA GGCGGGGGGT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCAGGG 2040  
 65 CTCTGATGAG GCATGATGTC AGCACCACTT GCCCTTGTTC CCAACTCACT CCAGGTGCAA 2100  
 CCTGATGAG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCCCTCAG 2160  
 CTCTCCCTGG AGTTGCACTT TGGAAAGCCAG GAGGTGAAGG GCCCGCTGCG GCAGGACCAG 2220  
 CGGTTCGTGC AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280  
 TGGGAGCTG ACAGGGCAGG GGCCTTGGC TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340  
 70 GTGGGCTGA GGCAGGCAGC CGAAGTGGG CCTGGGGGCA CCGTGGACCC CTATGCCCGG 2400  
 GTACAGCTCT CCAACAGGCG CGGACACAGA CATGAGACAA AAGTGACCG AGGCAAGCTC 2460  
 TGCCCGCTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGCTGGGTGG 2520  
 GCCTGGAAGG CTGGATGGGC CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580  
 GCTGGGTGGG CTTGAGCTAG GGCAGCAGGG CTTGGCTCAC GCCCTGCTCT CAGATCCCGC 2640  
 75 AGGCGGAGCT GCGAGGGGCG ACCCTGCAAG TGCACTTTT CAACTTCAAG CGCTTCTCGG 2700  
 GGCATGAGCC CTTGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGATCTG CAGCATGTTT 2760  
 TGGAGCTGT GTACCTGCTG GGCCTGCGCG CTGCCACTCA GGTGAGGTGC TGGTCAACAG 2820  
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CTTGCCCTAT GGGCCATGGG AAAGACAGGC 2880  
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAGATCAC CTTCCCGGGC 2940  
 80 TGAAGCCCTT CTTGCTGCCC ACAGCCCGAG CAGGTGGGGG AGCTGTGCTT CTCTCTCCGG 3000  
 TAGCTGCCCA GCTCAGGCGG GCTGACCGTG GTGGTGTGAG AGGCTCGAGG CTTGGTCCA 3060  
 GGCCTTGCA GACCTTACGT GAAGGTCCAG CTATGCTGA ACCAGAGGAA GTGGAAGAAG 3120  
 AGAAGACAG CCAACAAAAA GGCACGCGCG GCCCTTACT TCATGAGGC CTTCACTTCC 3180  
 CTGGTGGCCT TCAGCCAGGT CCAAGATGTG GACCTGGTGC TGGCTGTCTG GAGCCGAGC 3240  
 CTGCGCTCC GAACTGAGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300

CCCTGCGCAGC ACTGGGCGAGA CATGCTGGCC CACGCCCGGC GGCCCATTCG CCAGCGGCAC 3360  
 CCCTGCGGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCCG CCTTCGCGCTG 3420  
 CGCGTCCCTT TCGCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCG CTGAGCCACG 3480  
 GCATTGCCC AGGCCGCCCT GCAGGCCAC TGCAATAAAC GCCTTCTCCT GCC

**A80 Protein sequence:**

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Protein Accession #: CAB70885  
 Signal sequence: none found  
 Transmembrane domains: 69-85  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MGHPVPSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG QGDNPAKWGL QLSTDALSLA 60  
 STPGPRWALI AGALAAAGVLL VSCLLCAACC CRRHRKPKPR DKESVGLGSA RGTTHLVR 120  
 SGSLLTQSRE GLKSRLQSPG QRGEFSRDRG LTPTEAGR

**A81 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51  
 | | | | |  
 GGGGAACACC GGGCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60  
 TCCCTCGTGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCAGCG 120  
 CCTCGAGGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG CGCGGAGGCG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGGG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCGATCCAAA CGTATCTTAC 360  
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCGTGAATAA GGCAAGGGTC 420  
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCGCTGAGGG TGCTTCTGCT GTAGAGAAGG 540  
 AGACAGGCTG GTTGTGTGTT AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660  
 TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGGA 720  
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840  
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900  
 CCAAGTGGCT AGCCAGGGA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020  
 ACAATGCTCC CATGTTTGAC CCCAGAAAT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080  
 GCGATGAGT GCAGAGGCTG ACGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140  
 GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200  
 CTGAGGCTCA CGCTGATC CTGACCAACA GGAAGGGTTT GGATTTTGGG GCCAAAAACC 1260  
 AGCACACCCG GTACGTTGAA GTGACCAACG AGGCCCTTT TGTGCTGAAG CTCCCAACCT 1320  
 CCACAGCCAC CATAGTGGTC CAGCTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380  
 CTTCCAAAGT GGTGAGGTC CAGGAGGGCA TCCCACTGG GGAGCCTGTG TGTGTCTACA 1440  
 CTGCAGAAAG CCCTGACAG GAGAATCAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500  
 CAGGTTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCACCACTT GGCACGGGAA CCGTTCTGCT AACCTGATT GATGTCAACG 1680  
 ACCATGGCCC AGTCCCTGAG CCGGTGAGA TCACCATCTG CAACCAAGC CCTGTGGGCC 1740  
 ACGTGTCTGA CATCAAGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTC CAGGCCACG 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAAGAGCAG CTGACGCTGA TCAGGSCCAG TGTGTGGAC TGCCATGGCC 1980  
 ATGTGGAAGC CTGCCCCTGA CCGTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CTTCTTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAAGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGGC AACCCAGATG AATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCGCG CCTACGACAC CCTCTTGGTG TTGACTATG 2400  
 AGGCGAGCGG CTCGAGAGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCCC TCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGTGTGGCG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580  
 CACAGAGCAT CTCCAGGGG TCTCAGTTCC CCGTTCAGCT GAGGACTTCG GAGCTTGTCA 2640  
 GGAAGTGGCC GTAGCAACTT GCGCGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCTTAGCTT TTAGGATGAG AGGAATGTGG GCAGTTTGGC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC AGGTTGGCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 TGCTCAACCC TGTGTCTTGG GCTTGGGCTT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940  
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCACGA GCTGCTGGGC CCACTGGCCG 3000  
 TCTGTATTT CTGCTTTTCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTG TGCCATAGTT GCGCTTATT TTTTATTTTC CCGTGTGCGT TGCTATAGAT 3120  
 GAAGGGTGGG GACAACTGTG TATATGTACT AGAATTTTTT TATTAAGAA A

**A82 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)  
 Cellular localization: plasma membrane

10

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MGLPRGPLAS LLLLVQCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
    QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
    KGPPFQRLNQ LKSNKDRDRTK IPYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREBIAK 180
    YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
    DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
    TDMGDDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVQRLT VTDLDAPNSP 360
    AWRATYILMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
    PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRIIR 480
    DPAGHLAMDV DSGQVTAAGT LDREDEQFVR NNIYEVMLVA MDNGSPPTTG TGTLTLLTID 540
    VNDHGPFVPEP RQITICNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
    TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFIPVL 660
    25  GAVLALLFL LVLALLVRKX RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
    GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDITLLVF 780
    DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEDED
  
```

**A83 DNA SEQUENCE**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Probeset Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

35

```

1      11      21      31      41      51
|      |      |      |      |      |
40  AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCACGCGTG CTGTGGCCTC 60
    GGGGAGTGGG AATGATGAGGC AGGAGCCITC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
    CTCAGCATC ATGATTACCT CCCAAATACT ATTTTGTGA TTTGGGTGGC TTTTCTTCAT 180
    GCGCCAAATG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCCTCTCCGT 240
    GAGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
    45  GAATAGCAGC TCCCGTTATT TTCACTGGAA AATGAACCTG TGCGTAATTC TGCTGATCCT 360
    GGTTTTCATG GTGCCCTTTT ACATTGGCTA TTTTATGTG AGCAATATCC GACTACTGCA 420
    TAAACAACGA CTGCTTTTTT CCGTCTCTTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
    ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
    CATCAGCCGG GTTGGGTGTA TTGGAGTGAC TCTCATGGCT CTCTTTCG GATTGTGGTG 600
    50  TGTCACCTGC CCATACACTT ACATGTCTTA CTCTCTCAG AATGTGACTG ACACAGATAT 660
    TCTAGCCCTG GACCGCGGAC TGCTGCAAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
    GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
    TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
    TATTCAACAG GAGATGGATG CTTTGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
    55  TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTT 960
    TAATTTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
    CAATATGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
    TGTAATTTAT CTGGAATCC AATTGTATGT GAAGTTTGG TCCCAACACA TTCTCTTCAT 1140
    TCTGTGTGGA ATAATCATG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT 1200
    60  CTTTATGCC ATCTCTAGCA GTAAGTCCTC CAATGTCTT GTCTGCTAT TAGCACAGAT 1260
    AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320
    CCGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTGTGTT 1380
    TGATGTGATC TTCCTGTGCA GCGCTCTCTC TAGCATATCT TTCCTCTATT TGGCTCACAA 1440
    ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
    65  CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAATG GAACCCAGGC CTGACATTTT 1560
    ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCTCTC 1620
    AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTAAG 1680
    ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CCGAGAGGAG 1740
    CCAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
    70  TGAGCCAAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAGGTTA TAGCTTTGCC 1860
    TTGAGATGTA CTCATTAAAA TCAGAGACTG T
  
```

**A84 Protein sequence**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Protein Accession #: NP\_057418.1  
 Signal sequence: none found  
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402.  
 424-446  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
  
```

	MSFLIDSSIM	ITSQILFFGF	GWLFMRQLF	KDYEIRQYVV	QVIPSVTFAF	SCTMFELIIF	60
	EILGVLNSSS	RYFWKMNLC	VILLILVFMV	PFIYGFIVS	NIRLLHKQRL	LFSCILLWTF	120
	MYFFWKLQDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
5	VTDTLILALE	RRLLQTMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGFVGM	IKSVTTSASG	240
	SENLTILQOE	VDALIELSRQ	LFLETADLYA	TKERIEYSKT	FKGKYFNFLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGTDPVPT	RGIEITVNYL	GIQEDVKFWS	QHSIFILVGI	IIVTSIRGLL	360
	ITLTKFYAI	SSSKSSNVIV	LLLAIQIMGY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSAISSILF	LYLAHKQAPE	KQMAP			

## A85 DNA SEQUENCE:

Gene name: TTK protein kinase

Unigene number: Hs.169840

Probeset Accession #: M86699

Nucleic Acid Accession #: NM\_003318

Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

20	1	11	21	31	41	51	
	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGITTCACCT	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CGCCTCCCG	GGTTCAGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACTAATTT	180
	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCGT	240
25	ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAACCTG	300
	TGCTGGCTCG	ATTCTTTT	TGTTGTTGGA	TTTTTGAAC	AGGGTCTCCC	TTGGTCGCCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACTATAACC	TCCACCTCCT	GGTTTCAAGT	420
	GATCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	GCGTGCACCA	CCACACCCGG	480
	CTAATTTTGT	TATTTTATT	AGAGACAGGG	TTTCAACATG	TTGGCCAGCG	TGTTCTCAAA	540
30	CTCCTGGACT	CAAGGGATCC	GCCTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACAGT	CCTGACCTTA	TAATCTTAA	GTCAATTTTT	CTGGTCCATT	TCCTCTTAG	660
	GGTCTCACA	ACAAATCTGC	ATTAGCCGGT	ACAATAATCC	TTAATCTCAT	GATTCACAAA	720
	AGGAAGATGA	AGTGATTCAT	GATTTAGAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
	GGATGATGAT	CTTAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
35	TTTGGTTTAA	ATTAATATATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
	ATGTAAGTCT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCTCAG	960
	TGCAGTTTTC	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAATGAA	CAAAAGTGAGA	GACATTAATA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
40	AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAACT	GTTAACCATA	1140
	TTATGATGAT	GGCAACAAC	CCAGAGGACT	GGTTGAGTTT	GTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTGGTTAC	AGTCAAGCAA	1260
	TTGAAGCGCT	TCCCCAGAT	AAATATGSCC	AAAATGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
	GATTTGCTGA	ATTAAAGACT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAATGGA	1380
45	CCAGAGCAAA	CTGGAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
	CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
	TACCAGTACT	AATGCTGGAA	ATTGCCCTGC	GGAAATTTAA	CCTCAAAAAA	AAGCAGCTGC	1560
	TTTCAGAGGA	GGAAAAGAAG	AATTTATCAG	CATCTACSGT	ATTAACTGCC	CAAGAATCAT	1620
	TTTCCGGTTC	ACTTGGGCAT	TTACAGAATA	GGAAACACAG	TTGTGATTCC	AGAGGACAGA	1680
50	CTACTAAGC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
	ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCAATT	GGAAGAGTCC	1800
	CAGTTAATCC	GCTAAGTAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
	GTTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
	AACCAAGTGG	AAATGATCCC	TGTGAATTAA	GAAATTTAAA	GTCCTGTCAA	AATAGTCATT	1980
55	TCAGGAAGCC	CTGGGTGTCA	GATGAAAAGA	GTTCTGAAC	TATTATTACT	GATTCAATAA	2040
	CCCTGAAGAA	TAAACGGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAACT	AAAGAGTATC	2100
	AAGAACCAGA	GGTTCAGAG	AGTAAACAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAACCA	GAATCCTGCT	GCATCTTCAA	ATCACTGGCA	GATTCCGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTTTTCA	GTTTCAAAAC	2280
60	AGTCACCACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
	GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AAGAAATGAT	2400
	TTCCACCTGC	TTGTCAAGTG	TCAACACCTT	ATGGCCCAAC	TGCTGTGTTT	CAGCAGCAAC	2460
	AGCATCAAT	ACTTGGCACT	CCACTTCAAA	ATTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGTTTAAA	GGAAGAAATT	ATTCCATATT	AAAGCAGATA	GGAAAGTGAG	2580
65	GTTCAAGCAA	GGTATTTTCA	GTTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAAATAG	2640
	TGAATTAAGT	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATAAAT	ACAACACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCACGG	2760
	ACCAGTACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCAG	2880
70	TTACACAAAT	CCATCAACAT	GGCATTGTTT	ACAGTGATCT	TAAACCAAGT	AACTTTCTGA	2940
	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAAAATG	CAACCAAGTA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAGCAAA	3060
	TCAAGATAT	GTCTTCTCTC	AGAGAGAAATG	GGAAATCTAA	GTCAAGATA	AGCCCCAAAA	3120
	GTGATGTTG	GTCCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTT	3180
75	AGCAGATAAT	TAATCAGATT	TCTAAATTAC	ATGCCATAAT	TGATCTTAAT	CATGAAATTG	3240
	AATTTCCCGA	TATTCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
	ACCCAAACCA	GAGGATCTCC	ATTCTGAGC	TCCTGGCTCA	TCCATATGTT	CAAAATCAAA	3360
	CTCATCCAGT	TAAACCAATG	GCCAAAGGAA	CCACTGAAGA	AATGAAATAT	GTTCTGGGCC	3420
	AACTTGTGTT	TCTGAATTCT	CCTAACTCCA	TTTTGAAAGC	TGCTAAAACT	TTATATGAAC	3480
80	ACTATAGTGG	TGGTGAAGT	CATAATTCTT	CATCCTCCAA	GACTTTTGA	AAAAAAGGG	3540
	GAAAAAATAT	ATTGCAAGTT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
	GTATATCTCT	TGAATCCCTG	TGGAATCTCA	CATTGGAAGA	CAACATCACT	CTGAAGTGTG	3660
	ATCAGCAAAA	AAAAATTCAGT	GAGATTATCT	TTAAAGAAAA	ACTGTAAAAA	TAGCAACCAAC	3720
	TTATGGCACT	GTATATATGT	TAGACTTGTG	TTCTCTGTTT	TATGCTCTTG	TGTAATCTAC	3780
	TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GTATATTCTA	AAAAACTTTG	3840

TAAATAAAGT TTTGTGGCTA AAATGA

**A86 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51  
 15 MNKVRDIRNK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLKLEKNS 60  
 VPLSDALLNK LIGRYSQAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120  
 ANCKKPAFVH ISFAQFELSQ GNVKKSQKLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180  
 EEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDNRGQTT KARFLYGENM PPQDAEIGYR 240  
 20 NSLRQTNKTK QSCPFGRVFV NLLNSPDCDV KTDSDVVPFC MKRQTSRSEC RDLVVPKSKP 300  
 SGNDSCELRN LKSVQNSHFV EPLVSDEKSS ELIITDSITL KNKTESLLA KLEETKEYQE 360  
 PEVPESNQKT WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTPE QPVFVSQKQS 420  
 PPISTSKWED PKSICKTPSS NTLDDYMSCF RTPVVRKDFP PACQLSTPYG QPACFQQQKH 480  
 QILATPLQNL QVLASSSANE CTSVKGRIYS ILKQIGSGGS SKVFQVLNEK KQIYAIKYVN 540  
 25 LEEADNQTLN SYRNEIAYLN KLQQHSKII RLYDYEITDQ YIYMVMCCGN IDLNSWLKKK 600  
 KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPFANFLIV DMLKGLIDFG IANQMPPDQT 660  
 SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VMSLGCILYY MTYKGTFFQQ 720  
 IINQISKLHA IIDPNEHIEF PDIPKDLQD VLKCCCLKRDP KQRISIPELL AHPYVQIQTH 780  
 PVNQMAKGTI EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK 840  
 K

**A87 DNA SEQUENCE**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 40 GGGGCGACGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCGCCCCCT 60  
 CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CGGAGCGCG GGTAGCGCGT AGAGCGCGCG 120  
 CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCGCAG CTTCGTGGCG CTCTGGGCAC 180  
 45 CCTGTTCCT GCTGGCTCTC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240  
 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGGCGGA GATGACGCGC GAGATCCTCT 300  
 CCAITTTGGG CTGTGCCACG CGCCCGCGCC CGCACTTCCA GGGCAAGCAC AACTCGGCAC 360  
 CCAITTTCAT GCTGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGCG GGGCCGCGCG 420  
 GCCAGGGCTT CTCTACCTCC TACAAGGCCG TCCTCAGTAC CCAGGGCCCC CCTCTGCCCA 480  
 50 GCCTGCAAGA TAGCCATTTC CTCACGAGC CGGACATGGT CATGAGCTTC GTCAACCTCG 540  
 TGAACATGA CAAGGAATTC TTCCACCCAC GCTACCAACA TCGAGAGTTC CGGTTTGATC 600  
 TTTCAGGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCGGA ATTCCGGATC TACAAGGACT 660  
 ACATCCGGGA ACCTCTCGAC AATGAGAGCT TCCGATCAG CGTTTATCAG GTGCTCCAGG 720  
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCTTC TGGGCTTCGG 780  
 55 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACGAGCAA CCACTGGGTG GTCAATCCGC 840  
 GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCGAGGC ATCAACCCCA 900  
 AGTTGGCGGG CCTGATTGGG CGGCAGCGGC CCCAGAACAA GCAGCCCTTC ATGTGGCTTC 960  
 TCTTCAAGGC CAGGAGGTTC CACTTCGCGA GCATCCGCTC CAAGGGGAGC AAACAGCGCA 1020  
 GCCAGAACCG CTCGAAGAGC CCCAAGAAC AGGAAGCCCT GCGATGGGCC AACGTGGCAG 1080  
 60 AGAACAGCAG CAGCGACCG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140  
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTAAGCGGCC TACTACTGTG 1200  
 AGGGGGAGTG TGCCCTTCCCT CTGAACCTCT ACATGAAGCG CACCAACCA GCCATCGTGC 1260  
 AGAGCGTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320  
 AGCTCAATGC CATCTCCGTC CTCTACTTCC ATGACAGCTC CAAGCTCATC CTGAAGAAAT 1380  
 65 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCGACTAGCT CCTCCGAGAA TTCAGACCCT 1440  
 TTGGGGCCAA GTTTTCTCGG ATCTCTCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500  
 CTGCTTTTGG TGAGACCTTC CCCTCCCTAT CCCCACTTT AAAGGTGTGA GAGTATTAGG 1560  
 AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAGA 1620  
 TCCTACAGC TGTGACGGCA AAACCTAGCA GGAAAAAACA ACAAGCATA AAGAAAAATG 1680  
 70 GCGGGGCCAG GTCATTGGCT GGGAAAGTCT AGCCATGCAC GGAAGCTTTT CCAGAGGTAA 1740  
 TTATGAGCGC CTACAGCCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800  
 GGGCATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCTCTGA ATAAATGTCA 1860  
 CAATAAACG AATGAATG

**A88 Protein sequence:**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 Signal sequence: 1-30  
 Pfam domains: TGFb\_propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIIHRLRSQE RREMQREILS 60
   ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
   LQDSHFLTDA DMVMSFNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
   IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVDITA TSNHWVVNPR 240
   HNGLQLSVE TLDGQSINPK LAGLGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
10  QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
   GECAFPPLNSY MNATNHAIVQ TLVHFINFET VPKPCCAPTQ LNAISVLVFD DSSNVILKKY 420
   RNMVVRACGC H

```

**A89 DNA SEQUENCE:**

```

15  Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Nucleic Acid Accession #: AC012478
   Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

```

```

20  1      11      21      31      41      51
   |      |      |      |      |      |
   ATGCGCGCGG TGCCGCTGCC CGCCCGGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC 60
   GCTCCGCGCG CCGCGCCGAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
25  CGGAGTCCGC GGCACCCGCC CGGCCCGGGG CCGCGGAACA CCACCGGTTT TGGGTCTGGG 180
   CGCGCGGCGG GCAGCGGCGG CTCAGCTCC AACAGCAGTG GCGACGCTT GTGACCCCGC 240
   ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCGAG CGGTGATCGT GCGTTCGCC 300
   TTTACACCCC TCCTCATCGC CTGCTGCTGC CTGCGGCTCT TCAGGTCGGG AAAGAGGTTA 360
   AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
30  CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
   TCCTGCGCGG CTTGCGTGGG AGCTGAGCTG CCAGGCGTGC AGCGCTACT GACAGTTCTT 540
   GTGCCCCAC CTTTCATCCT CGACATTGAC CTTCCAGCAA GATCAGTGG AAGGCCTGAT 600
   GGTGGAATCA GACCTGGTAA AACCTGTTT CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660
   TCAGCTGCAA CCTGGGGTGT GAAGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720
35  GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTG AGGCATCTGC 780
   TCAGACTTGC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840
   TTTGGGCATC CTTTAAAGT GCCCCTACT TCTACTCCC ATGGTTTTCG ACAACTGCAG 900
   CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTAGCCA GAAACACCCG GGCTCCATCT 960
40  GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
   CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAAACCATG 1080
   AGTACTTGG GCTTGGATGT TTTCTGGT GCGGCCAGC GCGGCACCTT TTGTGAAGAC 1140
   AGAGCAGTGA CTAAGTTCTT CCAGGCTAGC TCTTCTCCA AACAGCTGGG CTGGAAGCCA 1200
   GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTC TCCGCTGAGC 1260
45  ACCATCCTCG TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCTT GACGCGGAGG 1320
   AGGGTGTTC GGCCTCGCGG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
   TGCTTTTGG TTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
   ATCTGTCTCC CTTGCTGTGC CTTGGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCTTGGCT CATTTGAGCA GAGCCACAA AAGGCAGCTG CTGCCCACCG GGAGCCTGTC 1560
50  AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
   GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCACGCTGA GGATGTCACT 1680
   CACCTCTGG GAGACTTGGG TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GCCAGAAGAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860
   TCCCCCGCAG AGCCCTGTT TCTGTCCAGG CCTTGA

```

**A90 Protein sequence:**

```

60  Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Protein Accession #: FGENESH predicted
   Signal sequence: 1-27
   Transmembrane domains: 94-115, 448-469
   Cellular Localization: not determined

```

```

65  1      11      21      31      41      51
   |      |      |      |      |      |
   MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
   AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTTLLIACIL LRVFRSGKRL 120
70  KRTRKYDIIT TPAERVEMAP LNEEDEDED STVPDIKYRV SLPAALRRQL PGQTLTLTVP 180
   VPPPFILID LPARCGRPD GGIRPGKTCF PANWHFVESW SAATWGVKDW TWKPSCVGGV 240
   ETKTNVMYKT PAPSCVSGIC SDCHQWARFH VTTMELLPP FGHFPKVPPT STPHGFRQLQ 300
   LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLPN PWHFVSATGS PIKTLTYQTM 360
75  STLGLDVFCG AGQRGTFCE RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPPLS 420
   THEVRLARD ARGQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEPV KRGPSSQLTR HTPCPGWGITH 540
   ANLQTFIDTQ QQEGPREDVT HFGGDLQDVA NFYLEEGBFQ DGRQKQNMV SEECPPLSLT 600
   CERLTGSHHF SSHSKWSWFL SPRQPLFLSR P

```

**EWING****A91 DNA SEQUENCE**

```

Gene name: G protein-coupled receptor 64
Unigene number: Hs.184942

```

Probeset Accession #: AA435577  
Nucleic Acid Accession #: NM\_005756  
Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60  
CTGCGGTCAG GGATGGTTTT CTCTGTGAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120  
GTTTACTGTA CGTTCAAGAT ATTCTGTGTC ATCATTGTGC TTCAATGTCG TCTGGTAACA 180  
TCCCTGGAAG AAGTACTGTA TAATCCAGT TTGTCAACCAC CACCTGCTAA ATTATCTGTT 240  
GTCAGTTTTG CCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300  
AGCTTACTCC CTTCAAACGA AACAGAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360  
GCTTCAGGCG TCAAAACCCA GAGAAATATC TGCAATTTGT CATCTATTGG CAATGACTCA 420  
GCAATTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT 480  
CAACATATAA CGAATGGCAG CTAACTGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA 540  
GAGCTCAACA AAACCTGACA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600  
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660  
TGTGCTGCAA TAGCGCTTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720  
TCTGTGAGGA TACCTGCCCC TTCTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780  
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840  
TCCATCCGAG TGGTGCCTCG GGCCACTGTG CTTTCCCAAG TCCCAAAAGC TACCTCTTTT 900  
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960  
CAACCCCTTT CACCACGCTT TCCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020  
CCACAGTCTG AAACGATCTT TTCCCTATG CCCCACACCC ATGTCTCCGG CACCCACGCT 1080  
CCTGTGAAAG CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140  
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200  
CAAGTGTGTC AGATGGAGAA GGCTGTGCTC TTGGGCGAGC TGGAGCCTAA CCTCGCAGGA 1260  
GAAATGATCA ACATGCTCAG CAGACTCCTT CATTCGCCGC CTGACATGCT GGCCCTCTG 1320  
GCTCAAGAT TGCTGAAGT AGTGGATGAC ATTGGCCTAC AGCTGAAGTT TTCAACACAG 1380  
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440  
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAAAATC TTCAGTTTTC TCTGGAAACC 1500  
CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCTCT CATCGCTGAT GAATAATTTA 1560  
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTTTTGA AACACCTGCT 1620  
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680  
GTTGCAAAAC TGACCGGTAC GAACTTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740  
AACCCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800  
GGCAGGAGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860  
ATCTGTACCT GTAGCCATCT AACAGCTTC GGCGTTCTGC TGGACCTATC TAGGACATCT 1920  
GTGCTGCCCT CTCAATGAT GGCTCTGAGG TTCAATACAT ATATTGGTTG TGGGCTTTCA 1980  
TCAATTTTTT TGTCATGAT TCTTGTAAAC TACATAGCTT TTGAAAGAT CCGGAGGAT 2040  
TACCTTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CTTGGTCTTC 2100  
CTCTGGACTC CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160  
TTTCTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCCTAGAAGC ATTCATATG 2220  
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTGTC 2280  
ATTGTGCGTT GGGGGGTAC AGCTGTGGTT GTGACCATCA TCTGACTAT ATCCCCAGAT 2340  
AACTATGGGC TTGGATCCTA TGGGAAATTC CCAATGGTT CACCGGATGA CTTCTGCTGG 2400  
ATCAACACAA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTG 2460  
CTGAACGTCA GCAATTTCTGA CTGGAGTAAA ACTGCTACTA ATGTTTAAAG AAGAGAGAG 2520  
CAACTGGGAG CCCAGCGAAA AACCAATATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580  
TTTTTACTGG GAATTAAGTT GGGCTTTGCC TTCTTTGCC TGGGACCAAT TAACGTGACC 2640  
TTATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700  
TTGTGTGCCA AAGAAATATG CAGGAAGCAA TGGAGGCGGT ATCTTTCTTG TGGAAAGTTA 2760  
CGGCTGGCTG AAATTTCTGA CTGGAGTAAA ACTGCTACTA ATGTTTAAAG AAGACAGACT 2820  
GTAAACCAAG GAGTGTCCAG CTCTTCAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC 2880  
TCCACCACAG TGCTAGTGAA TAATGATGTC TCAGTACAG CAAGCGGAAA TGGAAATGCT 2940  
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAAATG GAGATGTGTG CCTTACAGAT 3000  
TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCGGT 3060  
ATGGCTCTCA GAAGGACTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTTC 3120  
CTTCTCTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAAAT TTACCTTTTA 3180  
CACAAATGTA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240  
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300  
TTTAGACATT TCTGATTTGG TTCTTATCT TTCAATTTAT AAGAAGTTG GTTTTAAACA 3360  
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420  
TTTAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTGAGCCTG 3480  
TTGGTGAGTT TAGTTGTGCA TGCTTTGTT GTATATAAGC TAAATTTCTAG TGACCATGT 3540  
GTCAAAATC TTACTTCTAC ATTTTTTGT ATTTATTTTC TACTGTGTAA ATGTATTCTT 3600  
TTGTAGAATC ATGGTTGTTT TGCTCACGTT GATAATTCAG AAAATCCTTG CTGTTCCGC 3660  
AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720  
TCAAGAAATA ATGATCCGAG CCAGACTGAG AAAATGTAG CAGACAGTGC CACAGTTAGC 3780  
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840  
TGGGTGATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900  
GTGACAGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCATCCC CTGACCGCAT 3960  
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020  
AGAGGGATGA ACTGTATCCT AGACCATGTG TCAGGAAAT TGTGAACGTA GATGAGGTAC 4080  
ATACACTGCC CTATCTGAAA TCCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140  
CTTCTCTTAA AAGGTACAT ATATATGGAA AAAATCATA TTGCGTTCT TTAAGAGGCA 4200  
ACTGCAATGT ACATTGTTGA TTGTTATGAC TGTACACTC TGGCCAGCC AGAGCTATAA 4260  
TTGTTTTTAA AATGTGTCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320  
GGGAACGTGT CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380  
TATACAGGTC CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440  
TTATTAGGAA CATTTCAAAC CCTTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGCAATG 4500  
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560  
CTGACTGTAC TTTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTGTA TTTATATGTT 4620



**A92 Protein sequence**

**G protein-coupled receptor**  
Gene name: G protein-coupled receptor 64  
Unigene number: Hs.184942  
Protein Accession #: NP\_005747.1  
Signal sequence: 1-38  
GPS domain: 564-615  
Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
Cellular Localization: plasma membrane

	1	11	21	31	41	51	
15	MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSP	PAKLSVVSFA	60
	PSINEVETTS	LNDVTLSSLP	SNETEKTKIT	IVKTFNAGSV	KPQRNICLS	SICNDSAFFR	120
	GGIMVQYDKE	STVPQNGHAI	NTGLTVGSLV	SELKRSBLNK	TLQTLSEYTF	IMCATEAAGS	180
	TLCNTDFTIKL	NNTNMCAACAI	AALERVKIRP	MEKCCSVRI	PCPSSPEELG	KLOCLQDPLI	240
	VLCADHPRPG	PFSSQSIGIV	VRATLVLSQV	PHATCSAEPF	DPSPVTHNVF	SPICEIQPLS	300
	PQPSAPIASS	PAIDMPPQSE	TISSPMPQTH	VSGTPPPVIK	SFSSFTVSAP	ANMLTASAPF	360
20	QVDQIVNTSS	ISDLENQVLQ	MEKALSGSL	EPNLAGEMIN	QVSRLLHSPF	DVNVTPAQQR	420
	LKVVDDIGLQ	LISFNSTTISL	TSPSLALAVI	RNVASSENTF	TFVAQDPANL	QVSLQTAPE	480
	NSISGITIPLS	SLMNLNPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLSD	YSISVSSVANL	540
	TVRNLRNVT	VTLKHINPFS	DELTVRCVFN	DLGNGRGGG	WSDNGSCVIX	RINNETICTC	600
	SHLTSFGVVL	DLNSTRVFLPA	QMMLATPIY	IGCSLSIFL	SVTLVTYIAF	EKIRADYPSK	660
25	ILILQICRAIL	LNRSLVSLAS	WIALYKMQGL	ICSVAVFLHF	PLLVSTFTWMG	LEAFHYMLAL	720
	VKVFNTYIRK	YILKFCIVGW	GVPVVVTI	LTISPDNVGL	GSYGKFPNGS	PDDFCWNLIN	780
	AVFYITVVG	FCVIFLLNVS	MFIVVLVQLC	R1KKKKQLGA	QRKTSIQDLR	S1AGSLFLNG	840
	ITWGPAPFAN	GPVNVTFMYL	FAIFNTLQGF	F1F1FYCVAK	ENVRKQWRRY	L1CCKGLRLAE	900
	NSDMSKATN	GLKKQVTGKQ	VSSSSNLSQS	SNSTNSTRAL	LVNNDSCSVHA	SGNGNASTER	960
30	NGVFSKVONT	DQLCHDFTVN	QHMFNESKDS	CNGKGRMGLR	RTSKGRSLHF	IEQM	

## Fibrosis

### A93 DNA SEQUENCE

35 EGF-like domain  
Gene name: EGF-like-domain; multiple 6  
Unigene number: Hs.12844  
Probeset Accession #: N67551  
Nucleic Acid Accession #: NM\_015507  
Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
40	CGCGAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCCCCA	GCCCTTCCCC	AGGCGCGGAG	60
	CGCCCTTGCC	GGCGTGCTGC	GCCTCCCCCT	CCAGACTGCA	GGGACGAGC	CCGGTAACTC	120
	CGAGTGGAGG	GGAGGAGCCG	AGCGGCTGAG	GAGAGAGGAG	GGCGCGCTCT	AGCTGCTACG	180
45	GGGTGCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGGTA	240
	ATGCTCTCTC	CTCGGAGCGT	TGCGCTCCCG	CTGTCTCTCT	CCCTGGGTGC	AGGTGGTTTC	300
	GGGAACCGCG	CCAGTGCAAG	GCATCAAGGG	TTGTAGACT	CGCGACTGCA	GCCTGGGGTC	360
	TGTCACTATG	GAATCAAACT	GGCCTGCTCG	TACGGTGCTG	GAAGAAACAG	CACAGGGAATC	420
	TGTGAAGCTA	CTATCGAAAC	TGGATCTAAG	TTTGGTGAGG	CGGTGGGACT	AAACAATAATC	480
50	AGATGCTTTC	CAGGATACAC	CGGAAAAACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGGAATG	540
	AAACCCCGCG	CGATCCCAAC	CAGATGTGTG	AATACACAGC	GAAGCTACAA	GTGCTTTTTCG	600
	TCAGTGGGCC	ACATGCTCAT	GCCAGTAGCT	ACCTGTGTGA	ACTCTAGGAC	ATGTGCCCATG	660
	ATAAATCTGC	ATGACAGCTG	TGAAGACACA	GAAAGAGGCG	CACAGTGCCT	GTGTCCCATCT	720
	TCAGACATCC	GCGTCGGCCC	AAATGGAAAG	GACGTGCTAG	ATATTGATGA	ATGTGCGCTCT	780
55	GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGGGAAG	CTACTACTGC	840
	AAATGTCAAC	TTGGTTTTCG	ACTGCAAAT	ATCCAGTGGC	GATTGACTGT	TATAGATATA	900
	AAATGAATGA	CTATGGATAG	CCATACGTGC	AGACCCATG	CCAATTGCTT	CAATACCCAA	960
	GGGTCTCTCA	AGTGTAAATG	CAAAGCAGGGA	TATAAAGGAG	ATGGACTCTG	GTGTTCTGCT	1020
	ATCCTCGAAA	ATTCTGTGAA	GGAATGCTCT	AGAGCAACCT	GTACCAATCA	AGACAGAATC	1080
60	AAGAAGTTCC	TTGCTCAACA	AAACAGCATG	AAAGAAGGCG	CAAAAATTA	CAATGTATCC	1140
	CCGAAAGGCC	CCAGGACTCC	TACCCCTAAG	GTGAACTTGC	AGCCCTTCAA	TTATGAAGAG	1200
	ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GMAAATGAAA	1260
	GAGGCGGCTT	AGGATGAGAA	AAGAAGAAG	AGAAACCTCA	AGAAATGACAT	AGAGGAGCGA	1320
	AGGCTGGGAG	GAGATGTGTT	TTTCCCTAAG	TTAGATGAAG	CAGGTGAATT	GGCCCTGATT	1380
65	CTGGTCCAAA	GGAATAGCGT	AACTTCCAA	CTGGAACATA	AAGATTAA	TATCTCGGTT	1440
	GACTGACGAT	TCAATCATGG	GATCTGTGAC	TGGAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
	TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTTC	GGCCTTCCGA	1560
	GGTCAACAGA	AAGACATTTG	CCGATTGAAA	CTTCTCTCTAC	CTGACCTGCA	ACCCCAAGAC	1620
	AACTTCGTGT	TGCTCTTTGA	TATCCGGCTG	CGCGGAGACA	AAGTCGGGAA	ACTTGGAGTG	1680
70	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CACAGAGTGA	GATGAGAAAG	1740
	TGGAAGACAG	GGAAATGAA	TTGTGATCAA	GGAAGATGAT	TACCCAAAG	CAATCATTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGCG	GAAATCGCAG	TGGATGGCGT	CTCTCTGTGT	1860
	TCAGGCTTAT	GTCGACAGAT	CCTTTATTCT	GTGGATGACT	GAAATGGTCT	ATTCCTTATAT	1920
	TTGACTTTGT	ATGTGAGTTG	CTCGTTTATC	TTGATATTGC	ATCATAGGAC	CTCTGGCAAT	1980
75	TTAGAATTAC	TAGTCAAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGGCCT	2040
	TCTTGATATA	GATATGCCAA	TATTTGCITT	AAATATCAT	TCACCTGTATC	TCTTCAGTCA	2100
	TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGAGAA	GTGCACTTAT	CTCCCTCTCT	2160
	CAGTATATCT	GATTTTGATA	AGTAAGTTGA	TGAGCTTCTC	TTTACAACAT	TCTTCAACAT	2220
	TAGAAAAAAA	AGCACAGATA	ATGTTTAA	TGTTTGACTC	TTATGATACT	TCTTGGAAAC	2280
80	TATGACATCA	AAGATGAGCT	TTTGCTTAAT	TGCGTTAGCT	GGGTCTTCA	TAGCCAAACT	2340
	TGTAATATTA	AAATCTTTGT	AATTAATAA	TCCAAATCAT	CAAAAAAAA	AAAAAAA	

A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

1 11 21 31 41 51  
 15 MPLPWSLALP LLLSWVAGGP GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60  
 CEATCEPGCK FGECVGPWNC RCFPGYTGT CSQDVNECGM KPRPCQHRCV NTHGSYKCF 120  
 LSGHMLMPDA TCVNSRITCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS 180  
 GKVICPNRR CVNTFGSYIC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240  
 20 GSPKCKCKQG YKNGGLRCSA IPENSVEVL RAPGTIKDRI KLLAHKNSM KKKAKIKNVT 300  
 PEPTRTPTPK VNLQPFNYEE IVSRGONSHG GKKNEERMK EGLEDEKREE KALKNDIEER 360  
 SLRGDVFFPK VNEAGEFLGI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420  
 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFYRL AGDKVGLRV 480  
 FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGGKGTG EIAVDGVLLV 540  
 25 SGLCPDLSLS VDD

GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51  
 35 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GCGCGCTGTG 60  
 CCTGTGCTGT AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGAACAACCT TCACCAATGA 120  
 GTGCACATA CCAGGCAACT TCATGTGCAG CAATGAGACG TGCAATCCGG GCGCCTGGCA 180  
 40 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTCGAAATGT GGCACAACCT TCCTCCCTGT TGCACGCGG ATCCATTGCA TCATTGGTCG 300  
 CTTCCGGTGC AATGGGTTTG AGGACTGTTC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTGC CTTTGTCTCA CGGCCGCTA CCATGCAAG AACGGCTCT GTATTGACAA 420  
 GAGCTTCATC TGCATGAGC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 45 AAGTTCTCAA GAACCCGCGA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 TTACCCGAGC ATCACTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCTGCTGGCA CTGGCTTTCG ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660  
 GCACCGGCTG CAGCAGCTGT TGTGCTGTGC CGCCTGGTGT GTCTCTGACC ACCCCACCA 720  
 CTGCAACGTC ACCTACAAGC TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 GAATGCGTCG GAAGTAGGCT CCCCACCTCT CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840  
 50 TCGCTGGTAT GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGCCC GACTACCGCT CCGGTCCCG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960  
 CAGCAGCTCT CTGAGCGTGG AAGACACCG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020  
 GGGCAGCTGT CAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 55 AGTTATTCCA AAGCTCATAT GGGTTAATCT GCTCTGACT GTTGCCATTG TAACAATTG 1140  
 TGCTCATGGG AAGCTCTTTA AGCACTGTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GCATTCTCTT CCTCCCCAG ACTTCAGAGA TGTTTTCTG CGCTCTCAGT 1260  
 TGACATGATC TGTGTGCGT CTTTCTGTGC AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320  
 CACCCCTATT TTTCACTTA TTCTGTTTCT GTTGAGAGGA CAGCATATAA AACAGTATTG 1380  
 60 AATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATCTCTCT GCTGGGTAGT TACCTATAG CATTTGGGGA TTTGGGTTAG 1500  
 ATGATCTAAC CAGGAGGCCA TCACCTGGATG GTCACCCCCC CAAAAAATT CCATTTGAGC 1560  
 ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCCG TTCAGCAGAG TCAGTGGCCA 1620  
 AAGAAACTT TGGACGTGAG TAACACCTCT CAGCAGTCG AACGTTATT TGGTTTGTG 1680  
 65 AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTG CCCAAGAATG 1740  
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTAA AATAGGCAGG 1800  
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920  
 AACTGCCCTG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAGTC TGACCTGGCT 1980  
 70 GTATGTCCTT GTGGCCACA CCCAGCCTGT CTTGCTCAIT CATGCAGCCT CAACACTGGC 2040  
 CTCCAAAGTT CCCTTAACAC TTGCAAGATC CTTTCTACCT GTGCATTGG ACTTGAGGAC 2100  
 ACTGGTTCTT ATCAAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTGAGGCTG AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 75 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCAIT 2340  
 TGAACAGTGT TGTGTTGTTT TTCCCTTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400  
 AGCTGTCTCT TTTTGTGTTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAGGAGATC 2460  
 ACACCCCTGC CCCGCTGAGC CCCGTGATAA CAGTCACTC CAGACTAACC TGTGTGOCAG 2520  
 ACATTGTGTC ATTTGTGCAC TTTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580  
 80 AGAGGCACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640  
 TTCTCTGTGT CCAGTCAGCG ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAAAGTT 2700  
 AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760  
 CCACTCCGGG CAGCTGTAC CCATTGAGAA CTTCTTTCOG CAGCTGAAGA AATGTTCACT 2820  
 AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAAGAGT GGGGCTAAG TGGCATTGAG 2880

5 TGATCTCTGT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940  
 AACGTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAGAA CTTTGATGA CAGCCAGAAT GTGTAGAAC TCTGGCTGAA 3120  
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180  
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCACTTAG GAAAAACAAA TGGTTTTAGT 3300  
 AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 10 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420  
 TTTTGGGGGG GAGGGGGGTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTTC ATTTCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACAG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 15 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTTGT GTGTCGTTGC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780  
 TTATACCTTC TAATAAATT GCAGTTTCAT TCTTTCTGTT TGTGCAAAAG GWMCTAMARM 3840  
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCATCTCGGG 3900  
 TGGGGCGGG GGGCCACGT AGGTACGGG ACCACGGGG CCCAAACGG ACCCCAGAAG 3960  
 20 GAAACCCGG CCAAGAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGGCGCGGG 4020  
 GGAACCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGAACCC GATAGAGTAC G

25 A96 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 30 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 | | | | |  
 MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGANQCD GLPDCFDKSD 60  
 EKCEPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 40 KNLGLCIDKSF ICDGNQNCQD NSDEESCESS QEPGSGQVFV TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHQQRK NNLMTLHVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240  
 YVASQAQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PFYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEV

#### 45 LUNG

A97 DNA SEQUENCE  
 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 50 Unigene number: Hs.256897  
 Probeset Accession #: BE001836  
 Nucleic Acid Accession #: BE001836  
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 | | | | |  
 ATGGCCGTCA AATCTTTTTC CTTCAACACT GGAATGATG GGCTAGACCC AGACCCAATC 60  
 ATGTTAAGTA TGATAGGAGT CAGTGGCCCA GCTGGTGTGG AAGACAAGTG GGTCACTACTG 120  
 GGTTAGGCC CACATAGCAC TAAAGGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC 180  
 60 GGGAAATATG TCACTCTAA AAAAGATGTT TCTATTAGAA TTACTTACT CTTTCATGAA 240  
 AACATAGATG CTTCTCTTTT CTTGATTAGT GATGGCCATC AGTTAACCCA AGTGCACTCA 300  
 GAGAAGTCAA ATTCTGACAC AATCCAGCAA GTAACATATA AACTGATGG CCCAGTCGAA 360  
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAAG AGATTGAGA 420  
 AATTTTCTGA AGCTCTTGAA GCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480  
 65 AGAGCAAAGS CTACCACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540  
 GACAGCTACA CCTGTTTTC TCCTCATGC CTTGATCCCC AGAAGTCTA CTTTCACAGC 600  
 GCTGGAGCAC TCCCAAGCTG TGAATGTCAT CTCACCAACC TCAGCCAGAG TGTCAATTTC 660  
 TGTGAGAGAA CAAAGATTG GGGCACTTTC AAAATTAATG AAAGGTTTAC AAATGACCTT 720  
 TTGAATTCAT CTTCTGCTAT ATACTCCAAA TATGCAAAAT GAATTGAAAT TCAACTTAAA 780  
 70 AAAGCATATG AAAGAAATCA AGGTTTTGAG TGGTTTCAAG TCAACCAATT TCGAAATGGA 840  
 AGCATGTTG CTGGGTATGA AGTTGTTGGC TCCAGCAGTG CATCTGAAGT GCTGTGAGCC 900  
 ATTGAACATG TTGCGAGAA GGCTAAGACA GCCCTTCACA AGCTGTTTCC ATTGAAGAC 960  
 GGCTCTTTC GAGTGTTCGG AAAAGCCAG TGTAAATGACA TTGTCTTTGG ATTTGGGTCC 1020  
 AAGGATGATG AATATACCTT GCCCTGCAGC AGTGGCTACA GGGGAAACAT CACAGCCAG 1080  
 75 TGTGATCCT CTGGGTGGCA GGTGATCAGG GAGACTGTGT TGCTCTCTCT GCTTGAAGAA 1140  
 CTGAACAGA ATTTTCAGT GATTGTAGGC AATGCCACTG AGGCAGCTGT GTCATCCTTC 1200  
 GTGCAAAATC TTTCTGTCAT CATTOGGCAA AACCCATCAA CCACAGTGGG GAATCTGGCT 1260  
 TGGTGGTGT CGATTCTGAG CAATATTTC TCTCTGTGAC TGGCCAGCCA TTTCAGGGTG 1320  
 TCCAATTCAA CAATGGAGGA TGTGATCAGT ATAGCTGACA ATATCCTTAA TTCAGCTCAA 1380  
 80 GTAACCAACT GGACAGTCTT ACTGOGGGA GAAAGATATG CCAGCTCAGG GTTACTAGAG 1440  
 ACATTAGAAA ACATTGACAC TCTGGTGCTT CCGACAGCTC TTCCTCTGAA TTTTCTCGG 1500  
 AAATTCATTG ACTGGAAAGG GATTCCAGTG AACAAAAGCC AACTCAAAAG GGGTTACAGC 1560  
 TATCAGATTA AAATGTGTCC CCAAAATACA TCTATTCCCA TCAGAGGCCG TGTGTTAATT 1620  
 GGGTCAGACC AATTCAGAG ATCCCTTCCA GAAACTATTA TCAGCATGGC CTGTTGACT 1680  
 CTGGGGACAA TTCTACCCGT TTCCAAAAAT GGAATGTCTC AGGTCAATGG ACCTGTGATA 1740

5 TCCACGGTTA TTCAAACTA TTCCATAAAT GAAGTTTTC TATTTTTTC CAAGATAGAG 1800  
 TCAAAACCTGA GCCAGCCTCA TTGTGTGTTT TGGGATTTCG GTCAATTTGCA GTGGAACGAT 1860  
 GCAGGCTGCC ACCTAGTGAA TGAAACTCAA GACATCGTGA CGTGCCAATG TACTCACTTG 1920  
 10 ACCTCCTTCT CCATATTGAT GTCACTTTT GTCCCTCTA CAATCTTCCC CGTTGTAAAA 1980  
 TGGATCACCT ATGTGGGACT GGGTATCTCC ATTGGAAGTC TCATTTTATG CCTGATCATC 2040  
 GAGGCTTTGT TTTGGAAGCA GATTAAAAA AGCCAAACCT CTCACACACG TCGTATTGTC 2100  
 ATGGTGAACA TAGCCCTGTC CCTCTTGATT GCTGATGTCT GGTTTATTGT TGGTGCCACA 2160  
 GTGGACACCA CGGTGAACCC TTCTGGAGTC TGCACAGYTG CTGTGTTCTT TACACACTTC 2220  
 15 TTCTACCTCT CTTTGTCTT CTGGATGCTC ATGCTTGCCA TCCTGCTGGC TTACCGGATC 2280  
 ATCCTCGTGT TCCATACAT GGCACGAT TTGATGATGG CTGTGGATT TTGCCTGGGT 2340  
 TATGGGTGCC CTCTCATTAT ATCTGTCAAT ACCATTGCTG TCACGCAACC TAGCAATACC 2400  
 TACAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCCTGGCT 2460  
 TTTGTGTCC CTGCACCTGC TATTGTGGCT GTGAACTTCG TTGTGGTGTCT GCTAGTTCTC 2520  
 20 ACAAAGCTCT GGAGGCCGAC TGTGGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC 2580  
 ATCCGCTGG GGAAGAGCCT CCTCATTCTG ACCCTCTCG TAGGCTCAC CTGGGCTTT 2640  
 GGAATAGGAA CAATAGTGA CAGCCAGAAT CTGGCTTGGC ATGTTATTTT TGCTTTACTC 2700  
 AATGCATTCC AGGATTTTTT TATCTTATGC TTGGAATAC TCTTGGACAG TAAGCTGCGA 2760  
 CACTTCTGT TCAACAGTGT GTCTGCCCTA AGTTCTTGGA AGCAACACAGA AAAGCAAAAC 2820  
 25 TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAGCCTT TCAACCACT GCAAAACAAA 2880  
 GGCCATTATG CATTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940  
 GTCTCAATG AATAA

## A98 PROTEIN SEQUENCE

25 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 Unigene number: Hs.256897  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Pfam domain: 7tm\_2 [561-820]  
 30 Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 MHALLLCFSV LNSAGLSLL QSPVEEYQLL LQVYRDSKE KRDLRNFLKL LKPPILLWSHG 60  
 LIRIIRAKAT TDCNSLNGVL QCTCEDSYTW FPPSCLDPOQ CYLHTAGALP SCECHLNLS 120  
 QSVNFCERTK INGTFFKINER PTNDLLNSSL AIYSKYANGI EIQLKKAYER IQGFESVQVT 180  
 QFRNGSIVAG YEVVNGSSAS ELLSAIEHVA EKAKTALHKL FPLEDGSFRV FGKACQNDIV 240  
 40 PGFSGKDDY TLPSCSSYRG NITAKCESSG WQVIRETCVL SLLEELNKNF SMIVGNATEA 300  
 AVSSFVNLS VIIRONPST VGNLASVSI LSNISLSLA SHFRVSNSTM EDVSIADNI 360  
 LNSASVINWT VLLREKYAS SRLLETLENI STLVPPTALP LNFSPKFDW KGIPVNKSQL 420  
 KRGYSQIKM CPQNTSIPR GRVLIGSDQF QRSLEPETIS MASLTGLNLI PVSKNGNAQV 480  
 NGPVISTVIQ NYSINEVFLP PSKIESNLSQ PHCVFWDPSH LQWMDAGCHL VNETQDIVTC 540  
 45 QCTHLTSFSI LMSFPVPSTI FVVKWITYV GLGISIGSLI LCLILEALFW KQIKKSQTS 600  
 TRICMVNIA LSLILADVPF IVGATVDTT NPSGVCTAAV FPTHFFYLSL FFWMLMLGIL 660  
 LAYRIILVPH HMAQHLMMAV GFCLGYGCPL IISVITIAVT QPSNTYKRKD VCWLNWSNGS 720  
 KPLLAFFVPA LAIVAVNFV VLLVLTKLWR PTVGERLSRD DKATIIIRVGK SLLILTPLLG 780  
 LTWGPFGITI VDSQNLAWHV IFALLNAFQV RTVTITYCIV K

## A99 DNA SEQUENCE

55 Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 ProbeSet Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51  
 AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCCAGCGTG CTGTGGCCTC 60  
 GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120  
 CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTGTGGA TTGGGTGGC TTTTCTTCAT 180  
 65 GCGCAATTG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240  
 GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300  
 GAATAGCAGC TCCGTTATT TTTCTGGAA AATGAACCTG TCGTAATTC TGCTGATCCT 360  
 GGTTTTCATG GTGCCCTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420  
 TAAACAACGA CTGCTTTTCT CCGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480  
 70 ACTAGGAGAT CCCTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGTC 540  
 CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTTTCTG GATTGGTGC 600  
 TGTCACTGTC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660  
 TCTAGCCCTG GAACGGCGAC TGCTGCAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720  
 GATGCAATG GCAAGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780  
 75 TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAAGTCAA GGAAGTGAAT ATCTTACTCT 840  
 TATTCAACAG GAAGTGGATG CTTTGGAAAG ATTAAGCAGG CAGCTTTTCT TGGAAACAGC 900  
 TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTT 960  
 TAAATTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020  
 CAATATTGTT TTTGATCGAG TTGGGAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080  
 80 TGTGAATTAT CTGGGAATCC AATTGTATGT GAAGTTTGG TCCCAACACA TTTCTTCTAT 1140  
 TCTGTTGGA TTAATCATCG TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200  
 CTTTATGCC ATCTCTAGCA GTAAGTCTCT CAATGTCAAT GTCTGCTAT TAGCACAGAT 1260  
 AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320  
 CGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT 1380  
 TGATGTGATC TTCTGTGCA GCGCTCTCTC TAGCATACTC TTCTCTATT TGGCTCACAA 1440

	ACAGSCACCA	GAGAAGCAA	TGGCACCTTG	AACTTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAAATTTAGA	TATAAGAGGG	GGGAAAAATG	GAACCAAGGC	CTGACATTTT	1560
	ATAAACAAAC	AAATGCTAT	GGTAGCATTT	TTCACTTCA	TAGCATACTC	CTTCCCCCTC	1620
5	AGGTGATACT	ATGACCATGA	GTAGCATCAG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGGAGAGGAG	1740
	CCAAGAAACT	AAAGGTGAAA	AATACACTGG	AACTCTGGGG	CAAGACATGT	CTATGGTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTAA	GGTTCACATG	GAAGAGGTGA	TAGCTTTGCC	1860
	TTGAGATTGA	CTCATTAAAA	TCAGAGACTG	T			
10	<u>A100 Protein sequence</u>						
	Gene name: putative G-protein coupled receptor						
	Unigene number: Hs.16085						
	Protein Accession #: NP_057418.1						
	Signal sequence: none found						
15	Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446						
	Cellular Localization: plasma membrane						
	1	11	21	31	41	51	
20	MSFLIDSSIM	ITSQILPFGF	GWLFPMRQLF	KDYBIRQYVV	QVIFSUTFAP	SCTMFELIIF	60
	EILGLVNSSS	RYFHWKMNLC	VILLILVFMV	PFYIGYFIVS	NIRLLHKQRL	LPSCLLWLTF	120
	MYFFFKLGGP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTMSYFLRN	180
	VTDDILALE	RRLQTMDMI	ISKKRMAMA	RRTMPQKGEV	HNKPSGFWM	JKSVTTSASG	240
25	SENLTLIQOE	VDALIELSRQ	LPLETADLYA	TKERIEYSKT	PKGKYFNPLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDVPT	RGIEITVNYL	GIQFDVKFWS	QHSIFILVGI	IIVTSIRGLL	360
	ITLTKPPYAI	SSSKSSNVIV	LLLAQIMGY	FVSSVLLIRM	SMPLYRTII	TEVLGELQFN	420
	FYHRNFDVIF	LVSALSSILF	LYLAHKQAPE	QKMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]						
	Unigene number: Hs.19322						
	Probeset Accession #: AA088458						
	Nucleic Acid Accession #: AA088458						
35	Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)						
	1	11	21	31	41	51	
40	GCCCTTGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAA	GAGGTGCTGC	TGCAGGGTTT	GGAGATGATG	120
	CGCGGGGGCC	CGGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCGCG	180
	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAAGGTACA	AGAGGTGGCC	CGGTGCCTGG	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCCCTGCC	CCGTCCTCC	TCCGGGGCCC	CCTGCCCTGC	CCTGAAGTCC	360
45	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
	CTCACCCAGT	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAAGTCG	480
	CGGCTCATTG	AGCAGCTGTT	TGAGGCCCGC	GCCCTGAGCC	AGCAGGACGG	GGGACCTCTG	540
	GATTCCACCT	TCATCTAGTC	CTTGTGGGCC	GGGTGGGGCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTGA	GGGTGGGGCC	CCCATCGCAC	CCACCTCTC	TGGCTGGAGA	CCCCCGGCAG	660
50	GCCACGGCAC	AGTCCCGGAG	TGGGGCGCTT	CCTGCCGGCC	TGCGCAGATG	GGCTCCCCAG	720
	GCCTGCCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTCTGGGCTC	CTGGTTGYTG	780
	ACATGGGCTG	GGGGCTCTCT	TGAGTCCGCA	TAGTCCGCGC	CTACTACTGG	CCGCTGTGAG	840
	TGAGCAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCCCGG	TTTCCAGCGG	TGCCGCCCTG	900
	GGTCCCTTGA	TCAGGGAAAG	GCACTGCCCA	CGCCAGGCTG	CACCTTCAAC	AACGGGCAGC	960
55	AGAGGGCGCG	GGCGGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGTCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TCCGACGAGC	GGAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAAGCGGG	GGAGCTGCGC	TGGCTGGGGA	GCCCCAGGGA	TAGCGTTCGG	ACTTCAGGTT	1140
	CTGGCCACAG	CTGAGGGAAC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GGAGAGAGCTT	1200
	GGCCTGCATG	TGCTCCAC	AGACCTGGGG	GTGATGGCCT	TCCCTCTCT	GGCGGGGAOG	1260
60	TTGCCCCAGC	TTGAGTCCCA	CAACAATCC	TGTGAGCCTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCACGTCA	TAGGCAAAAG	CTGTTTCCCC	CGACTCAGGA	TTTCAAGGCG	1380
	CTGGGGTCTT	GCTCACCCCC	CTTTGCTCTC	ACGCCAGGCC	TGTCCCCAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAGC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCCTGCCCA	GGCCCACTCC	CGCTGGTGTCT	1560
65	GGAGTAGCCA	CTGGTGGGGG	GGCCCTGCTC	AGCCCAACCT	GGAGGGTCCC	AGTGTACCCA	1620
	GAACCAAGGG	CACGGCAACA	GCATCGATGG	GTTCTGCAGC	CCAGGGCCCC	CGATGCCGGG	1680
	TCAGTGTGTG	TGGGGGCGAG	GGCCTCGAT	GCGGGGTGAG	TGGTGGGGGG	GCGCAGGGCC	1740
	CCCGATGCCG	GGTCAGTGCG	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCACTTTGGT	1800
	ACACTGTCCG	ACAAGGCACC	TGTCTCAGAG	GAGGGGCCCT	GGCAGGCAGC	GTGGCAACTC	1860
70	CCTTCGCGAG	CCAGCTCCA	TGCTAACCTG	CCACAGCAA	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCAG	GACAGGCCCA	AGTCAGCCCA	GCATGCAGCT	1980
	GCCCTCTTAC	CTCAAGATG	GGAGTGGGCT	TCCAGGGGGA	CATAAGGATG	TCAGGCTCTG	2040
	ACCTCTCTGG	CAGGAAGAGG	TGCAGGTCT	GAGGGCTGT	GCCCCACAGC	CCAGCACACC	2100
	AGGTGGAATG	CAGCGCAGTG	GTTGGGCCAG	TGGCAGCCAG	GGAGAAAGCC	CCCGTCAGCA	2160
75	GGCTGGGGTC	TGCCCAACAG	GGCCTCCCCA	CGTCTGCCTT	TGAGGGTGCC	TGCCATGCCC	2220
	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGACC	GCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCTCCG	GAAAAATGCG	CTTTCAGCCT	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATAG	GTCCTCCGAG	TTTACAGCTT	GAAATCAGGC	TAGTGAGTGG	CCCTGGAGAG	2460
80	CACGAGGGGA	GAAATTAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCTCG	CCTGGAGCCT	GCCCTAGGAC	GCTGGGGGGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	ATCCGGCTCT	ATCCGGGAGG	TGCCAGTAGC	GTGTGAGGCT	ACATACAGTG	2640
	CGGTGCACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
	CAGAAGTGTC	CCAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTGTGTTG	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CGGGCGCTGG	TGGTTCAGCG	2820

CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

**A102 DNA SEQUENCE**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ACCGGGCACC GGACGGCTCG GGTACTTTTC TCTTAATTA GGTATGCCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120  
 CCACTACATC TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCTCG AATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTGTGC ACCAGATGCA 300  
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGTGTGT CACAGCTGCT TCGTGGAAAG CCACTGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAGCTG GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT TCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTCG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCAGCCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGACAA TCACGCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGGCGGCCA 1140  
 CTCAGTTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGGAAGA TGCTCTGGAC GTCCAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTGCC TGAACACGCG GGCCGTCCCT TTGATTTCCT ACAAGATCTG CAACCCACAG 1320  
 GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT AGTACGGGGA CAGCGGGGGG CCCTGTGGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCCAGCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCAGGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCGGA 1620  
 TCCTCCCTCG GACTCCCTGT TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGCG CCGAAAGAGG CACCCCTTCA TCTGATTCCA GCACAACCTT 1740  
 CAACTGCTCT TTGTGTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGTTTCA AGCGATTCTC 1860  
 TTGCTCTCAG TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACC CAACCTAATT 1920  
 TTGTATTTTT AGTAGAGACA GGGTTTCACT ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCTGCTC TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040  
 ACGCTAGGCC TCACGCTCCT TTCTGATCTT CACTAAGAAG AAAAAGAGCA GCAACTTGCA 2100  
 AGGGCGGCGT TTCCCATCGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160  
 ACGAGATAAG CAGTTATGTG ACCTCAGCTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACCAAGCCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCTCTCTA GGGACCAGAA 2280  
 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCTAT TTTCTGATTT TCTTTGTAGC ATTTGGTGTCT TGACGTATTA 2400  
 TTGTCTTTTG ATTCCAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAA

**A103 Protein sequence:**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGENDPFAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLEPLKFFP IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVP 120  
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEQGFRFEEFV SIDHLLPDDK 180  
 VTALHHSVTV REGCASHVTV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240  
 LCGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VVHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLFNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA 360  
 AVPLISNKIC NHRDVGII SPSMLCAGYL TGGVDSQQGD SGGPLVCQER RLWLKVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 ATGCACACCG TGGCTACGTC CGGACCCAAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC 60

GGCTGCCCGG GCTGTGGGCG CAACGCCTCG GACGGCCCGC TCCCTTGGCC GCGGGCCGTG 120

GACGCCTGGC TCGTGCCGCT CTCTTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180

TCGCTGGTCA TCTACGTCAT CTGCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240

ATCGCCAAAC TGGCGGCCAC GGAAGTGACC TTCTCTCTGT GCTGCGTCCG CTTCACGGCC 300

15 CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360

ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420

TGGTACGTGA CGGTGTTCCC GTTGGCGGCC CTGCACCGCC GCACGCCCGC CCGTGGCGCTG 480

GCTGTGAGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTCGCCCTG 540

20 CACGCGCTGT CACCGCGGCC GCGGCGCTAC TGCACTGAGG CCTTCCCGAG CCGCGCCCTG 600

GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCGCTC GCTCGCCACC 660

TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGGTGCG CCGCGCGGCC 720

GCGGATAGCG CCCTGCAAGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGCGCAAG 780

GTCTCGCGCG TCGTGGCGCG CTGTGGTCTG CTCTTCGCGC CCGTGGGGG CCGCATCCAG 840

25 CTGTCTCTCG TGCTGCAAGC GCTGGGCCCC GCGGCGCTCT GGCACCCACG CAGCTACGCC 900

GCCTACGCGC TTAAGACTG GGTCACTGCG ATGTCTTACA GCAACTCCCG CAGTGAACCG 960

CTGCTCTACG CCTTCTCTGG CTGCACTTTC CGACAGGCGT TCCGCGCGGT CTGCGCCCTG 1020

GCGCGCGCGC GCGCGCGCGC CCGCGCGCGC CCGGACCCCT CGGACCCCGC AGCCCCACAC 1080

GCGGAGCTCG ACCGCTCTGG GTCCCAACCG GCGCGCAGAA GCGAGGGAGC 1140

30 AGTGGGCTCG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm\_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

1 11 21 31 41 51

45 MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA ALMLLGLVGN 60

SLVIYVICRH KPMRTVTNFI IANLAATDVT PLLCCVPFTA LLYPLPGWVL GDFMCKFVNY 120

IQQVSQVATC ATLTAMSVDR WYVTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180

HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240

ADSLAQQVIL AERAGAVRAK VSRVAAVVL LFAACWGIQ LFLVLQALGP AGSWHPRSYA 300

50 AYALKTKAHC MSYNSALNP LLYAFILGSHF RQAFRRVCPC APRRRRRPRR PGSPDPAAPH 360

AELHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

A106 DNA SEQUENCE

Gene name:

integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM\_002214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

60 CCCAGAGCGG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGAGC 60

CTGCGGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAGCTGCG AACTAATGGT 120

GTTGGCCTCC CTGCCCCACT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180

65 TCCCTCGAC CTGCGCGCGG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240

TAGGGTGGT TCCCCCCCAG CTGCGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTCG 300

CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360

TGTCCCGGAG CAGGCTCGCG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCGGGGCCCT 420

TGGCGGTGGA AGGAGGTGCT TCTGCGGAG ACCGCGGAC CCGCGTGCC GAGCGGGAG 480

GGCGGTAGG GCGCTGAGAT GCGGAGCGGT GCGCGGGGCC GCTTACCTGC ACCGCTTGCT 540

70 CCGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAACGCT CCTAGCGACA CTCGCCGCG 600

GGCCCGAGG TCGCCCGGGA GCGGAGCCCC GCGTCCGAA GGCAGCCAGG CCGCGGGCGC 660

GGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITTAAC GCTGCATTG 720

TCTGCCGCA AAAGACCGG CGAGGTCCCG CCTCGTCTCT CTGGGCGAGC TGGGTGTTT 780

75 CACTGTGCTT TGGACTGGG CAAGGTGAAG ACAATAGATG TGCACTTTC AATGCGCAT 840

CCTGTGCGAG GTGCTTGGC CTGGGTCCAG AATGTGATG GTGTGTTCAA GAGGATTTC 900

TTTCAGGTG ATCAAGAGT GAAGTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960

GCTCAGTTGA TTCAATAGA TACCATCTG TGCAATGAT AATACCCACT GAAATAGAA 1020

TTAATACCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GGTGCGAGGA GCGCAAGCTA 1080

80 ATTTTATGCT GAAAGTTTCT CCTCTGAAGA AATATCTCTG GATCTTTTAT TATCTTGTG 1140

ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAA TTCGTTGGA AACGATTAT 1200

CTAGAAAAT GGCATTTTTC TCCGTGACT TTCGTCTGG ATTGGCTCA TCGTTGATA 1260

AAACAGTTT ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCA TGCACTGACT 1320

ACAATTTAGA CTGCATGCT CCGCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA 1380

TCACTGAGT TGAGAAAGCA GTTCATAGC AGAAGATCTC TGGAAACATA GATACACCAG 1440

5 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620  
 ACGTCAAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680  
 ACAACAACAT TAATGTCATC TTTGCAGTTC AAGGAAACA ATTTTCATTG TATAAGGATC 1740  
 TTCTACCCCT CTGGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800  
 ATAATTTGGT AGTGAAGCC TATCAGAAGC TCATTTTACA AGTGAAGGT CAGGTGGAAA 1860  
 ACCAGGTACA AGGCATCTAT TTTAACAATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920  
 CAGGCATGGA AGGATGACGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980  
 10 TTACAAATGAA AAAATGTGAT GTCAAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040  
 GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTGAG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAG TGTTCCTCAGT 2160  
 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTT TCTGAGAGT TGCAAGTCAC 2220  
 15 ACAAGGATCA GCCTGTTTGC AGTGGTTCGAG GAGTTTGTGT TTGTTGGGAA TGTTCATGTC 2280  
 ACAAAATTA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340  
 CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520  
 20 CACCGATGCC AGGAGCATC GGCCTGTTCT GTGAACACTG CCCACCTGT TATACAGCCT 2580  
 GCAAGGAAAA CTGGAATGTT ATGCAATGCC TTCAACCTCA CAATTTGTCT CAGGCTATAC 2640  
 TTGATCAGTG CAAACCTCA TGTGCTCTCA TGGAAACAAC CATTATGTC GACCAACTT 2700  
 CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTT ATAGTTACAT 2760  
 TCTTGATTGG GTTGCTTAAA GTCTCATGAT TTAGACAGGT GATACTACAA TGGAAATAGTA 2820  
 25 ATAAATTA GCTCTCATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATTC 2880  
 TGCAAGTGT TTGCAAGA GCACTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACCTCTAA AAAAAAGATT 3000  
 TTAACACTT AATGGGAAAC TGGAAATGTT AATAATGCT CCTAAAGATT ATAATTTTAA 3060  
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC 3120  
 30 GAAGACTGAC AAGTATCCT ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTAATCTGTT TTGAGACTAG TGTGTTGTA GCATTTTACT GTAATATATA 3240  
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTT AGCATTGTGT 3360  
 CACTACAGG GTACAGTAAT CCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 35 TATATTCTAA GGTGCCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTAAATCTTA 3540  
 AAGATTATTT GCTTTTAAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT 3600  
 TTTGCAAGAT GGATACTAAT TCCAGATTG TCTCTCTTT GCCTTTATGT TTTGTTTTCT 3660  
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 40 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780  
 GAATGTAA

A107 Protein sequence:

45 Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 50 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane

55 1 11 21 31 41 51  
 MCGSALAFFT AAFVCLQND RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60  
 LGPECGNCVQ EDFISGGSR ERCDIVENLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120  
 60 GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKINSVG NDLSRKMAFF 180  
 SRDFRLGFGS YVDKTVSPYI SIHPERIHNO CSDYNLDCMP PHGYIHVLSL TENITEPEKA 240  
 VHRQKISGNI DTPEGGPDAM LQAAVCESHI GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV 300  
 VPNDGNCHLK NMVYVKSTTM EHPSLGLQSE KLIDNNINVI FAVQKGQFHW YKDLLPLLP 360  
 65 TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420  
 NVTSENDELFP NVTVMKKCD VTGGKQYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480  
 CVDETFLDSK CFQDENKCH FDEDQFSSES CKSHKQDPVC SGRGVCVCGK CSCHKIKLKG 540  
 VYGYKCEKDD FSCPVYHGNL CAGHGECEAG RCQCPGSGWEG DRQCPGSAQA QHCNVNKGQV 600  
 CSRGRTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660  
 70 CALMEQHYV DQTECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKKIKSSS 720  
 DYRVASAKKO KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETPRCNF

A108 DNA sequence

75 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 ATGCTGTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60  
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GTGCGGCACA CCTCCCGAGG GCGAGGCAGC 120  
 GACCGGAGAG GGGAGAGCCG GCGGAGGCTC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGGOGAG CCGCCCGCCT GGATCGCGCC CCAGCAGCAG 240



5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60

CCGCGGCCGC GCACGAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCT 300  
 CGCTGCGTTC CTGAGCGTTTC CCGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360  
 TCCGAGCAGC AGCCCCGGGG GCCTTCTGAC TGACATCCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCCTGGAC CTAGGGCCCG GCGTGTGCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540  
 CCGCGCGGAA AGCGCGCGG GACAGTCAGT GACGAGGCC GGGGGTCGCC GGGGCCAOGA 600  
 CTCTCTGGAG ACCGTCTCTG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
 TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCTGGAA CCGCGCTTCG CTCCTGCAGC 720  
 TGCTGTGGC TGCGCTGCTG GCGGCGGGGG CGAGGGGCCA GCGGCGAGTA CTGCCACGGC 780  
 TGGCTGGAGC CGCAGGCGGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 GGGGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGGCGGAG 900  
 GCGCGCTGG ACCAGGGCGG CTGGGACAAT GACCGCCAGC AGGCGCTTGG CGAGCCTGGC 960  
 CCGCGCGGCA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGG AGGTGCGGCC CCCACCGTG AGGGCTGGC AGCGGTGCTC CCTGGAAGGC 1080  
 TCCCGGAAAG GAAGCGAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140  
 CGCGATTCC CAGCTCTCTC ACGCGCGGCG CCCTCTCCCG TGCAGCGGCG CGCTTGTCCC 1200  
 ATCTAGTGC CGTCTCTCAT TGTGGGCTCC GTGTTTGTG CCTTTATCAT CTGGGGTCC 1260  
 CTGTGGCAG CCTGTTGCTG CAGATGTCTC CGGCTTAAGC AGGATCCCCA GCAGAGCCGA 1320  
 GCGCCAGGGG GTACCGCTT GATGGAGACC ATCCCATGA TCCCGAGTGC CAGCACCTCC 1380  
 CGGGGTGCT CCTCAGGCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCAACTCC 1440  
 GGGCGCGGCG GCGCCCAAC AAGGTCACAG ACCAACTGTT GCTTGGCGGA AGGACCATG 1500  
 AACACGTGT ATGTCAACAT GCCCAGCAAT TTCTCTGTGC TGAACGTGCA GCAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT AGTGGGGSTA CAGCGTGCAG 1620  
 CAOGACTCTG AGGCCATGAG AGCTGTGCCA CCTTTATGG AGGCGCTGCA GCCTGGCTAC 1680  
 AGGCAGATTG AGTCCCGCTT CCTCAGACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTGC GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860  
 GCTTCATTGG CCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920  
 CATCCAGGGT ATCATTTGAT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAAATTTA TAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100  
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTTCC CTTTACTGG GACTTTTTTT 2160  
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220  
 TGGTGCATG TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCCTGCCCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCAT GGCTAATTTT TTGTATTTTT 2340  
 TGTAGAGATG TGTGCTTTAC ATGTTGGCTG GGTGCTCTC ACTCTCTGA CCTCAAGCAA 2400  
 TCTGCTGTC TCAGCCTCCC AAAGTGTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460  
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520  
 ATTCATAAAG GAAACCTGTT TGAACCTGTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580  
 GGCACACCTT AATTTCAATG TAAAGAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640  
 GGGCTATTAG TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700  
 TTAAGAGAG ACTGAATAA ATTGTATAGT TACTTAACTA ATGAAGCAT TTCAGAACTC 2760  
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCCCTC 2820  
 TTGATTGTAT CTAAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTTT 2880  
 TATATTGAAA TCATAAACTA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCCTG 2940  
 TGGTATGGT TGGCGTTTC CTCTGTTTG GTTTTCAGAG CCCAATGCT ATATAGTCTC 3000  
 GAGTGCAAGT AATTACTATA CTTGTAATG AAGATCAGTA TTTCTGCTA GATCTGATAA 3060  
 AAAAAATTTT TTGCTTAGT TATAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCTCTA GCCATAAACC GAGACTTGGG ATGAAATTTA AACGAGATAC GATTACTTTT 3180  
 GCAGATCAT AAGCTTTTTT TACTCTTGT ATCAAATGG CTTATTTTTC AGGCACATAAG 3240  
 GATTGTAAAG AGAAAGCTT TTCAACGAAG GATTGCTTT CTCTCCAC ACTGTTCTG 3300  
 ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360  
 CAAATTCAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACAGTATT TTGTAATTAA ACAAATGCTC 3480  
 GTATGGTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540  
 TGTTTCTATG GTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTATAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAATAA TTTTATGATG 3660  
 TGAATAAAAA AAAAAAATAA AAAAAAATAA

# A109 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

70  
 75  
 80

1 11 21 31 41 51  
 MLGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLDWRAAA 60  
 GEAEKGNRGE PPANIRAAQQ PRPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPEA 120  
 SGRQPRGSD CIPRFPSSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180  
 PRGRRTGTVS DEARGSPGPR LLGDRPALSG DALSAPEVVP CGALAARPSF HPFTPLRSCS 240  
 CCLRCWRRG RPSGGEYCHG WLDAQGVWRI GFQCEPFDG GDATICGSC ALRYCCSSAE 300  
 ARLDQGGCDN DRQQAGEPG RADKDGPRRL GRASCLRGTO GDGEGAPFPV RAWQRCSPG 360  
 SPKRGQLLRA FPGLLPRARR RGFPSPPRG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420  
 LVAACCCRL RPKQDPQQR APGGRNLMET IPMIPASST RGSSSRQSSST AASSSSSANS 480  
 GARAPPTRSQ TNCCLPEGTM NRVVNMPTN FSVLNCQOAT QIVPHQGYL HPPVGYTVQ 540  
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQMYPAV TV

## A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCAGAG TTCTTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCCTGA GGAITGTCAA TACTCTCAAG CACTAAGAA AGTATTGACC 300
   CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTATGCTAT 360
15 GAACCCACTG ATAAGAATT ATCACCCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTG 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTACCC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAACT CAAATTTCAT 600
   GAAGAAAAAC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
20 TTAATTATTA GTTTTTTTAA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
   TCTGAAAAAA AAAAAAATA AAAAAAATA

```

25 A111 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

30

```

1      11      21      31      41      51
|      |      |      |      |      |
35 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQSKSK 60
   PLMVIHLED CQYSQALKKV FAQNEBIQEM AQNKFRIMNL MHETTDKNLS PDGQYVPRIM 120
   FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

40

A112 DNA SEQUENCE  
 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

```

1      11      21      31      41      51
|      |      |      |      |      |
50 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
   AATCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCTC GGGGCGAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCG CGAAGGGCCT 300
   GCAGTGGCAG TCGGCTCTC CAAGGACCGA TCCACTGTC AGGTGCTGGA CTGGGCCACA 360
   GGGAACTGGT TCTCTGCTCG TTTGACACAC TTCAAGAGAG CTCTGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAAT CACAGAAAAA AGCCAGGAGC TTGSCATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
   AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGACACC CCACTGGGTC 720
   CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCGA CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
   TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
   ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCAGTCCA 960
65 GCAACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTCAA TGCAGACGAT 1080
   GCGTACCAGG GGGAAAGTCAG CGAGAAGATG ATGTGTGTCAG GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGCATCG TTAGCTGGGG CTATGCTGTC GGGGGCCCGA GCACCCGAGG AGTATACACC 1260
   AAGGCTCAGC CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

```

75 A113 Protein sequence:  
 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

80

```

1      11      21      31      41      51
|      |      |      |      |      |
5  MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPRIIAL LSLASIIIVV VLIKVILDKY 60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPFDEGP AVAVRLSKDR STLQVILDSAT 120
GNWPSACFDN FTEALAEATAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GPCLSGSLVS LHCLACGKSL KIPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHV 240
LTAACHCFRKH TDVFNWKVRA GSKLGSFSPS LAVAKIIIE FNMYPKQND IALMKLQPL 300
TFSGTVRPIC LPFFDEELTP ATPLNIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
10 AYQGEVTEKM MCAGIPEGGV DTCQGDSSGP LMYQSDQWHV VGVVSWGYGC GGPSTPGVYT 420
KVSAYLNIWY NWWKAEL

```

A114 DNA SEQUENCE:

```

15 Gene name: TTK protein kinase
Unigene number: Hs.169840
Probeset Accession #: M86699
Nucleic Acid Accession #: NM_003318
Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

```

```

20      1      11      21      31      41      51
|      |      |      |      |      |
25  GGAATTCCTT TTTTITTTT TTTGAGATGG AGTTTCACCTC TTGTTGGCCA GGCTGGAGTG 60
CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCTCCCG GGTTCAGCG ATTCTCCTGC 120
CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180
CTTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
ACCTCAGGTG ATCCACTTGC CTGGGCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300
TGCTGGCTG ATTCTTTT TGTGTTGGA TTTTGAAC AGGCTCTCCC TTGTCGCC 360
AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTCAGT 420
GATCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGCACCA CCACACCGG 480
CTAATTTT TATTTTAT AGAGACAGGG TTTCACCATG TTGGCCAGG TGTTCCTCAA 540
CTCCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAA GTCGCCAGAT TACAGGTGTG 600
AGTCACCATG CTTGACCTTA TAATCTTAA GTCATTTT CTGCTCCATT TCTTCTTAG 660
GGTCCTCACA ACAATCTGCT ATTAGCGGT ACAATAATCC TTAACCTCAT GATTACAAA 720
AGGAAGATGA AGTGATTCAT GATTTAGAAA GGGGAAGTAG TAAGCCACT GCACACTCCT 780
GGATGATGAT CCTAATCCA GATACAGTAA AATGGGGTA TGGGAAGSTA GAATACAAA 840
TTTGTTTAA ATTAATTATC TAAATATCTA AAAACATTT TGGATACATT GTTGATGTA 900
ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTGGGT CCATCTTTC ATTTCCCGC 960
TGCAGTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAAATG ACAATTGATT 1020
CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080
CGATGATGAT CTAATAATCT TCTGCTGATA CTACAGATAA CTCGGGAAC GTTAAACCAA 1140
TTATGATGAT GGCAACAAC CCAGAGGACT GGTGAGTTT GTTGCTCAA CTAGAGAAA 1200
ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTGTITAC AGTCAAGCAA 1260
TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTGCTAGA ATTCAAGTGA 1320
GATTTGCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAATGG 1380
CCAGAGCAAA CTGCAAGAAA TTTGCTTTT TCTCATATATC TTTTGACAA TTTGAACGTG 1440
CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG 1500
TACCACCTAG AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCAAAAAA AAGCAGCTGC 1560
TTTCAGAGGA GGAAGAAAG AATTTATCAG CATCTACGCT ATTAAGTCC CAAGAATCAT 1620
TTTCCGGTTC ACTTGGGCTT TTACAGAATA GGAACAACAG TTTGATTC AGAGGACAGA 1680
CTACTAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740
ACCGGAATTC ATTGAGACAA ACTAACAACA CTAAACAGTC ATGCCCATTT GGAAGAGTCC 1800
CAGTTAACTT TCTAATATG CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGATCTT 1860
GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGTTGTG CTGGATCTA 1920
AACCAGTGG AAATGATTC TGTGAATTAA GAAATTTAAA GTCTGTTC AAATAGTCAT 1980
TCAAGAGACC TATGGGTGCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATA 2040
CCCTGAAGAA TAAACGGGAA TCAAGTCTTC TAGCTAAAT AGAAGAACT AAAGAGTATC 2100
AAGAACCAGA GGTTCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160
GTATTAACCA GAATCTGTCT GCATCTTCAA ATCACTGGCA GATTCGGAG TTAGCCGAA 2220
AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC 2280
AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGT AAGACACCAA 2340
GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTAGAAC TCCAGTTGTA AAGATGACT 2400
TTCCACCTGC TTGTCACTG TCAACACCTT ATGGCCAAAC TGCCGTGTT CAGCAGCAAC 2460
AGCATCAAT ACTTGCACT CCACTTCAA ATTTACAGGT TTAGCATCT TCTTCAGCA 2520
ATGAATGCAT TTCCGTTAAA GGAAGAATTT ATTCATATT AAAGCAGATA GGAAGTGGAG 2580
GTTCAAGCAA GGTATTTT CAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
TGAATTTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700
TGAATAAACT ACAACACAC AGTGATAAGA TCACTCCGACT TTATGATTAT GAAATCAGG 2760
ACCATGATAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAA 2820
AGAAAAATC CATGATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG 2880
TTACACCAAT CCATCAACAT GGCATTGTT ACAGTGATCT TAAACCACT AACTTTCTGA 2940
TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAATG CAACCATGAT 3000
CAACAAGTGT TGTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060
TCAAGATAT GTCTTCTCCT AGAGAGAAATG GGAATCTAA GTCAAGATA AGCCCAAAA 3120
GTGATGTTG GTCTTAGGA TGTATTTGT ACTATATGAC TTACGGGAAA ACACCATTT 3180
AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG 3240
AATTTCCCGA TATTCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTGTT TAAAAAGGG 3300
ACCCAAAAA CAGGATATCC ATTCCTGAGC TCCTGGCTCA TCATATGTT CAAATCTCAA 3360
CTCATCCAGT TAACCAATG GCCAAGGGAA CCACTGAAGA AATGAATAT GTTCTGGGCC 3420
AATTTGTTG TCTGAATCT CTAACCTCCA TTTTGAAGC TGCTAAAACT TTATATGAAC 3480
ACTATAGTGG TGGTGAAGAT CATAACTCT CATCTCCAA GACTTTTGA AAAAAAGGG 3540
GAAAAAATG ATTTGCAAGT ATTCGTAATG TCAGATAGGA GGTATAAAAT ATATTGGACT 3600
GTTATCTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660
ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3720

```

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780  
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAAGCTTG 3840  
TAAATAAAGT TTTGTGGCTA AATGA

**A115 Protein sequence:**

Gene name: TTK protein kinase  
Unigene number: Hs.169840  
Probeset Accession #: M86699  
Protein Accession #: NP\_003309  
Signal sequence: none found  
Transmembrane domains: none found  
Protein Kinase Domain: 510-775  
Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	FKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	SLLKLEKNS	60
VPLSDALLNK	LIGRYSQAIE	ALPPDKYQON	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISFAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	INLQKKQLLS	180
BEEKKNLSAS	TVLTQAQESFS	GSLSHLQNRN	NSCDSRGQTT	KARFLYGENM	FPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDSDVVPFC	MKRQTSRSEC	RDLVVPGSKP	300
SGNDSCELRN	LKSVQNSHFK	EPLVSDEKSS	ELIITDSITL	KNKTESSLLA	KLEETKEYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHITFE	QPVFSVSKQS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTPVVKNDFF	PACQLSTPYG	QPACFQQQQH	480
QILATPLQNL	QVLASSANE	CISVKGRIS	ILKQIGSGGS	SKVFQVLNEK	KQIYAIKYVN	540
LEEADNQTLN	SYRNEIAYLN	KLQHSKDKII	RLYDYEITDQ	YIYMMECCN	IDLNSWLKKK	600
KSIDWERKS	YWKMLAEVH	TIHQHGVHS	DLKPANFLIV	DGMLKLIDFG	IANQMOPDIT	660
SVVKDSQVGT	VNYMPPEAIK	DMSSRENGK	SKSKISPKSD	VWSLGCILYV	MTYGKTPFPQ	720
IINQISKLHA	IIDPNHEIEF	FDIPEKDLQD	VLKCLLRDP	KQRISIPELL	AHPYVQIQTH	780
PVNQMAKGT	EEKYVLQGL	VGLNSPNSIL	KAATLYEHY	SGGESHSNS	SKTFEKKRGK	840
K						

**OVARIAN****A116 DNA SEQUENCE**

Gene name: G protein-coupled receptor 39  
Unigene number: Hs.85339  
Probeset Accession #: AA349893  
Nucleic Acid Accession #: NM\_001508  
Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGGCTTCAC	CCAGCCTCCC	GGGCAGTGAC	TGCTCCCAA	TCATTGATCA	CAGTCATGTC	60
CCCGAGTTTG	AGGTGGCCAC	CTGGATCAAA	ATCACCCCTA	TTCTGGTGTA	CCTGATCATC	120
TTCTGATGAG	GCCTCTCTGG	GAACAGCGCC	ACCATTCGGG	TCACCCAGGT	GCTGCAGAAG	180
AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
TTGGTGTTC	TCATCGGCAT	GCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCTGACC	300
ACGTCCAGCT	ACACCTGTCT	CTGCAAGCTG	CACACTTTCC	TCCTCGAGGC	CTGCAGTAC	360
GCTACGCTGC	TGCACGTGCT	GACACTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTACCCCC	420
TTCAAGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTGTCTTGG	480
GTCACTCCG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTTG	540
GTGAACGTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCGC	CCACCAAGAG	600
CAGCCCGAGA	CCTCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
CAGTCCAGCA	TCTTGGGGC	CTTCTGGTGC	TACCTGTGG	TCCTGCTCTC	CGTAGCCTTC	720
ATGTCTCTGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGC	780
ACGCGGCTCT	CGCAGCTGAG	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCG	840
ACCATCATCT	TCTGAGGCT	GATTGTGTGT	ACATTGGCGG	TATGCTGGAT	GCCCAACAG	900
ATTCCGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCAGGACT	GGAGGAGGTC	CTACTTCCGG	960
GGGTACATGA	TCCTCTCTCC	CTTCTCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
CGCTCCTGT	ACACGCTGTC	CTCGCAGCAG	TTTGCGGGGG	TGTTCTGTGA	GGTCTGTGTC	1080
TGCGCGCTGT	CGCTGCAGCA	CGCCAAACCC	GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140
ACCACCGACA	GCGCCGCTT	TGTGCAGCGC	CCGTTGCTCT	TGCGCTCCCG	GCGCCAGTCC	1200
TCTGCAAGGA	GAAGTGAAG	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCCAG	1260
TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACCAAGC	1320
AATTCTGCTG	CAGAGAATGG	TTTTCAGGAG	CATGAAGTTT	<u>GA</u>		

**A117 Protein sequence:**

Gene name: G protein-coupled receptor 39  
Unigene number: Hs.85339  
Probeset Accession #: AA349893  
Protein Accession #: NM\_001508, NP\_001409  
Signal sequence: none found  
Pfam domains: 7tm\_1 [72-172, 224-344]  
Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
Cellular Localization: plasma membrane

1	11	21	31	41	51	
NASPSLPGSD	CSQIIDHSHV	PEFEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60

KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120  
 ATLLHLVLTLS FERYIAIHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFMAGTEYPL 180  
 VNVPSHRLGT CNRSSTRHHE QPETSNSIC TNLSSRWTVF QSSIFGAFVW YLVVLLSVAF 240  
 MCWMMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIIFLRLIVV TLAVCWMPNQ 300  
 IRRIMAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360  
 CRLSLQHANH EKRLRVHAHS TDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPO 420  
 SKSQSLSLES LEPNSGAKPA NSAAENGQFE HEV

**A118 DNA sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.87223  
 Probeset Accession #: AA250737  
 Nucleic Acid Accession #: NM\_001203  
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGCGGGGCGG GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTCGCGAGA CCGCGGCGCT 60  
 GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGTGGGAGTT CAGCCTACTC TTTCTTAGAT 120  
 GTGAAAGGAA AGGAAGATCA TTTTCATGCT TGTGATATAA GGTTCAGACT TCTGCTGATT 180  
 CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300  
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360  
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTGCTGCTT GGTCACTTCT 480  
 GGTGCTCTAG GACATAAGG CTCAGATTTT CAGTGTGCGG ACACCTCCAT TCCTCATCAA 540  
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600  
 CTGCTCCAT TGAAAAACAG AGATTTTGTG GATGACCTTA TACACCACAG GGCCTTACTT 660  
 ATATCTGTGA CTGCTGTAG TTTGCTCTTG GTCTTATCA TATTATTTTG TTACTTCGGG 720  
 TATAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780  
 ATTCTCTCTG GACATACCTT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
 TCAGGCTCTC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTGAGT GGTGAAACAG 900  
 ATTGAAAAG GTGCGTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGCGGA AAAGGTAGCT 960  
 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020  
 ACAGTGTTGA TGAGGACATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080  
 GGTCTCTGTA GCTAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCTTA CTCTTCTGTC 1200  
 AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260  
 CATCGAGATC TGAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320  
 GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
 ACTCGAGTTG GCACCAAGCG CTATATGCTT CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440  
 AATCACTTCC AGTCTTACAT CATGCGTGAC ATGTATAGTT TTGGCTCTAT CCTTTGGGAG 1500  
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560  
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620  
 CGCCCTCAT TCCCAAAACG GTGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GTTAAAGAAA 1740  
 ACCTTGCCCA AATGTGAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAGTAAG 1800  
 CATCTCTGCA GAAAGCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920  
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTGTA GCGCGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT

**A119 Protein sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCPTMIEED 60  
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECKNDLHPTL PPLKNRDFVD 120  
 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
 EQSQSSSGSGS GLPILLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFPFTTEAS 240  
 WFRETEYIQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KNGTCCCIAD LGLAVKFPISD 360  
 TNEVDIPPNT RVGTRKYMPP EVLDESILNRN HFQSYIMADM YSFLGLINEV ARRCVSGGIV 420  
 EBYQLPHYDL VPSDPSYEDM REIVCIKLR PSPPNRWSSD ECLRQMKLM TECWAHPAS 480  
 RLTLARVKKT LAKMSQSQDI KL

**A120 DNA SEQUENCE**

Gene name: LIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Probeset Accession #: U41060  
 Nucleic Acid Accession #: NM\_012319.2  
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	CTCGTGCCGA	ATTCCGACAG	AGACCGCGTG	TTCGCGCCTG	GTAGAGATTT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAC	CAAACTCTGC	CGCGTGGCCG	GGCGGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCTG	ACCTTTGCCC	180
5	TCTCTGTAC	AAATCCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTGGAAGGGT	360
	TCAGAAAATT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
10	ACCACGACCA	TCAGTCAGAC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
	AGCATCACTC	AGACCAGCAG	CATCACTCTG	ACCATGATCA	TCAGTCTCAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAAG	CGAAAAGCTC	TTTGCCGAGA	CCATGACTCA	GATAGTTTCA	600
	GTAAAGATCC	TAGAAACAGC	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAAGGACAGT	GTAGTGCTA	GTGAAGTGAC	CTCACTGTG	TACAACTCTG	720
	TCTCTGAAGG	AACCTCACTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
15	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTCAATC	AAAGAGCCGG	GTGAGCCGGC	840
	TGGCTGGTAG	GAATCTGTGA	GTGAGCCCG	AAAAGGCTT	ATGATTATCA		900
	GAAACACAAA	TGAAAATCCT	CAGGAGTGT	TCAATGCATC	AAAGTACTG	ACATCTCATG	960
	GCATGGGCAT	CCAGTTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
20	TCACCAAAAT	TGATGCTAGA	TCTTGTCTGA	TTCATACAAG	TGAAAAGAA	GCTGAAATCC	1080
	CTCCAAAGAC	CTATTCATTA	CAATAGCCT	GGGTGGTGG	TTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCTT	GTCTCTGCTG	GGGTTATCT	TAGTGCTCT	CATGAATCGG	GTGTTTTTCA	1200
	AATTTCTCCT	GAGTTTCTCT	GTGGCACTGG	CCGTGGGAC	TTTGAGTGT	GATGCTTTTT	1260
	TACACCTTCT	TCCCATTTCT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
25	CAATGAAAT	GAAAGAGGGA	CCACTTTTCA	GTCACTGTCT	TTCTCAAAAC	ATAGAAGAAA	1380
	GTGCTATTT	TGATTCACG	TGGAAGGGTC	TACAGCTCT	AGGAGGCCGT	TATTTTCATG	1440
	TTCTTGTGA	ACATGCTCTC	ACATTGATCA	AACAATTAA	AGATAAGAAG	AAAAGAATC	1500
	AGAAGAAACC	TGAAAATGAT	GATGATGCG	AGATTAAGAA	GCAGTTGCTC	AAGTATGAAT	1560
	CTCAACTTTC	AACAAATGAG	GAGAAAGTAG	ATACAGATGA	TGAACTGAA	GGCTATTTAC	1620
30	GAGCAGACTC	ACAGAGAGCC	TCCCACTTTG	ATTCTCAGCA	GCGCTGAGTC	TGGAAGAAG	1680
	AAGAGGTGAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
	CTCAGCTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCCGG	GTGCCCACTT	1920
35	TGGCTGAGAT	GGTGATGAG	GGTGATGCG	TGCACAAAT	CAGCGATGGC	CTAGCAATTG	1980
	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTGTCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTCTTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CCTTTATAAT	GCATTGTCAG	CCATGCTGGC	GTATCTTGGA	ATGCAACAG	2160
	GAATTTTCAT	TGCTCATATT	GCTGAAAATG	TTTCTATGTG	GATATTTGCA	CTTACTGCTG	2220
40	GCTTATTCAT	GTATGTGCT	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
	GTGACCATGG	ATGATGCGG	TGGGGGTATT	TCITTTTACA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTTGGAAT	TATGTTACTT	ATTTCATAT	TGAACATAA	AATGCTGTTT	CGTATAAAT	2400
	TCATGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
45	TTGTATTGAA	TATGTCTGTC	TGTTACAAAG	TCAGTTAAAG	GTACGTTTAA	ATATTAAAT	2580
	TATTTCTATC	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAGAG	ATTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAATGT	CTTTAATGCT	2700
	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAAGTCTGCG	2760
	TGTTTAGGAA	TAAAGATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAAATTTA	2820
50	AGCAAGAGAA	TAAAGAGAGAA	AAGAGAAAGAA	TCTGAGAAAT	GGGGAGGCAT	AGATTCTTAT	2880
	AAAAATCACA	AAATTTGTGT	TAAATTAGAG	GGGAGAAATT	TAGAATTAAG	TATAAAAAGG	2940
	CAGAATTAGT	ATAGAGTACA	TTCATTAAAC	ATTTTGTCTA	GGATTATTTT	CGTATAAAAC	3000
	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAC	TTTGATAAT	ACAGAAATCT	3060
	AAATATATTT	AATGAATTCA	AGCAATATAC	ACTTGACCAA	GAAATTGGAA	TTTCAAAATG	3120
55	TTGCTGCGGG	GTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	3180
	TATTTGCCAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGGTT	ACCTGGTTTA	3240
	CAAAATTATC	AGAGTAGTAA	AACITTTGATA	TATATGAGGA	TATTAATACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTTCAGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTTG	3360
	GAGCAATTGT	CTTTATATAC	GATACTGTAG	CCATACCTAGG	CCTGTCTGTG	GCATTCTCTA	3420
60	GATGTTTCTT	TTTTACACAA	TAAATTCCTT	ATATCAGCTT	G		

**A121 PROTEIN SEQUENCE**

Gene name: LIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Protein Accession #: NP\_036451  
 Signal sequence: 1-21  
 Pfam domain: Zip[591-743]  
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
	MARKLSVILI	LTFALSVTNP	LHELKAAAFP	QTTEKISPNW	ESGINVDLAI	STRQYHLQQL	60
	FYRYGENNSL	SVEGRFKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDHEHSDH	120
75	EHSDHDS	HNNHAASGKN	KRKALCPDHD	SDSSGKDPFN	SQKGAAHPR	HASGRNRVND	180
	SVSASEVST	VNTVSEGT	FLETIETPRP	GKLFPKDVSS	STPFSVTSKS	RVSRLAGRKT	240
	NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMGIQV	PLNATEFNVL	CPALINQIDA	300
	RSCLHTSEK	KAEIPPKTYS	LQIAWVGFI	AISIISFLSL	LGVLVPLMN	RVFFKFLLSF	360
80	LVALAVGTLG	GDAPLHLLFH	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIESAYFDS	420
	TKWGLTALGG	LYFMLVEHV	LTLIKQFKDK	KKNQKQKPN	DDVVEIKKQL	SKYESQLSTN	480
	EEKVDITDKT	EGVLRADSQE	PSHFDSSQPA	VLEEEVIMIA	HAHPQEVYNE	YVPRGCKNKC	540
	HSHFMDTLQG	SDDLHSHHHD	YHHILHSHH	QNHHPHSHSQ	RYSREELKDA	GVATLAWMVI	600
	MGDGLHNFSD	GLAIGAAFT	GLSSGLSTSV	AVFCHLPHE	LGDFAVLLKA	GMTVQKAVLY	660
	NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720

RWGYFFLQNA GMLLGFGLM LISIFEHKIV FRINF

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50

1	11	21	31	41	51	
COGCAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCCCCA	GCCCTCCTCC	AGGCCGCGAG	60
CGCCCTGTC	CGCGTGCCCTG	GCCTCCCTCT	CCAGACTGCA	GGGACAGCAC	CCGGTAACTG	120
CGAGTGAGAG	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	CGCGCGGCTT	AGCTGCTACG	180
GGTCCCGGTC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
ATGCCTCTGC	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
GGGAACGGCG	CCATGGCAAG	GCATCACGGG	TGTTAGCAT	CGCACGTCA	GCCTGGGGTC	360
TGTCACTATG	GAACATAACT	GGCTGTCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
TGTGAAGTCA	CATCGGAACC	TGGATGTAAG	TTTGGTGAGT	GGTGGGACC	AAACAAATGC	480
AGATGCTTTC	CAGGATACAC	CGGGAACACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACAG	GAAGCTACAA	GTGCTTTTGC	600
CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
TCAGGACTCC	GCCTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCTTCT	780
GGTAAAGTCA	TCTGTCCCTA	CAATGGAAGA	TGTGTGAACA	CATTGGAAG	CTACTACTGC	840
AAATGTGACA	TGTGTTTCGA	ACTGCAATAT	ATCAGTGGAG	GATATGACTG	TATAGATATA	900
AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
GGTCTCTTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
ATCCCTGAAA	ATTCTGTGAA	GGAAATCCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
AAGAAGTTTC	TGTCTCAACA	AAACAGCATG	AAAAAGAAGG	CAAAAATTAA	AAATGTTACC	1140
CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
ATAGTTTCCA	GAGGCGGGGA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAAAAGAAA	1260
GAGGSGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCTGTATT	1380
CTGGTCCAAA	GGAAGAGCGT	AACCTCCAAA	CTGGAACATA	AAGATTAA	TATCTCGGTT	1440
GACTGCGAGT	TCAATCATGG	GATCTGTGAC	TGGAACAGG	ATAGAGAAGA	TGATTTGAC	1500
TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
GGTCACAAGA	AAGACATTGG	COGATTGAAA	CTTCTCCTAC	CTGACCTGCA	ACCCCAAAGC	1620
AACTTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
TTTGTGAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
TGGAAGACAG	GGAAAAATCA	GTGTATCA	GGAACTGATG	CTACCAAAG	CATCATTTT	1800
GAAGCAGAAG	GTGGCAGGGG	CAAAACCGGC	GAAATGCGAG	TGGATGCGCT	CTTGCTTGTT	1860
TCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
TTGACTTGT	ATGTCAGTTC	CCTGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
TTAGAAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCCT	2040
TCCTGTATA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCACTGTATC	TTCTCAGTCA	2100
TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAT	GTCACTTTAT	CTCCCTCTCT	2160
CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
TAGAAAAAAA	AGCAGAGAGA	AATGTTTAA	TGTTTGACTC	TTATGATACT	TCTTGGAAAC	2280
TATGACATCA	AAGATAGACT	TTTGCTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340
TGTATATTTA	AATCTTTTGT	AATAATAATA	TCCAAATCAT	CAAAAAAAA	AAAAAAA	

55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

65  
 70  
 75  
 80

1	11	21	31	41	51	
MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	EGECVGNPKC	RCPPGYTGKT	CSQDVNECGM	KPRPCQHRVC	NTHGSYKFC	120
LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
KGVICPYNRR	CVNTFGSYIC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTQ	240
GSFKCKCKQG	YKNGLRCSA	IPENSVEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNTV	300
PEPTRTPPK	VNLQPFNYEE	IVSRGNSHB	GKKGNBEKMK	BGLEDEKREB	KALKNDIEER	360
SLRGDVFPFK	VNEAGEFGLI	LVQRKALTSK	LEHKDLNISV	DCSFNHCICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPALA	GKKKIDIGRLK	LLLPDLQPQS	NFCLLPDYRL	AGDKVGKLRV	480
FVKNSNNALA	WEKTTSEDEK	WTKGKIQLYQ	GTDATKSIIF	EAERGKGTG	EIAVDGVLLV	540
SGLCPDLSLLS	VDD					

80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51  
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60  
CTGCCACCTG GGGCGGTGCG GGGCCGAGAG CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120  
CGATGCAAGT GCGCTCACTG CGAGCTGCGG CCGCGACAG CTTCGTGGCG CTCTGGGCAC 180  
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240  
GCTTCATCCA CCGGCGCTCC CGCAGCCAGG AGCGCGGGGA GATGACGCGC GAGATCCTCT 300  
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360  
CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCGG 420  
GCCAGGGCTT CTCTACCCG TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480  
GCCTGCAAGG TAGCCATTTC CTCACGAGC CCGACATGGT CATGAGCTTC GTCACCTCG 540  
TGGAAATGA CAAGGAATTC TTCCACCCAC GCTACCAACA TCGAGAGTTC CGGTTTGATC 600  
TTTCCAAGT CCGAAGGGG GAAGCTGTCA CGCAGCCGA ATTCCGGATC TACAAGGACT 660  
ACATCCGGGA ACGCTTCGAG AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720  
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCCT TGGGCTCCGG 780  
AGGAGGCGG GCTGTGTTT GACATCACAG CCACAGCAAA CCACTGGGTG GTCACCTCGG 840  
GGCACAACCT GGGCGCTGAG CTCTCGGTGG AGACGCTGGA TGGGCGAGAG ATCAACCCCA 900  
AGTTGGGGG CTTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960  
TCTTCAAGGC CACGAGGTC CACTTCCGCA GCATCCGTC CACGGGAGC AACAGCGCA 1020  
GCCAGAACCG CTCGAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080  
AGAACAGCAG CAGCGACGAG AGGCAGGCCT GTAGAGAGCA CGAGCTGTAT GTCAGCTTCC 1140  
GAGACCTGGG CTGGCAGGAT TGGATCATCG CGCCTGAAGG CTACGCGGCC TACTACTGTG 1200  
AGGGGGAGTG TGCCTTCCCT CTGAATCCT ACATGAACG CACCAACCA GCCATCGTGC 1260  
AGACGCTGGT CCACTTCATC AACCCGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCAAGC 1320  
AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380  
ACAGAAACAT GTGTGTCCGG GCCTGTGGCT GCACTAGCT CCTCCGAGAA TTCAGCCCT 1440  
TTGGGGCCAA GTTTTCTGG ATCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500  
CTGCCCTTTG TGAGACCTTC CCTCCCTAT CCCCACCTT AAGGTGTGA GAGTATTAGG 1560  
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGT GCAGCATCCA ATGAACAAGA 1620  
TCCTACAAGC TGTGAGGCA AACCTAGCA GGAAGAAAA ACAACGCATA AAGAAAAATG 1680  
GCGGGGCGAG GTCAATGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740  
TTATGAGCGC CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800  
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860  
CAATAAAGC AATGAATG

## A125 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195  
Probeset Accession #: BE616633  
Protein Accession #: NP\_001710.1  
Signal sequence: 1-30  
Pfam domains: TGFb\_propeptide [37-281]  
Transmembrane domains: none found  
Cellular Localization: secreted

50 1 11 21 31 41 51  
MHVRSRLAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE RREMQRILS 60  
ILGLPHRPPR HLQMKHNSAP MFMLDLNLYM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120  
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGAVT AAEPRYKDY 180  
IRERPDNETF RISVYQLQE HLGRESDLFL LDSRTLWASE EGWLVEFDIT TSNHVVNPR 240  
HNLGLQLSVE TLDQGSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFERS IRSTGSKQRS 300  
QNRSKTPKQK EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAAYCE 360  
GECAFPINISY MNATNHAIVQ TLVHFIPNET VPKPCCAPTQ LNAISVLIFD DSSNVILKKY 420  
RNMVVRACGC H

## A126 DNA SEQUENCE

Gene name: integrin, beta 8  
Unigene number: Hs.52620  
Probeset Accession #: AA479726  
Nucleic Acid Accession #: NM\_002214  
Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51  
CCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCGAGCTTC CTCCCTGCC AGCCAGGACG 60  
CTGCGCACTT GTCCTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120  
GTTGGCCTCC CTGCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180  
TCCCTCGAC CTGCGCGGCG TACCCTCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240  
TAGGGTGTT TCCCCCCAG CTTCGGGCTT TGTTCGGTT TGATTGTGTT TGGCTCTTG 300  
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCT 360  
TGTCCCGAG CAGGCTGCGG AGCCTTGCA GAGCCTCTC TCCAGTCGCC GCGGGGCCCT 420  
TGGCGTGA AGGAGGTGCT TCTCGGGAG ACCGCGGAC CGCGCTGCC GAGCGGGAG 480  
GGCGGTAGGG GCGCTGAGAT GCGGAGCGGT GCGCGGGCCC GCTTACCTGC ACCGCTTGCT 540  
CGAGGCGCG GGTCCGCTCT GCTAGGCTGT CGGAAAAGT CCTAGCGACA CTGCGCGCG 600  
GGCCCGGAG TCGCCCGGGA GGCAGAGCCC GCGTCCGGAA GGCAGCCAGG CGCGGGCGC 660  
GGGGCGGCT GTTTTGCAIT ATGTGCGGCT CGGCCCTGGC TTTTITTACC GCTGCATTG 720  
TCTGCTGCA AACGACCGG CAGAGTCCCG CCGTCTTCT CTGGGAGCC TGGGTGTTTT 780



5  
10  
15  
20  
25  
30  
35  
40  
45  
50

CACTTGTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840  
 CCTGTGCCAG GTGCCTTGGC CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900  
 TTTCAAGTGG ATCAGAAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960  
 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAATGAAA 1020  
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080  
 ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140  
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTAT 1200  
 CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTGCTTGG ATTGGCTCA TACGTTGATA 1260  
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAGGAT TCATAATCAA TGCAGTGA 1320  
 ACAATTTAGA CTGCATGCC CTCCATGGAT ACATCCATGT GCTGCTTTG ACAGAGAACA 1380  
 TCACATGAGT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440  
 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGGAAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 GCAAAATGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620  
 ACGTCAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680  
 ACAACAATC TAAAGTCTAT TTTGCAGTTC AAGGAAAACA ATTTCTTGG TATAAGGATC 1740  
 TTCTACCCCT CTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACTCA 1800  
 ATAATTTGGT AGTGAAGCC TATCAGAAAGC TCATTTTCTG AGTGAAGTT CAGGTGAAA 1860  
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCATCTG TCCAGATGGG TCCAGAAAAGC 1920  
 CAGGCATGGA AGGATGAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980  
 TTACAATGAT TAAATGAGT GTCCAGGAG GAAAAACTA TGCAATAATC AAACCTATTG 2040  
 GTTTTAATGA AACGCTAAA ATTCAATAC ACAGAACTG CAGCTGTGAG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACTTTCT AGATTCCAAG TGTCTTCAAG 2160  
 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220  
 ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTTGGAAA TGTTCATGTC 2280  
 ACAAAATGAA GTGTGAAAAG GTGTATGGAA AATACCTGTA AAAGGATGAC TTTTCTTGTG 2340  
 CATATCACC TGAATATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAAA GGGCCAAAGT TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520  
 GCACGATCC CAGGAGCATC GGCCTGTTCT GTGAACACTG CCCACCTGT TATACAGCCT 2580  
 GCAAGGAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTTGTCT CAGGCTATAC 2640  
 TTGATCAGTG CAAACCTCA TGTGCTCTCA TGAACAACA GCATTATGTC GACCAAACTT 2700  
 CAGAATGTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760  
 TCTGATTGG GTTGCTTAAA GTCTGTATCA TTAGACAGGT GATACTACAA TGAATAGTA 2820  
 ATAAATATTA GTCTCATCA GATTACAGAG TGTACGCTC AAAAAAGGAT AAGTTGATC 2880  
 TGCAAGATG TTGCAAGA GCAATCACCT ACGGAGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATT 3000  
 TTAACACTT AATGGGAAAC TGAATTTGT AATAATTGCT CCTAAAGATT ATATTTTAA 3060  
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGTTGT ACATCGAAC 3120  
 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGATG TTACTACTGT TTGAGACTAG TGTGTTTGT GCACCTTACT GTAATATATA 3240  
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCTACGCTT CCGAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360  
 CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 TATATTTCAA GGTGCAAAA CACTTCAACA GTTGGTGGT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT TTTGCTGTTT TCACTCTTTC AAGAGGTGAA CAGATACAC CTTAATCTTA 3540  
 AAAGATTAT GCTTTTAAA GTGTGTAGT TTATGATGT GTGTTTATG TTTGCTTAT 3600  
 TTTGCAAGT GATACATA TCCAGATT TCTCTCTT GCCTTTATG TTTGTTTCT 3660  
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780  
 GAATGTTAA

55 A127 Protein sequence:  
 Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 60 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane

65  
70  
75  
80

1 11 21 31 41 51  
 | | | | |  
 MGSALAPFT AAFVCLQND RGPASPLWAA WVPSLVILGL QGEDNRCASS NAASCARCLA 60  
 LGPECGWCQV EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120  
 GEVSIQLRPG ABAFMKLKVH PLKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSSRMAPP 180  
 SRDFRLGPGS YVDKTVSPYI SIHPERIHQ CSDYNLDCMP PEGYIHVLSL TENITEFEKA 240  
 VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRL LVMTDQTS HL ALDSKLAGIV 300  
 VPNDGNCHLK NNIVYKSTM EHPSLGQLSE KLIDNNINVI FAVGQKQFHW YKDLLPLLP 360  
 TIAGEIESKA ANLNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420  
 NVTSIDVLF NVIVTMKKCD VTGGKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKG 480  
 CVDETFLDSK CFQDCENKCH FDEDFSSSES CKSHKDQPV C SGRGVCVCGK CSCHKIKLKG 540  
 VVGKVCEDD FSCPVYHGNL CAGHECEAG RCQCFSGWEG DRQCPCPSAA QHCVNKSGQV 600  
 CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660  
 CALMEQHYV DQTSCEFPSP SYLRIFITF IVTFLIGLKL VLIIRQVILQ WNSNKIKSSS 720  
 DYRVASAKID KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

A128 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942  
 Probeset Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

1      11      21      31      41      51
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
CTCGCGGTCA GGATGGTTTT CTCTGTCAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTACTAGA CGTTCAAGAT ATTCTTGTC ATCATTGTTC TTATGTGCTG TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTACCAC CACCTGCTAA ATTATCTGTT 240
GTCAAGTTTG CCCCTCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAAATCA CTATAGTAAA AACCTTCAAT 360
GCTTCAGGCG TCAAAACCCA GAGAAATATC TGCAATTGTG CATCTATTTG CAATGACTCA 420
GCATTTTCTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCAGAAAT 480
CAACATATAA CGAATGGCAC CTTAACATGA GTCTGTCTCT TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AAACCTTGCA AACCTTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TGTGTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
TCTGTACAGA TACCCTGCC TCCCTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTC TTCCAGCCAA 840
TCCATCCGAG TGGTGCTCTG GGCCACTGTG CTTTCCGAGG TCCCCTAAGC TACCTCTTTT 900
GCTGAGCCTC CAGATTATTCT ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCCGAGCG TTCACTCTCC ATAGCTTCCA GCCCTGCCAT TGACATGCC 1020
CCACAGCTCG AAGCTGCTCT TCCCTCTATG CCCCACCCAT ATGCTCCGG CACCCCACT 1080
CCTGTGAAAG CCTCATTTTC CTCTCCACCC GTGTCTGCC CTGGAATGT CAACACTACC 1140
AGCGCACCTC CTGTGCGAGC AGACATCGTC AACACCAGCA GTATTCTGA TCTTGAGAAC 1200
CAAGTGTGCG AGATGGAGAA GGCTCTGTCC TTGGGCGACC TGGAGCCTAA CCTGCAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCCCGCG CTGACATGCT GGCCCTCTG 1320
GCTCAAGATG TGCTGAAAGT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAACACG 1380
ACTATAAGTC TAACCTCCCC TTCCTTGGCT CTGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCACACAAA CTACCTTTGT GGCCCAAGAC CCTGCAAAAT TTCAGGTTTC TCTGAAACC 1500
CAAGCTCCTG AGAACAGTAT TGGCACAAAT ACTCTTCCTT CATCGCTGAT GAATAATTTA 1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTGTGA AACACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680
GTTGCAAAAC TGACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
AACCAGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800
GGCAGAGGAG CTGCTGTCAG CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860
ATCTGTACCT GTAGCCATCT AACAGCTTC GCGCTTCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCGAG CTCCTAATGAT GGCTCTGACG TTCATTACAT ATATTGGTTG TGGGCTTTCA 1980
TCAATTTTTC TGTCAGTGAC TCTTGTAACC TACATAGCTT TTGAAAAGAT CCGGAGGGAT 2040
TACCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCGTGTCTTC 2100
CTCTGCACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC CTGCTATCTC AGTGGCTGTA 2160
TTTCTTCAAT ATTTCTCTT GGTCTCATT ACATGGATGG GCTGAGAAGC ATTCCATATG 2220
TACCTGCCCC TTGTCAAAGT ATTTAATACT TACATCGAA AATACATCTT TAAATCTGCG 2280
ATTGTGCGTT GGGGGGTACC AGCTGTGTT GTGACCATCA TCCTGACTAT ATCCCAGAT 2340
AACTATGGCG TTGGATCCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTCTGCTGG 2400
ATCAACAACA ATGCAATATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTGT 2460
CTGAACGTCA GCATGTCAT TGTGGTCTG GTTCAGCTCT GTCGAATTAA AAGAAGAGAG 2520
CAACTGGGAG CCCACGGA AACCAGTATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580
TTTTTACTGG GAATAACTTG GGGCTTTGCC TTCTTTGCC GGGGACCGAT TAACGTGACC 2640
TTCATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700
TGTGTGGCCA AAGAAAATGT CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA 2760
CGGCTGGCTG AAAATTCTGA CTGGAGTAAA ACTGCTACTA ATGTTTAAAG GAAGCAGACT 2820
GTAAACCAAG GAGTGTCCAG CTCTTCAAAT TCCTTACAGT CAAGCAGTGA CTCCACTAAC 2880
TCCACCACAC TGCTAGTGAA TAATGATTGC TCAGTACAGC CAAGCGGGA TGGAAATGCT 2940
TCTACAGAGA GGAATGGGCT CTCTTTTAGT GTTCAGAAAG GAGATGTGTG CCTTCAAGAT 3000
TTCACTGAAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT 3060
ATTGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATT 3120
CTTCTTCTTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
TTTAGACATT TCTGATTGCG TTTCTTATCT TTCATTTTAT AAGAAGGTTG GTTTTAAACA 3360
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
TTTAAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTCAGCCTG 3480
TTGGTGAGTT TAGTTGTGCA TGCCCTTGTT GTATATAAGC TAAATCTAG TGACCCATGT 3540
GTCAAAAATC TTACTTCTAC ATTTTITTTT ATTTATTTTC TACTGTGTAA ATGTATTCTT 3600
TTGTAGAATC ATGGTTGTTT TGCTCACTG GATAATTGAG AAAATCCTTG CTCGTTCCGC 3660
AAATCTCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
TCAAGAAATA ATGATCCAG CCAGACTGAG AAAATGTAAAG CAGACAGTGC CACAGTTAGC 3780
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCGAG CACAGCCCTA 3840
TGGGTGATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
GTGCAGGACC TGTACAGCCA AACACAGCAT CCAATATGAA TCCCACATCC CTGACCGCAT 3960
CCCCAGTAGT CAGATTATAG AATCTGACCC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
AGAGGAGTAG ATAGTCTACC AGACCATGTG TCAGGAAAAT TGTGAACGTA GATGAGGTAC 4080
ATACACTGCC GCTTCTCAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATT 4140
CTTCTCTTAA AAAGGTACAT ATATATGAAA AAAATATCATA TTGCGTTCTT TTAAGAGGCA 4200
ACTGCATGGT ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCCGACC AGAGCTATAA 4260
TTGTTTTTAA AATGTGCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGAACTAGTC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGCT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCTCT AAGTACATCC 4440
TTATTAGGAA CATTTCAAAC CCGTTTGTAG TAAGTCTTTC ACTAAGGTTT TCTTGCAAT 4500
ATTTCAGTGT AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTAGTG 4560

```

CTGACTTGTC TTTGCAATAT TTCTTTCTG ATTTATTAA TTTCTTGTA TTTATATGTT 4620  
 AAAATCAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

# A129 Protein sequence

Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60  
 PSSNEVETTS LNDVTLSLLP SNETEKTIT IVKTFNAGSV KPORNICNLS SICNDSAPFR 120  
 GEIMFQYDKE STVPQNQHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAGS 180  
 TLNCTFTIKL NMTNNAACAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240  
 VCLADHFRGP PFSSSQSIPV VPRATVLSQV PKATSFAPPP DYSPVTHNVP SPIGSIQPLS 300  
 PQPSAPIASS PAIDMPQSE TISSPMPQTH VSGTTPPVKA SFSSPTVSAP ANVNTTSAPP 360  
 VQTDIVNTSS ISDLENQVLQ MEKALSLSL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL 420  
 LKVVDDIGLQ LNFSTNTISL TSPSLALAVI RVNASSFNIT TFVAQDPANL QVSLETQAPE 480  
 NSIGTITLPS SLMMNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVSSSVANL 540  
 TVRNLTNRVT VLKHNINPQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600  
 SHLTSFGVLL DLSRTSVLPA QMALTFITY IGCGLSSIFL SVTLVTYIAF EKIRRDYPSK 660  
 ILIQLCAALL LNLVFLDLS WIALYKMQGL CISVAVFLHY FLVSTFTWMG LEAFHMYLAL 720  
 VKVFNTYIRK YILKFCIVGW GVPVVVVVII LTISPDNYGL GSYGKFPNGS PDDFCWINNN 780  
 AVFYITVVG YFCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840  
 ITWGFAPFAW GGVNVTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE 900  
 NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGMASTER 960  
 NGVSFSVQNG DVCLHDFGK QHMFNEKEDS CNKGKRMALR RTSKRGSLLH IEQM

# A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Probeset Accession #: AA460530  
 Nucleic Acid Accession #: NM\_003667  
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GTGGGCGCAA CGGCGACCTC AGTCCCGGCC GCGCTTCTCC TCGCGGCCCA GCGCGTGGG 60  
 TCAGGAACGC GCGCTCTGGC GCTGCGAGCG CCGCTGAGT TCGAGAAGCC CACGGAGCGG 120  
 CGCCGCGGCG CGCAGCGGCC GTAGCAGTCC GGTGCTGCTC TCGCGCCGCG TCGCGCTCGT 180  
 GGCCCGCTAC TTGCGGCACC ATGGACACCT CCGCGCTCGG TGCTGCTCCTG TCCTTGCTCG 240  
 TGCTGCTGCA CTGCGGACCC GGGGGCAGCT CTCCAGGTC TGGTGTGTTG LCGAGGGGCT 300  
 GCGCCACACA CTGTCAATTG GAGCCCGAGC GCAGGATGTT GCTCAGGGTG GACTGCTCCG 360  
 ACCTGGGGCT CTGCGAGCTG CTTTCAACCC TCAGCGTCTT CACTCTCTAC CTAGACCTCA 420  
 GTATGAACAA CACCGTCCAG CTGCTCCCGA ATCCCGTGCC CAGTCTCCGC TTCTGAGGAG 480  
 AGTTACGCTG TCGGGGAACG GCTCTGACAT ACATTCCCAA GGGAGCAATC ACTGGCCTTT 540  
 ACAGTCTTAA AGTTCTTATG CTGCAGAATA ATCAGCTAAG ACAGTACCC ACAGAAGCTC 600  
 TGCAGAAATT GCGAAGCCTT CAATCCCTGC GTCTGGATGC TAACCAATC AGCTATGTGC 660  
 CCGCAAGCTG TTTAGTGGC CTGCAATCCC TGAGGCACTT GTGCTGGAT GACAATGCTG 720  
 TAACAGAAAT CCGCGTCCAG GCTTTAGAGG GTTTATCGGC ATTGCAAGCC ATGACCTTGG 780  
 CCTGGAACAA AATACACCA CATTACGACT ATGCTTTGGG AAACCTCTCC AGCTTGTGAT 840  
 TTCTACATCT CCATAACAA AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC 900  
 ACAGCCTAGA GACTTTAGAT TTAATTTACA ATAACTTGA TGAATCCCC ACTGCAATTA 960  
 GGACACTCTC CAACCTTAAA GAATAGGAT TTCATAGCAA CAATATCAGG TCGATACCTG 1020  
 AGAAAGCTTT TGTAGGCAAC CTTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC 1080  
 AATTGTGTGG GAGATCTGCT TTTCAACATT TACCTGAATC AAGAACAATG ACTCTGAATG 1140  
 GTGCTCTACA AATAACTGAA TTTCTGATT TAATGGAAC TGCAAACTCG GAGAGTCTGA 1200  
 CTTTAACTGG AGCACAGATC TCATCTCTTC CTCAACCGT CTGCAATCAG TTACCTAATC 1260  
 TCCAAGTGTG AGATCTGTCT TACAACCTAT TAGAAGATTT ACCCAGTTT TCACTCTGCC 1320  
 AAAAGCTTCA GAAAATTGAC CTAAGACATA ATGAAATCTA CGAAATTAAG GTTGACACTT 1380  
 TCCAGCAGTT GCTTAGCCTC CGATCGCTGA ATTTGGCTTG GAACAAAATT GCTATTATTC 1440  
 ACCCACTCTC ATTTTCCACT TTGCCATCCC TAATAAAGCT GGACCTATCG TCCACCTTCC 1500  
 TGTGCTCTTT TCCTATAACT GGGTTACATG GTTTAACTCA CTTAAATTA ACAGGAATC 1560  
 ATGCTTACA GAGCTTGATA TCATCTGAAA ACTTTCCAGA ACTCAAGGTT ATAGAAATGC 1620  
 CTTATGCTTA CCAAGTCTGT GCATTGGAG TGTGTGAGAA TGCTTATAAG ATTTCTAATC 1680  
 AATGGAATAA AGGTGACAC AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT 1740  
 TTCAGCTCTA AGATGAACGT GACCTTGAAG ATTTCTGCTG TGACTTTGAG GAAGACCTGA 1800  
 AAGCCCTTCA TTCAGTGCAG TGTTCACCTT CCCCAGGCCC CTTCAAAACC TGTGAACACC 1860  
 TGCTTGATGG CTGCTGATC AGAATTGGAG TGTGGACCAT AGCAGTCTG GCACTTACTT 1920  
 GTAATGCTTT GGTGCTGATC ACAGTTTTC GATCCCTCT GTACATTTC CCCATTAAAC 1980  
 TGTTAATTTG GGTGATGCA GCACTGAACA TGCTCACGGG AGTCTCCAGT GCGGTGCTGG 2040  
 CTGCTGTGGA TGGCTTCACT TTTGGCAGCT TTGCAAGACA TGGTGCCTGG TGGGAGAATG 2100  
 GGGTTGGTTG CCATGTCAAT GGTTTTTTGT CCATTTTTCG TTCAGAAATC TCTGTTTTC 2160  
 TGCTTACTCT GGCAGCCCTG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA 2220  
 CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCATTTTGT CTGTCCTCTG CTGGCCTTGA 2280  
 CCATGCCCCC AGTTCCTCTG CTGGGTGGCA GCAAGTATGG CGCCTCCCTC CTCTGCTGTC 2340  
 CTTTGCCTTT TGGGGAGCCC AGCAACATGG GCTACATGGT CGCTCTCATC TTGCTCAATT 2400  
 CCGTTTGTCT CCTCATGATG ACCATTGCTT ACACCAAGCT CTACTGCAAT TTGGAACAAG 2460

5 GAGACCTGGA GAATATTGGS GACTGCTCTA TGGTAAAACA CATTGCCCTG TTGCTCTTCA 2520  
 CCAACTGCAT CCTAACTGCG CCTGTGGCTT TCTTGTCTTT CTCCTCTTTA ATAAACCTTA 2580  
 CATTTATCAG TCTGAAGTA ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTCTCTGCAT 2640  
 GTCTCAATCC CCTTCTCTAC ATCTTGTTC AATCTCAGTT TAAGGAGGAT CTGGTGAGCC 2700  
 TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAAT 2760  
 CTGATGATGT CGAAAAACAG TCCCTGTGACT CAACTCAAGC CTGGTAACCC TTTACCAGCT 2820  
 CCAGCATCAC TTATGACCTG CCTCCAGTT CCGTGCCATC ACCAGCTTAT CCAGTGAGCTG 2880  
 AGAGCTGCCA TCCTTCTCT GTGGCAATTG TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940  
 10 AATGTTTTCA AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000  
 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

15 A131 Protein sequence  
 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 20 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 MDTSLRLGVL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLENPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120  
 LQNNQLRHVP TEALQNLRLSL QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240  
 30 LNYNNLDEFP TAIRTLNLK ELGFHSNNIR SIPEKAFVGN PSLLTIHFYD NPIQFVGRSA 300  
 FQHLPELRTL TINGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360  
 YNLLEDLPSF SVCQKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHPNAPST 420  
 LPSLKLKLDL SNLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPAYQCC 480  
 AFGVCENAYK ISNQWKNKDN SSMDDLHKKD AGMFQAQDER DLEDFLDDE EDLKLHVSQ 540  
 CSPSPGPFKP CEHLDDGWL I RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 35 AVNMLTGVS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASE SVFLLTLAAL 660  
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGE 720  
 STMGYMVALI LLSLCLFLMM TIATYKLYCN LDKGDLNIW DCSMVKHIAL LLFNCILNC 780  
 PVAFLSPSSL INLTFISPEV IKFILLVVVP LPACLNPLLY ILFNPHEKED LVSLRKQTYV 840  
 40 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSITYDL PPSVSPSPAY PVTESCHLSS 900  
 VAFVPL

45 A132 DNA SEQUENCE  
 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Probeset Accession #: U25128  
 Nucleic Acid Accession #: NM\_005048  
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 GGCGGGTGGC CCGGGCCCGA CCACCCAGC TCGCGTCTGT TACTGGCCAC AAGTTTGCTC 60  
 TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGCG TCTGGAGSAG GGTCCCTGCT 120  
 55 TCTTCTTACA GCGTTCCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCAGC TCTGGGGTTG 180  
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATC GCACCATAC 240  
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300  
 AGCTCAACTC CAGAGGGGAG AAGGTAATTG TTCCCTGAA TGGGATGGAC TCATTGTGTG 360  
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGCT CCTCTTATA TTTATGACTT 420  
 60 CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480  
 CAGCTTAAT AAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT 540  
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600  
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTTACTTCA GACGATTGCA 660  
 TTGCACTAGG AACTATATCC ACATGCACCT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720  
 65 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780  
 AATAATGCGA GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCAATAA 840  
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATT 900  
 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCTT TTTGGGACAC 960  
 CAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTCGAGC 1020  
 70 ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGCAGAGTGC TGGGAACCTA GTGCTGGAGA 1080  
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140  
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200  
 CACAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCGTGCTC TAGTCTTTGG 1260  
 AGTGCAATAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320  
 75 CGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA 1380  
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440  
 CTCGGTGGAC TGGAAAGGGA CACCGCCATG TGGCAGCGCG AGATGCGGCT CAGTGCTCAC 1500  
 CACGTCAGC CACAGCACA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560  
 TATCTCTGSC AAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCCTTTACC 1620  
 80 TGGCTATGTC TGGAGTAAT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC 1680  
 CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740  
 GGAATCTAAC CACAGACACTG AAGGATGCCA AGGAGAAATC GAGGATGTTT TCTGAATGGA 1800  
 CATTGTGGC TGACTTTTAT GGGCTGTGCC AATGGCTGGT TGTGTGAGAG GGCTTGCTG 1860  
 ATACTCTTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920  
 TTTTAGGCTC CATGAATTGG TCCTGTAA TACTAACGAC ATGAAAATGC AAGTGCTAAT 1980

5 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040  
 GCTCTGTGAT TGTTCAATTT TTCTGTCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100  
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160  
 ATTTTCCTTT TAGAACTAG TATTCTCTTA TTCTTACTT TAATGTACTT CTATCACTGC 2220  
 ATTTATTTTG CCGTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280  
 GATCTAAGAA CAAGTACTTG CTGGAAATT AGTTGGCTGG ACATTGTATAA AATAATGCAT 2340  
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAAATT CTCAAAAAAG AATATTTTAC 2400  
 ACATCCCTTC TTTTGAATGG CCTCTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460  
 10 TTCTTTGTAA ACCATGTGAT GTGGAAAGAT TTCCTCAGTT AGTGAGCTTG TGCTGCAAAA 2520  
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCTTG 2580  
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640  
 T

15 A133 PROTEIN SEQUENCE  
 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Protein Accession #: NP\_005039.1  
 Signal sequence: 1-25  
 Pfam domain: 7tm\_2 [141-420]  
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419  
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 | | | | | |  
 MAGLGASLHV WGLWMLGSSCL LARAQLDSGD TITIEEQIVL VLKAKVQCEL NITACLQEGE 60  
 GNCFEPMDGL ICWPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120  
 NYSDCLRLFIQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180  
 30 MHLFVSPMLR ATSFIVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240  
 VMFIYFLATN YYWILVEGLY LHNLIFFVAF SDTKYLWGF I LGWGFPAAF VAAWAVARAT 300  
 LADARCEWLS AGDIKIWIQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360  
 LAKSTVLVLV VFGVHIYIVF CLPHSFTGLG WEIRMHCELF FNSFGCFVFS IICYCNGEV 420  
 QAÉVKKMWSR WNLSDVDWKRT PFCGSRRCGS VLTVTTHSTS SQSQVAASR MVLISGKAAK 480  
 35 IASRQPDISH TLPGYVWSNS EQDCLPHSPH EETKEDSGRQ GDDILMEKPS RPMESNPDE 540  
 GCQGETEDVL

A134 DNA sequence  
 Gene name: ESTs  
 40 Unigene number: Hs.128899  
 Probeset Accession #: AA983251.  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 | | | | | |  
 ATGCTGTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCACAGTA CACTCCCAGG 60  
 GGAAGAAGAAC TTCGTGGGA GGCCTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC 120  
 GACCCGGAGA GGGAGAGCCG GCGGAGGCT GCGGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 50 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240  
 CCGCGGCGCG CGCCAGCTGG CAGAGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300  
 CGCCTGCGTC CTGAGCGTTC CCGGGGAGAG GTCCGCTTGC CAGTGAACC TCCAGAGGCT 360  
 TCCGAGCAGC AGCCCGCGGG GCCTTCTGAC TGCACTCCGA GATTTCATC AGCAGTGTCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 55 GCTCCTGGAC CTAGGGCCCG GCGTCTGCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540  
 CCGCGCGGAA AGCGCGCGCG GACAGTCACT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600  
 CTTCTCGGAG ACCGCTCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAGG GGTGGTGCCA 660  
 TGTGGGGGCG TCGCCTCTCG TCGCTCTCTT CATCTCGGAA CGCCGCTTCG CTCTGCGAGC 720  
 TGCTGTCTGC TCGCTCTGCT GCGCGGCGGG CGAGGGCCCA CGCGCGAGTA CTGCCACGGC 780  
 60 TGGCTGGAGC CGCAGGGGCT CTGGCGCATC GGCCTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 GCGCAGCCCA CCATCTGCTG CCGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCGAG 900  
 GCGCGCCTGG ACCAGGGGCG CTGGGACAAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960  
 CGGGCGGACA AAGACGGGCG CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGGAGACGCG AGGGTGCGCC CCACCGGTG AGGGCCTGGC AGCGGTGCTC CCTGAAGGC 1080  
 65 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC 1140  
 CGCGGATTC CATCTCTTCC ACGCGGCGCG CCTCTCCGCC TGCAGCGGCC GCGCTTGCCC 1200  
 ATCTACGTGC CGTCTCTCAT TGTGGCTCC GTGTTTGTGC CCTTTATCAT CTTGGGGTCC 1260  
 CTGGTGCGAG CTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320  
 70 GCGCCAGCGG GTAACCGCTT GATGGAGACC ATCCCATGA TCCCCAGTGC CAGCACTTCC 1380  
 CGGGGGTGGT CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440  
 GGGGCGCGGG CGCCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG 1500  
 AACCAAGCTG ATGTCAACAT GCCCAAGAAAT TTCTCTGTGC TGAAGTGA CAAGGCCACC 1560  
 CAGATGTGCG CACATCAAGG CAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620  
 CAGGACTCTG TGCCCTGACC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680  
 75 AGGCAGATTG AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTGAG GTGGAACTGC GCACATGTGC GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860  
 GCTTCATTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920  
 CATCCAGGGT ATCATTTGAT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 80 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTAT TTTTATTAT TATTTCTTTT 2100  
 TTGTTGTTGA CTGCAAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTCTT 2160  
 TTTTCTTTT TTTTCTTTAA TCAGACAGGG TCTTGTCTG TTGCCAGGC TGGAGTGCAG 2220  
 TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCCTGCCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGATTTT 2340

5  
10  
15  
20  
25

TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400  
 TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460  
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520  
 ATTCTAAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580  
 GGCACACCTT AATTTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640  
 GGGCCTATTT TGTCCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTACA 2700  
 TTA AAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760  
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAAT CATCCCTTC 2820  
 TTGATTGTAT CTAAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCITTTT 2880  
 TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940  
 TGGTTATGGT TTGGCGTTTC CTCTGTTTG GTTTTCAGAG CCCATGTCT ATATAGTCTC 3000  
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCTA GATCTGATAA 3060  
 AAAATTTTC TTGCTTATGT TATAAAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTT 3180  
 GCAGATCAT AAGCTTTTTA TACTCTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240  
 GATTGTAAAG AGAAAGCTT TCACACGAAG GATTGCCCTT CTCTCCCACT ACTGTTCTTG 3300  
 ATTTCTCTC TCTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATAT 3360  
 CAAATTTCAAG TGAATTTATT TTGTGTCTT TACTTATAT AAAAAAAGAT AACTTTAAG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAAGTAT TTGTAATTAA ACAATCGCT 3480  
 GTATGTATG GTCTTCTACA CATTATGTC TATAGATATC TATGATCAT CTTTCTATTC 3540  
 TGTTCATAG CTGAATTAAG TAAACCAAGT GTTGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGA AAAAAA AAAAAA AAAAAA

30

**A135 Protein sequence**  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

35  
40  
45

1 11 21 31 41 51  
 MLSGFLMSPS TQHQAOYTPG GKLFWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKGNRGE PPAWIRAQQQ PRPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPEA 120  
 SGRQPRGPSD CIPRFPASASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEAGSG 180  
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVVP CGALAARPS PPGTPLRSCS 240  
 CQWLRCNRG RGPSEYCHG WLDAQGVWRI GFQCPERFDG GDATICGSC ALRYCCSSAE 300  
 ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPV RAWQRCSPG 360  
 SPKGRQLLRA FPGLLPRARR RGFPPSPRGG PSPLQRPALP IYVPELIVGS VFVAFIILGS 420  
 LVAACCCRCL RPKQDPQQR APGNRLMET IPMIPSASTS RGSRRQSSST AASSSSSANS 480  
 GARAPPTRS TNCCLPBGTM NNYYNMPN FSVLNCQQT QIVPHQGYL HPPYVGYTVQ 540  
 HDSVMTAVP PFMDGLQPGY RQIQSPFPH NSEQKMPAV TV

50

**A136 DNA SEQUENCE**  
 Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 ProbeSet Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60  
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120  
 CAGCAAAAGT ACACACACCT GGTTCGAATT CAAACCAAG AAGAGATTGA GTACCTAAAC 180  
 TCCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAAGT CAACAATGTG 240  
 TGGGTCTGGG TAGGAACCCA GAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300  
 GAACCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360  
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAAT TGTGAACGTG 540  
 ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAACTTC 600  
 AGCTACAATT CTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCACT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCTG CAATGTGGTT 720  
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGA 780  
 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840  
 GCCCAGAGCC TTCAGTGATC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
 CCTGTGGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020  
 TTGCAGGGAC CAGCCAGGT TGAATGCACC ACTCAAGGSC AGTGACACA GCAATCCCA 1080  
 GTTTGTGAAG CTTTCAAGT CACAGCCTTG TCCAACCCG AGCGAGGCTA CATGAATTGT 1140  
 CTCTCTAGTG CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200  
 GGTTTGTGTG TGAAGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260  
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCC GAAGGGTTTG 1320  
 GTGAGGTGTG CTCATTCCTC TATTGGAGAA TTCACCTACA AGTCTCTTG TGCCTTCAGC 1380  
 TGTGAGGAGG GATTGTGAAT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440  
 TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAATGTT CAAGCTGGC AGTTCGGGGA 1500  
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTGT 1560  
 CCTGAAGGAT GGAGCTCAA TGGCTCTGCA GCTGGACAT GTGAGGCCAC AGGACACTGG 1620  
 TCTGGCTGTC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
 CTCTCTGCTG CTGGACTCTC CCTCTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740

TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800  
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5 **A137 Protein sequence:**  
Gene name: Selectin E (endothelial adhesion molecule 1)  
Unigene number: Hs.89546  
Probeset Accession #: M24736  
Protein Accession #: NP\_000441  
10 Signal sequence: 1-22  
Transmembrane domains: 555-573  
C-lectin domain: 23-139  
Cellular Localization: plasma membrane

15  
1 11 21 31 41 51  
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKKEIEYLN 60  
SILSYSPSYW WIGIRKVVNV WVVVGTQKPL TEEAKNAPG EPNNRQKDED CVEIYIKREK 120  
20 DVGMMNDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180  
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
ECDAVTNPAN GFVECFQNPQ SFPWNITCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300  
AVTCRAVRQP QNGSVRCSSS PAGEFTFKSS CNFTCEGFM LQGPQVVECT TQGWTOQIP 360  
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420  
25 EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAPS CEEGFELYGS TQLECTSQGQ 480  
WTEEVPSQCV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRL CLRKAKKFVP ASSCQSLES 600  
GSYQKPSYIL

30 **A138 DNA SEQUENCE:**  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
35 Nucleic Acid Accession #: AA487468  
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60  
CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGCTCACAG TTCTTCCAA CCTTGCCATT 120  
GCAATAAAA AGSAAAAGAG GCTCTCTCAG ACACCTCTCA GAGGATGGG AGATGACATC 180  
ACTTGGGTAC AAACATTATGA AGAAGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
45 ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAGAA AGTATTGCC 300  
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
GAAACCACTG ATAAGAAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAAT CATGTTTGTA 420  
GACCTTCTT TAAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
TATGAGCCTC GCGATTATACC CCTATTGATA GAAACATGA AGAAGCATT AAGACTTATT 540  
50 CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT 600  
GAAGAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660  
TTACTATTTA GTTTTITTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTITAAA 720  
TCTGAAAAA AAAAAA AAAAAA

55 **A139 Protein sequence:**  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
60 Protein Accession #: none found  
Signal sequence: 1-23  
Transmembrane domains: none found  
Cellular Localization: secreted

65 1 11 21 31 41 51  
MLHLSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQYEE GLFYAQKSKK 60  
FLMVIHLED QYSQLKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNS PDGQYVPRIM 120  
70 FVDPSTLVRA DIAGRYNRL YTYEPRDLPL LIENMKKALR LIQSEL

**A140 DNA SEQUENCE**  
Gene name: TMPRSS3a  
Unigene number: Hs.298241  
Probeset Accession #: AI538613  
75 Nucleic Acid Accession #: AB038157  
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTGATGCC GTGTGAGCCA 60  
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGTGC CTACTATCTC TTCCGTGGTG 120  
CCATCTACAT TTTTGGGACT CGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240

TCATTCGGAT CGCTTTTGG CCTTGATGAT TTGAAAAATAA GTCCTGTTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTGCT CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCAATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACCGAAATGT TGCCTGTGCC CAACCTGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGGT TACCTTGCA GTCACAGCCT GTGGTCATAG AAGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCAGCCCTCT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGAATTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGGACAA TCCAGGCCCA TCCACATGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTACAGTCCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGGGAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTGTC TGAACCAAGC GGCCTGCCCT TTGATTTCCT ACAAGATCTG CAACCAAGG 1320  
 GACGTGTAGC GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCGTG TCACTCTCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTGT AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTG GACTCCCTG TAGGAACTG CACACGAGCA GACACCTCTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCTGTTGTTA AGCGATTCTC 1860  
 TTGCTCAGC TTCCCTCAGC GCTGGGACCA CAGGTGCCCG CCACACACCC CAACATAATT 1920  
 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGTCTCT AAACCCCTGA 1980  
 CCTCAATGA TGTGCTGCT TCAGCTCTCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040  
 AGCCTAGCC TCACCTCTCT TCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTCT 2160  
 ACAGATAAG CAGTTATGTG ACCTACGTG CAAGGCCACC AACAGCCAT CAGAAAAAGC 2220  
 GCACCAGCCC AGAAGTGACG AACTGCAGTC ACTGCAGTT TTTCTCTCTA GGGACCCAGAA 2280  
 CCACACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTTGTAGC ATTTGGTGTCT TGACGTATTA 2400  
 TTGTCTTTG ATTCCAAATA ATATGTTTCC TTCCTCATA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAA

**A141 Protein sequence:**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFPF IIVIGIIALI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLFQVF 120  
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEQPFREFV SIDHLLPDDK 180  
 VTALHSHSVV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240  
 LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLFNSEE NFPDGVKVCWT SGWGEDTGA GDASPLVSHA 360  
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQCGD SGGPLVQER RLWKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEHQMRL DLKT

**A142 DNA SEQUENCE**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CCAACAGAT TTGCAGATCA AGGAGAACC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60  
 CTGAGATCTT TGCATAGCT ACATCTCTAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120  
 CGGCTGCTCC TATTGCTGAG CTGCTGGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180  
 AGACCCAGCT GTGCTCTGG ATGTTTTTAC CACAAGTCCA ATTGCTATG TTAATCTCAG 240  
 AAGCTGAGGA ACTGGTCTGA TGCAGAGCTC GAGTGTCACT CTTACGGAAG GGGAGCCAC 300  
 CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360  
 CAGAGAAGCC AGCCGATATG GATTGGCTCT CACGACCCAC AGAAGAGGCA GCACTGGCAG 420  
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480  
 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540  
 AACAAAGGCC AACACTTCTCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600  
 AACTCTCTCA CCAGCCCGCT CCTCTTCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660  
 TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAGGGGCC CTACTACACT GGCTTTTTTA 720



GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780  
 CCCCCCATC CCTTTCACCA GTATCCTTCT TCCCTCCTCC CTTGTCTCTG GCTGTCTCGA 840  
 GCAGCTTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900  
 AAAGATTGGA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960  
 ACACCCCTTCT GCCTCTCTCT CATGCTCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020  
 TTTTCTCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080  
 TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

**A143 Protein sequence:**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

1 11 21 31 41 51  
 MASRSMRLLL LLSCLAKTV LGDIIMRPSG APGWYFHKSN CYGYFRKLNN WSDAELEQCS 60  
 YNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120  
 KSMGGNKHCA EMSNNNFLT WSSNECNKRO HFLCKYRP

**A144 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51  
 GGGGAACACC GGGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60  
 TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120  
 CCTCGAGACC GTGCGCGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACGTGTGG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCGATCCAAA CGTATCTTAC 360  
 GAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCGTAAAAAT GGCAGGGGTC 420  
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540  
 AGACAGGCTG GTTGTGTTGT AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660  
 TCATGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGGA 720  
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840  
 AGGACCCACA CGACCTCATG TTCAACAATC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900  
 CAGTGGGCTT GGACCGGGAA AAGTCCCTGT AGTACACACT GACCATCCAG GCCACAGACA 960  
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020  
 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCTGAG AATGCAATG 1080  
 GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCACCTCA CCAAGTGGC 1140  
 GTGCCACCTA CCTTATCATG GGGGCTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200  
 CTGAGACCTA CGCTGACATC CTGACCAACA GGAAGGGTTT GGATTTGAG GCCAAAAACC 1260  
 AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCACCAACT 1320  
 CCACAGCCAC CATAGTGGTC CAGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC 1380  
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GAGCCTGTG TGTGTCTACA 1440  
 CTGCAGAAAG CCCTGACAA GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500  
 CAGGTTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTGACCC 1560  
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCCACTACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGCCC AGTCCCTGAG CCCGTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740  
 ACGTGTGAA CATACGGAC AAGGACCTGT CTCCCAACAC CTCCCTTTC CAGGCCACG 1800  
 TCACAGATGA CTACAGATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTCT CTGAAGCAGG ATACATATGA CGTGCACTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGAAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGAGGCC CTTCTACTCT CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGCTCTG 2220  
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCCCG CCTACGACAC CCTCTTGGTG TTGCACTATG 2400  
 AGGCGAGCGG CTCGAGAGCC GGTCCCTTGA GCTCCCTCAC CTCTCCGCCC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGTGGCGG GGAGGACGAC TAGGCGGCTT GCTTCAGTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTCA 2580  
 CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTCA 2640  
 GGAAGTGGCC GTAGCAACTT GGGGAGGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCTC TTAGGATGAG AGGAATGTGG GCAGTTTGGC TTCAGCAGTG AAAACCTCTC 2760  
 CACCTGGGCC AGGGTTGCTT CAGAGGCCAA GTTTCAGGAA GCCTCTTACC TGCCGTAAAA 2820  
 TGCTCAACCC TGTGTCTGCG GCTGGGCTG GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCACTTAAT TTTTTTTTTT AATGCTATCT 2940

TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAAG GCTGCTGGGC CCACTGGCCG 3000  
 TCCTGCATT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTG TGCCTAGGTT GCCCTTATT TTTATTTTC CCGTTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTT TATTAAGAA A

#### A145 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 ProbeSet Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 MGLPRGPLAS LLLQLVCWLQ CAASEPCRAV PREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDHV VAPISVPENG 120  
 KGFPFQRLNQ LKSNKDRDRTK IFYSITGPGA DSPPEGVFAV EKETGWLILLN KPLDREELAK 180  
 YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSGST TAVAVVEILD ANDNAPMFDP QXEAHVFPEN AVGHEVQRLT VTDLADPNPS 360  
 AWRATYILMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMPD DSGQVTAAGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLLID 540  
 VNDHGFPVEP QKITICNQSP VRHVLNITDK DLSPTSFPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDK HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFLF LVLLLVVRKK RKIKEPLLLP EDDTRDNVYF YGEEGCGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

#### A146 DNA SEQUENCE:

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 ProbeSet Accession #: M86699  
 Nucleic Acid Accession #: NM\_003318  
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGAATTCCTT TTTTITTTTT TTTGAGATGG AGTTTCACCT TTGTTGGCCA GGCTGGAGTG 60  
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCTCCCGG GGTTCAGCGC ATTCTCCTGC 120  
 CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180  
 CTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240  
 AACTCAGGTG CAGGATCTGC CTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAACCTG 300  
 TGCTGGCTG ATTCTTTTTT TGTGTGTGGA TTTTGAAC AGGCTCTCCC TTGGTGGCCC 360  
 AGGCTGGAGT GCAGTGGTGC GATCTGGCT CACTATAACC TCCACCTCCT GGTTCCAAGT 420  
 GATCTCCCA CAAGTAGCTC CTGAGTAGCT GTGATTACAG CGGTGCACCA CCACACCCGG 480  
 CTAATTTTTG TATTTTTATT AGAGACAGGG TTTCAACATG TTGGCCAGGC TGTCTCATAA 540  
 CTCTGGACT CAGGGATCC GCCTGCCTCC ACTTCCCAA GTCCCGAGAT TACAGGTGTG 600  
 AGTCACCATG CCTGACCTTA TAATCTTAA GTCATTTTT CTGCTCCATT TCCTCCTTAG 660  
 GGTCTCTACA ACAATCTGCG ATTAGCGGT ACAATAATCC TTAACCTCAT GATTCACAAA 720  
 AGGAAGATGA AGTGATTATC GATTTAGAAA GGGGAAGTAG TAAGCCCAT GCACACTCCT 780  
 GGATGATGAT CCTAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA 840  
 TTTGGTTTAA ATTAATTATC TAAATATCTA AAACATTTT TGGATACATT GTTGATGTGA 900  
 ATGTAAAGCT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTCCCCAG 960  
 TGCAGTTTTT TGTAGAAATG GAATCOGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT 1020  
 CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080  
 AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAAC GTTAACCCAA 1140  
 TTATGATGAT GGCAAAACAC CCAGAGGACT GGTGAGTTT GTTGCTCAA CTAGAGAAAA 1200  
 ACAGTGTTC GCTAAGTAT GCTCTTTTAA ATAAATGAT TGGTCGTAC AGTCAAGCAA 1260  
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGTAGA ATTCAAGTGA 1320  
 GATTGTGCTA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG 1380  
 CCAAGAGCAA CTGCAAGAAA TTTGCTTTT TGCATATATC TTTTGCACAA TTTGAACGTG 1440  
 CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCCTCAAAA AGCTGTAGAA CGTGGAGCAG 1500  
 TACCACTAGA AATGCTGGA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560  
 TTTCAAGAGA GGAAGAAGAG AATTATACAG CATCTACGGT ATTAAGTGC CAAGAATCAT 1620  
 TTTCCGGTTG ACTTGGGCAT TTACAGAATA GGAACAACAG TGTGATTC AGAGGACAGA 1680  
 CTACTAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740  
 ACCGGAATTC TTGAGACAAA ACTAACAAAA CTAACAGTC ATGCCCATTT GGAAGAGTCC 1800  
 CAGTTAACTT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGTACCTT 1860  
 GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGTTGTG CCGGATCTA 1920  
 AACCAAGTGG AATGATTTC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980  
 TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATAA 2040  
 CCTGAAGAA TAAAACGGAA TCAAGTCTTC TAGCTAAATT AGAAGAACT AAAGAGTATC 2100  
 AAGAACCAGA GGTCCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160  
 GTATTAAACA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCGGAG TTAGCCCGAA 2220  
 AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAA 2280  
 AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGT AAGACACCAA 2340

GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT 2400  
 TTCCACCTGC TTGTGAGTTG TCAACACCTT ATGGCCCAACC TGCCTGTTC CAGCAGCAAC 2460  
 AGCATCAAT ACTTGCCACT CCACCTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520  
 ATGAATGCAT TTCCGGTTAAA GGAAGAATTT ATTCATATT AAAGCAGATA GGAAGTGGAG 2580  
 5 GTTCAAGCAA GGTATTTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640  
 TGAACCTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700  
 TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG 2760  
 ACCAGTACAT TAACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2820  
 10 AGAAAAATC CATTGATCCA TGGGAACGCA AGAGTACTG GAAAAATATG TTAGAGGCAG 2880  
 TTCACACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCACT AACTTTCTGA 2940  
 TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAATG CAACAGATA 3000  
 CAACAAGTGT TGTAAAGAT TCTCAGGTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060  
 TCAAAGATAT GTCCTCTCC AGAGAGAATG GGAAATCTAA GTCAAGATA AGCCCCAAA 3120  
 15 GTGATGTTG GTCCTTAGGA TGTATTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180  
 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG 3240  
 AATTTCCCGA TATTCCAGAT AAGATCTTC AAGATGTGT AAAGTGTGT TTAATAAGGG 3300  
 ACCCAAAACA GAGGATATCC ATTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360  
 CTCATCCAGT TAACCAATG GCCAAGGGA CCACTGAAGA AATGAAATAT GTTCTGGGCC 3420  
 20 AACTTGTTG TCTGAATTCT CTAACCTCCA TTTTGAAAGC TGCTAAAAC TATATGAAC 3480  
 ACTATAGTGG TGGTGAAAGT CATAATCTT CATCTCCAA GACTTTTGA AAAAAAGGG 3540  
 GAAAAAATG AATTGCAATT ATTGTAATG TCAGATAGGA GGTATAAAT ATATTGGACT 3600  
 GTTATACTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660  
 ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3720  
 25 TTATGGCACT GTATATATTG TAGACTTGT TTCTCTGTTT TATGCTCTTG TGAATCTAC 3780  
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAATCTTG 3840  
 TAAATAAAGT TTTGCGCTA AAATGA

**A147 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51  
 MNKVRDIKNK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLKLEKNS 60  
 VPLSDALLNK LIGRYSAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120  
 ANCKKFAFVH ISFAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLS 180  
 45 EEEKNLNSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR 240  
 NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRESC RDLVVPVSGSKP 300  
 SGNDSCELRN LKSVQNSHFQ EPLVSDKSS ELIITDSITL KNKTESSLLA KLEBTKEYQE 360  
 PEVPESNQKQ WQAKRKSECI NQNPAAASNN WQIPELARKV NTEQKHTTFF QPVFVSVSKQS 420  
 PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFF PACQLSTPYG QPACFQQQQH 480  
 50 QILATPLQNL QVLASSANE CISOVKRIYS ILKQIGSGGS SKVQVQVLEK KQIYAIKYVN 540  
 LEEADNQTLQ SYRNEIAYLN KLQHQHSDKII RLYDYEITDQ YIYMVMECCN IDLNSWLKKK 600  
 KSIDFWERKS YWKNMLEAVH TIHQHGIHVS DLKPANFLIV DGMKLIDFG IANQMOPDIT 660  
 SVVDSQVGT VNYMPEPAIK DMSSSRENGK SKSKIIPKSD VWSLGCILYI MTYKTKPFQ 720  
 IINQISKLHA IIDPNHEIEF PDIEPKDLQD VLKCKLKRDP KORISIPELL AHPYVQIQTH 780  
 55 FVNQMAKGT EEMKYVLQQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK 840  
 K

**A148 DNA SEQUENCE**

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTCTTTTAAA TTTCTTTCTA GGATGTTTCA TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGGA TGAATGGACA 120  
 70 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCTGTTT TATTTTITTT 180  
 TCTAATTTCT TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240  
 TACCTGTTGG CTAATTTAGC TGCTGCGGAT TTCTTCGCTG GAATTCGCTA TGTATTCTCG 300  
 ATGTTTAAAC CAGGCCAGT TTCAAAAAC TTGACTGTCA ACCGCTGGTT TCTCCGTCAG 360  
 GGGCTTCTCG ACAGTACTCT GACTGCTTCC CTCACCAACT TGCTGTTTAT CGCCGTGGAG 420  
 75 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAA GAGGGTGACA 480  
 CTGCTCATTT TGCTTGTCTG GGCATCGGCC ATTTTATATG GGGCGGTCCC CACTGCGGC 540  
 TGAATTGCC TCTGCAACAT CTCTGCTGCT TCTTCCCTGG CCCCATTITA CAGCAGGAGT 600  
 TACCTGTTT TCTGGACAGT GTCCAACTCT ATGGCCCTTC TCATCATGGT TGTGGGTGAC 660  
 CTGCGGATCT ACCTGACGT CAAGAGGAAA ACCAACGTCT TGCTCCGCA TACAAGTGGG 720  
 80 TCCATCAGCC GCCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780  
 GCGTTTGTGG TATGCTGGAC CCGGGGCTCG GGGTTCCTGC TCCTCGACGG CTTGAACCTGC 840  
 AGGCAGTCT GCGTCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGCGGCT GCTCAACTCC 900  
 GTCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960  
 ATGATCTGCT GCTTCTCTCA GGAGAACCAC GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020  
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAACCTCTG GATGCCTCTC GGGCCACCCA GGTGATGACT 1140  
GTCTTAGG

5 A149 Protein sequence:  
Gene name: endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor, 7  
Unigene number: Hs.258583  
Probeset Accession #: NM\_012152  
Protein Accession #: NP\_036284  
10 Signal sequence: none found  
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
Cellular Localization: plasma membrane

15 1 11 21 31 41 51  
MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFF CLFIPFNSNL VIAAVIKNRK 60  
FHEFPFYLLA NLAAADFFPAG IAYVPLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120  
LVIAVERHMS IMRMVRHNSL TKKRVTLIL LVWAIAIFMG AVPTLGWNCI CNISACSSLA 180  
20 PIYSRSYLVF WTSVNLMAFL IMVVYLRIY VYVKKRTNVL SPHTSGSISR RRTPMKLMKT 240  
VMTVLGAFVW CWTPLGLVLL LDGLNCRQCG VQHVKNRFLI LALLNSVNP IYYSKDEDM 300  
YGTMKMIMCC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

## 25 Prostate

A150 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.293616  
30 Probeset Accession #: AW043782  
Nucleic Acid Accession #: none found  
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51  
AGCAACGAGC CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GCGCGCTGTG 60  
CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAAACAACT TCACCAATGA 120  
GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180  
40 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
GTGAAATGT GGGCCAACT TCTTCCCTTG TGCCAGCGGC ATCCATTGCA TCATTGGTCTG 300  
CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
AAACCCCTCTG CTTTGTCTCA CCGCCGCTCA CCACTGCAAG AACGGCCTCT GTATTGACAA 420  
GAGCTTCATC TGCATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
45 AAGTTCTCAA GAACCCGGCA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
TTACCCGAGC ATCACCCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
CTGCTGGCA CTGCTCTTGC ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCGCT 660  
GCACCGGCTG CAGCACCTCTG TGCTGCTGTC CCGCTTGGTG GTCTGGGACC ACCCCACCA 720  
CTGCAACGTC ACCTACAAAG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
50 GAATGCGTCG GAAGTAGGCT CCCCACCTCT CTACTCCGAG GCCTTCTGCTG ACCAGAGGCC 840  
TGCGTGGTAT GACCTTCCCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
CGACCTGCCC CCTTACCGCT CCGGTCCGCG GAGTGCCAAAC AGTGCCAGCT CCCAGGCAGC 960  
CAGCAGGCTC CTGAGCGTGG AAGACACAGC CCACGCGCGG GGGCAGCCTG GCCCCAGGGA 1020  
GGGCACTCAT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
55 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140  
TGCTCATGGG AAGCTCTTTA AGCAGCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
AACTATGTCT AACTTCCCTT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GGTCTCTCAGT 1260  
TGACATGATC TGTGTGCGT CTTTCTGTC AGGTCACTCT TCCTTGGGA CCGGAGATCA 1320  
CACCTCATCT TTTACATTA TTCTGTTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380  
60 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
CGCTGGAGCC AATTCTCTCT GCTGGGTAGT TACCTTAGAG CATTTGGGGA TTTGGGTTAG 1500  
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCAACCCCC CAAAAAATT CCAATTGAGC 1560  
ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAG TTGAGCAGAG TCAGTGGCCA 1620  
AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTCCG AACGTTATTG TGGTTTGTG 1680  
65 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTG CCAAGAAGATG 1740  
CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG 1800  
GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920  
ACCTGCCGTG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980  
70 GTATGTCCCT GTGSCCACA CCCAGCCTGT CTTGCTCATC CATGCAGCCT CAACACTGGC 2040  
CTCCAAAGTT CCCCTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTGG ACTTGAGGAC 2100  
ACTGTCTCT ATCAGAGGTG AGAGCCATGT TCAATACCT CAGCAAGCTC TCCTGGCTCC 2160  
CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
GGTCAGGCTC AGGCTCTTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
75 AGACAAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340  
TGAAACAGTG TGTGTGTTT TTCCCTTCTA GTTAAGGAC TATTTATATG TGTATAGGAA 2400  
AGCTGTCTCT TTTTGTGTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460  
ACACCTTGGC CCGCTGAGC CCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520  
ACATTGTGTC ATTGTGTCAC TTTGAGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580  
80 AGAGGGACTC CTCTCTCCCT CCGTGATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640  
TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAACGTT 2700  
AGGTGTTGTT TGGTCAAGAAA CCACACTGAC TGATGAGGGG TAAATGAGAA CAGGTAGAG 2760  
CCACTCCGGG GAGCTGTCTC CCATTGAGAA CTCTTCTCG CAGCTGAAGA AATGTTCACT 2820

AACCTGTTTG ACGCTAATTA AACAGAGGCC TGCAGGAAGT GGGGCTAAAG TGGCATTTCAG 2880  
 TGATCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTACAGAA 2940  
 AAGCTAGCCA CTGGTATTTT GTTTGTGTTA AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTTRA AATAGCACTT GAGTATTTT 3060  
 5 CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTTCATCT CTTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180  
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATAGT 3300  
 10 AGATAAGGGA TGCTACTATA TGCTTTTITA AACAAACAG GGACATTTTT ATTATAGATT 3360  
 TGATTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCACACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCCAACCAG 3540  
 AAATAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600  
 15 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTGT GTGTGCTTGC TTTTGTGTT GTGGTTAGGC TTGGTTTGT TTTTAAATTT 3780  
 TTATACTTTC TAATAAATT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840  
 AAMMAAAAC AMYWTGTTGG GGGCTTGGGC CTCGGAAGAA GTTTTAAAC CCACTTCGGG 3900  
 20 TGGGGCGCG GGGCCACGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960  
 GAAACCTCG CCAAGAAAAA GSTGGCGAGA ATTCCTCACA CCAGAAAAAA ACGCGCGGG 4020  
 GGAAACCGCA GAGTGTGCG TAAACACAC CGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

25 A151 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 30 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

35  
 1 11 21 31 41 51  
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60  
 40 EKECPKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCDPG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSF ICDGQNNQD NSDEESCESS QEPGSGQVFPV TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHQRKR NMLMLPVHR LQHPVLLSRL VVLDHPRHCN VTYNVNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPAP YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASQAASS LLSVEDTSHS PQPQPQEGT AEPRDSEPSQ GTZEV

45 A152 DNA SEQUENCE  
 Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 50 Probeset Accession #: T48536  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 GTCATATTGA ACATTCACGA TACCTATCAT TACTCGATGC TGGTTGATAAC AGCAAGATGG 60  
 CTTTGAACCT AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAGAACCT GGATACCAAC 120  
 CGGAAACACC CTATCCCGCA CAGCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180  
 CTCAGTACTA CCGTCCCCC GTGCCCCAGT ACGCCCGAG GGTCTGACG CAGGCTTCCA 240  
 ACCCGTCTGT CTGCACGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300  
 60 AGAAAGCACT GTGCATCACC TTGACCCCTG GACCTTCCTT CGTGGGAGCT GCGCTGGCCG 360  
 CTGGCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCGACT 420  
 CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480  
 GGGAGGACGA GAATCGGTGT GTTCGCCCTT ACGGACCAAA CTTCATCCTT CAGATGTACT 540  
 CATCTCAGAG GAAGTCTCTG CACCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 65 GGGCGGCTGT CAGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG 660  
 ATGACAGCGG ATCCACCAGC TTTATGAAG TGAACACAAG TGCCGGCAAT GTCGATATCT 720  
 ATAAAAAAT GTACCAAGT GATGCCTGTT CTCAAAGC AGTGGTTTCT TTACGCTGTT 780  
 TAGCTCGCG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840  
 CGCTCCCGG GGCCTGGCCC TGGCAGGTCA GCCTGCACTG CCAGAAGCTC CACGTGTGCG 900  
 70 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960  
 TTAACAAATC ATGGCATTGG ACGGCATTTG CGGGGATTTT GAGACAACTT TTCTGTTTCT 1020  
 ATGAGACCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAGACCA 1080  
 AGAACAAATG CATTCGCGTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140  
 AACCAGTGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATT 1200  
 75 CCGGGTGGG GGGCACCGAG GAGAAAGGGA AGACCTCAGA AGTGCTGAAC GCTGCCAAGG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAC CTGATCACAC 1320  
 CAGCCATGAT CTGTGCGCGC TTCCTGCAGG GGAAGCTCGA TTCTTGCCAG GGTGACAGTG 1380  
 GAGGGCTCTT GGTCACTTCG AACACAAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440  
 80 GTTCTCGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTACAGG 1500  
 ACTGGATTTA TCGACAAATG AAGGCAACG GCTAATCCAC ATGGTCTTCG TCCTTGACGT 1560  
 CGTTTTCAGA GAAACAAATG GGGCTGGTTT TGCTTCCCG TGCAATGATT ACTCTTAGAG 1620  
 ATGATTACGA GGTCACTTCA TTTTATTTAA ACAGTGAAC TGCTTGGCTT TGGCACTCTC 1680  
 TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCAGGCC TGCTCTCCTT AACCCCTTGT 1740

CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800  
 GTTGGAGGCT GCCCCCATTTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGGG 1860  
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920  
 GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGTGGTAGT 1980  
 TCCCCAGCCT ACTTCACAAG GGGATTITTC TGATGGGTTT TTAGAGCCCTT AGCAGCCCTG 2040  
 GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100  
 AAGGGGAACA GAAACATTTT TGTTCCTATG GGGTGAAGAT ATAGACAGTG CCCTTGGTGC 2160  
 GAGGGAAGCA ATTGAAAAAG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220  
 CATTGGGTGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCTCTC CTGACCTGTC 2280  
 TCCTAGCACC CTGGAGAGTG AATGCCCTTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340  
 ATGTGGGCTT CTTCAGGCTT GATAGTCATT GGAATTTAG GTCCATGGGG GAAATCAAGG 2400  
 ATGCTCAGTT TAAGGTACAC TGTTCCTATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460  
 CTGAGTTCAA AGCCATCTT

**A153 Protein sequence:**

Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 Probeset Accession #: T48536  
 Protein Accession #: NP\_005647.1  
 Signal sequence: none found  
 Transmembrane domains: 85-107  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60  
 SNPVVCTQPK SPSTGVTCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120  
 DSSGTCTNPS NWCDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VCQDDWNENY 180  
 GRAACRDMGY KNNFYSSQGI VDDSGSTFSM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240  
 CLACGVNLS SRQSRIVGGE SALPGANPWQ VSLHVNVDH CCGSIITPEW IVTAAHCEVK 300  
 PLNNPWHWTA FAGILRQSFM FYGAGYQVQK VLSHPNYDSK TKNDIALMK LQKPLTFNDL 360  
 VKPVCLFNP MMLQPEQLCW ISGNATPEEK GRTSEVLNAA KULLIETQRC NSRYVYDNL 420  
 TPAMICAGFL QGNVDSQCGD SGGPLVTSNN NIWMLIGDTS WSGSCAKAYR PGVYGNVMVF 480  
 TDWIYRQMK NG

**A154 DNA SEQUENCE**

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039

Unigene number: Hs.129179  
 Probeset Accession #: AI694767  
 Nucleic Acid Accession #: AI694767  
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CAGAGAGGCT GTATTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60  
 GGGGTCACAC ATTCTCTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCACAGTTC 120  
 AGCTTCTTCA TGATGGTGGG TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCCTA 180  
 ATAGGCTTCC CTGGTTTAGA AGAGGCTCAG TTCTGTTGGC CCTTCCCATT GTGCTCCCTC 240  
 TACCTTATG CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGGGGAC TGAGCACAGC 300  
 CTGCATGAGC CCATGTATAT ATTTCTTTGC ATGCTTTTCA GCATTGACAT CCTCATCTCC 360  
 ACCTCATCCA TGCCCCAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTIT 420  
 GATGCTTGTC TGCTACAGAT GTTGGCCATC CACTCTCTAT CTGGCATGGA ATCCACAGTG 480  
 CTGCTGGCCA TGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGGG CCATGCCACA 540  
 GTACTTACGT TGCTCTGCTG CACCAAAATT GGTGTGGCTG CTGTGGTGCG GGGGGCTGCA 600  
 CTGATGGCAC CCTTCTCTGT CTTCATCAAG CAGCTGCCCT TCTGCGCTC CAATATCCTT 660  
 TCCCATTCCT ACTGCTTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720  
 AATGTGCTCT ATGGCTTAT CGTCACTATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780  
 TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTTGGGCT TGACACGTGA AGCCACGGCC 840  
 AAGGCATTGG GCACTTGGCT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900  
 ATTGATTGT CCATGGTGCA TCGCTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCATC 960  
 TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020  
 ACAAGGAGA TTCGACAGCG CATCCTTCGA CTTTTCATG TGGCCACACA CGCTCAGAG 1080  
 CCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTACAGAT CCTCTGATTC AGATTTTAAT 1140  
 GTTAACATTT TGGAGACAG TATTCAGAAA AAAAATTTC TTAATAAAAA TACAACCTAG 1200  
 ATCCTTCAA TATGAACTG GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTCTTT 1260  
 GTTTCTTGC ACCATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320  
 TTTTCATTTT ACCATGCGAT CCAATCTAA ACTGCTTCTA CTGATGGTTT ACAGCATTCT 1380  
 GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA 1440  
 TAAACACAGA ATATAATAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500  
 ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560  
 AAATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620  
 AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680  
 ATGGACCTCT TTTTCTCTAT TTAATTTTCT TATCAACCTT TTAATTAGGC AAAGATATTA 1740  
 TTAGTACCTT CATGTAGCG ATGGGAAAAAT TGATGTTTCA TGGGGATCAG TGAATTAAT 1800  
 GGGGTATAC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860  
 GGAAGAACTG TTAAGAGAC CAACAGGCTA GTGGGTTAGA GATTTCAGA GTCTTACATT 1920  
 TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGTATTAG GAATTTCTCT 1980  
 GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGCTCTGG TCCAATTGCC 2040  
 AATTACCTGT GTCTTGAAG AAGTGATTC TAGGTTCAAC ATTATGGAAG ATTCTTATTC 2100  
 AGAAAGCTCT CATAGGCTT ATAGCAAGTT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160  
 TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220  
 TGAAGATAAC ATTGGCTTT TGAGTGTGAC TGTAGTCTG AAAAGTGGG AATCTTCAGG 2280

5  
10  
15

```

ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGGAACAGGG ACTTTGAGAC CGGGAAAGCA 2340
ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATTACATA 2460
TACTAAAACA TGTGATCATA TATGTGGTAA GTTTCATTTT CTTTTCATAT CCTCAGGTTC 2520
CCTGATATGG ATTCCTATNA CATGCTTTCA TCCCCTTTTG TAATGGATAT CATATTTTGA 2580
AATGCCTATT TAATACTTGT ATTTGCTGCT GGACTGTAG CCCATGAGGG CACTGTTTAT 2640
TATTGAATGT CATCTCTGTT CATCATGAC TGCTCTTTGC TCATCATTTA ATCCCCCAGC 2700
AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTTC TCAAACTGA 2760
TTCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTTCCTTGA TTTGGTATTA 2820
TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAGGTGAC ATGTGCAATT TTTATACCTG 2880
GCTCATAAAA CCTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTTGGGAAGC 2940
TATGTGTTAC ACAGAGTTAA TTAACCNAA AGGCCTGGNA ATTTTGTGN AANNAAACTG 3000
TGGCCNNGAG GCCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCCCTTT GTANTTTGGT 3060
AAGGAGGCCA GTTGGATAAG TGAAAAATAA AGTACTATTG TGTC

```

**A155 PROTEIN SEQUENCE**

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039  
 Unigene number: Hs.129179  
 Protein Accession #: not available  
 Signal sequence: none found  
 Pfam domain: 7tm\_1 [43-293]  
 Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295  
 Cellular Localization: not determined

30  
35

```

1 11 21 31 41 51
MVPDNGNESS ATYFILIGLP GLEEAQFWLA FPLCSLYLIA VLGNLTIIYI VRTEHSLHEP 60
MYIFLCMLSG IDILISTSSM PKMLAIFWFN STTIQPDACL LQMPAIHSLS GMESTVLLAM 120
AFDRYVAICH PLRHATVLTIL PRVTKIGVAA VVRGAALMAP LPVFIKQLPF CRSNILSHSY 180
CLHQDVMKLA CDDIRNVVYV GLIVIIISAIG LDSLLISFSY LLILKTVLGL TREAAKAFG 240
TCVSHVCAVF IFYVPPFGLS MVHRFSKRDR SPLPVILANI YLLVPPVLNP IVYGVKTKEI 300
RQRILRLPHV ATHASEP

```

**A156 DNA SEQUENCE**

Gene name: vasoactive intestinal peptide receptor 1  
 Unigene number: Hs.198726  
 Probeset Accession #: X77777  
 Nucleic Acid Accession #: NM\_004624.1  
 Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

45  
50  
55  
60  
65  
70  
75  
80

```

TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCCGCC TCACTCATGC 60
CTCCTCCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGTTGGCGG GTTAGCGGGC 120
TGGTGGTGGC GGGGGCCGGG GCTCGCTCTC GGGGAGCGCG GGGCGGATCT CGCGGCGCAG 180
GCGGCGGGCG CGAGGTGGGG GTGCGCGCGC GGAGGCGGCT CGAGCTTCGT GCTGCGGCGT 240
CGCTCTTGGG CTCTCTCGTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300
ACAGAGCAGT CTTGGAGGAG GCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360
GGGACAACCT CACCTGCTGG CCAGCCACCC CTCGGGGCCA GGTAGTTGTC TTGGCCTGTC 420
CCCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCCGCAA TGTAAGCCGC AGCTGCACCG 480
ACGAAGCCTG GACGCACCTG GAGCCTGGCC CGTACCCCAT TGCTGTGGT TTGGATGACA 540
AGGCAGCGAG TTTGGATGAG CAGCAGACCA TGTCTACGG TTCTGTGAAG ACGGCTACA 600
CCATTGGTGA CGGCTGTGCC CTCGCCACCC TTCTGGTGGC CACAGCTATC CTGAGCCTGT 660
TCAGGAAGCT CCATGTCACG CGGAAGTACA TCACATGCA CCTCTTCATA TCCTTCATCC 720
TGAGGGCTCG CGCTGTCTTC ATCAAAGACT TGGCCCTCTT CGACAGCGGG GAGTGGGACC 780
AGTGCTCCGA GGGCTGGGTG GGCTGTAAAG CAGCCATGGT CTTTTCCTAA TATTGTGTCA 840
TGGCTAACTT CTCTGGCTGG CTGGTGGAGG GCCTCTACCT GTACACCCGT CTGCGGCTCT 900
CCTTCTTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960
GCACATTCAC CATGGTGTGG ACCATCGCCA GGATCCATTT TGAGGATTAT GGTCTGTCTA 1020
GGTGTGGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCCTCACTT 1080
CCATCTTGGT AAACCTCATC CTGTTTATTT GCATCATCCG AATCCTGTCT CAGAAACTGC 1140
GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACTC AAGGCTAGCC AGGTCCACAC 1200
TCCTGCTGAT CCCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CGGGACAATT 1260
TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TGCTGTGGG GTCTTTCAG GGTTTTGTGG 1320
TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380
GGCGCTGGCA CTTGAGGGGC GTCTGTGGCT GGAACCCCAA ATACCGGCAC CGGTGGGAG 1440
GCAGCAACGG CGCCACGTGC AGCACGACGG TTTCCATGCT GACCCGCGTC AGCCAGGTG 1500
CCCGCGCTC CTCCAGCTTC CAAGCGAAG TCTCCCTGGT CTGACCACCA GATCCACAGC 1560
CCAAGCGGCC CCTCCGCCCC CTTCCTCACTC GCAGCAGAGC CGGGGACAG AGGCCTGCC 1620
GGGCGCGCCA CGCCCGGGCC TGGGCTGGGA GGCTGCCCCC GGGCCCTGGG TCTCTGGTCC 1680
GGCACTCTCT AGAGAAAGCA GOCCTAGAGC CTGCTGGAGG CGTTCTAGC AAGTGAGAGA 1740
GATGGGAGCT CCTCTCTGG AGGATGCAGG TGGAACTCAG TCATTAGACT CCTCTCCAA 1800
AGGCCCCCTA CGCCAATCAA GGGCAAAAG TCTACATACT TTCATCTGA CTCTGCCCCC 1860
TGCTGGCTCT TCTGCCCAAT TGGAGGAAG CAACCGGTGG ATCCTCAAAC AACACTGGTG 1920
TGACCTAGG GCAGAAAGGT TCTGCCCGGG AAGGTCAACA GCACCAACAC CACGCTAGTG 1980
CCTGAAATTT CACCATGCT GTCAAGTTC TTTGGTTAA GCATTACCAC TCAGGCATTT 2040
GACTGAAGAT GCAGCTCACT ACCTATTCT CTCTTAAGC TTAGTTATCA GCTTTTAA 2100
GTGGGTATT CTGGAGTTT TGTTTGGAGA GCACACCTAT CTTAGTGGT CCCCACCGAA 2160
GTGAGCTGGC CCTCGGGTGA GTCTGGTGGG AGGACGGTGC AACCCAAGGA CTGAGGAGT 2220
CTGAAGCTTC TGGGAAATGA GAAGGCAGCC ACCAGCAAT GCTAGGTCTC GGACTAAGCC 2280
TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GGACTCTGT ACACAGCCA 2340
TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTTGTCCACC 2400
CACCTATGTG CCAACTGTGG TAACTAGGCT CAGAGATGTG CACCATGGG CTCTGACAGA 2460

```

5  
AAGCAGATCC TCACCTGCT ACACATACAG GATTGAACT CAGATCTGTC TGATAGGAAT 2520  
GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACGAGCCAG ATCCTCTTGG 2580  
TTATTTGTTT ACCACTTGTA TTATTAATGC CATTATCCCT GAATTCOCCT TGCCACCCCA 2640  
CCTCCCTGAG AGTGTGGCTG AGGAGGCCTC CATCTCATGT ATCATCTGGA TAGGAGCCTG 2700  
CTGGTCACAG CCTCTCTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CTAACCCACA 2760  
CCTCTGCCAG AAGATCCCCT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820  
GGAAAAAAA AAAA

10 A157 Protein sequence:  
Gene name: vasoactive intestinal peptide receptor 1  
Unigene number: Hs.198726  
Probeset Accession #: X77777  
Protein Accession #: JC2195  
Signal sequence: none found  
15 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430  
Cellular Localization: plasma membrane

20  
1 11 21 31 41 51  
MPPFPLLSLR RLGGWSAVT RLVVAAAGAR SRGGRGGRG AGGGGRGGVA RRRRLRLRAA 60  
RSLGSSSLQE ECDYVMQIEV QHKQCLEEAQ LENETIGCSK MWDNLTCWPA TPRGQVVVLA 120  
CPLIPKLFSS IQGRNVRSC TDEGWHLEP GPYPACGLD DKAASLDEQQ TMFYGSVKTG 180  
25 YTIYGLSLA TLLVATAILS LFRKLHCTRN YIHMFLFISF ILRAAVFIK DLALFDSGES 240  
DQCSSESVGC KAAMVFFQYC VMANFFWLLV EGLYLYTLA VSFPSERKYF WGYILIGWGV 300  
PSTFTMWIT ARIHFEDYGL LRCWDTINSS LWWIKGPIL TSILVNFIK ICIRILLQK 360  
LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFPD NFKPEVKMVF ELVVGSFQGF 420  
VVAILYCFIN GEVQALRRK WRRWHLQGV LWNPKYRPS GSGNATCST QVSMLTRVSP 480  
GARRSSSFQA EVSLV

30 A158 DNA SEQUENCE  
Gene name: ESTs  
Unigene number: Hs.29383  
Probeset Accession #: AW207206  
35 Nucleic Acid Accession #: AL133619  
Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

40  
1 11 21 31 41 51  
ATGAGCGGTG CGGGGGTGGC GGCTGGGAGC CGGCCCCCCA GCTCGCGGAC CCGGGGCTCT 60  
CGGGCGCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCGGCA GAGCCCGCAG 120  
CTCAGGCAGA GCGAGCCGCA GAAACGGAAC CTGGACCTGG AGAAAGCCCT GCAGTTCCTG 180  
CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240  
45 GAAACAAGG GTGAGCGGCG GCGGGGCCCT AGGCCCGCCC TGCCCTCCCA GGCACACTCA 300  
ACACTGCGCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360  
GGGGGAACAC AGGACGGGGA GCGCCCTCCAG ACTGTCTCTG CCCACCTGGC TGCACTGGCC 420  
CCTGTATGCG AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC GCCTACTCTT 480  
AGCGGTGGCT GGAAGATGTT ATGCAGCCAA GCACAGCAGC TGCTGCTCTC GGGGAAGCCA 540  
GGGCTGAGG TCATTGCAAG GCGGCAGGTG GCCACAGGCT GCTCCCCAGA CCTCCTCTCT 600  
50 CCAAGTAGAG CTGAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660  
CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
GCAGCAACCA TGGGACAAA GGGAGGAAGC AGAGTCTGT TCCCTTGCCA CTGTCTCAAG 840  
GCACTTCCCC ATCCTGACAG CCGCCCCCAC CCAGCCGAGC ATCCTGGGCT GTGGTCTCAA 900  
55 GCCTACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGG 960  
TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCTTA GGGCTCTCCC TTCCAGGGA 1020  
GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
CTGTCTGGG CAAAGTGTGG CCAAGTCCG CAGCCCGAGC CCTCAGTGC TGGGGAAGCT 1140  
60 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTCCGGACCT GCTGTTCAT GTGTCCCAAG 1200  
GAGTGTGAGT GGAAGAGGCG CAGGCTTCC CAGGAGGAGT TGGGTAGAGC CCGGAGGAGC CAGCCCTGCC 1260  
AGGCTGAGG AGGCTCTCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGGG 1320  
GGGCTAGAG CCGACACTGT GCGCTCTCTT GCAGACAGCC TCTCATGTC AAGCTTCCAG 1440  
TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CAGGCCGGCC 1500  
65 TCCTTCAACA AGCAAGATT AAAAGCTGAC GTCTCCGAGA AGGCCAGCTT GGAAGAGGAG 1560  
CCCTACTTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAGGGCA GGCCAGAAAG 1620  
GAGAAAGCAG AGGCTCTTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680  
AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCTGCG CCCTTCCCTT GCGAAAGCCC 1740  
70 ACCACACTTA GGCAGTGGGA AGTGTCTATC CGCGAGCTGT GGAATACCAA CCTCTGCAG 1800  
ACCAAGAGG TGCGGACCTT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGAGGCC 1860  
CCGAGGAGAG CTAGCTTTCC CAGGAGCCAA GAAGCCAGCG ATTTCCCAA GGTCTCCACC 1920  
AAGAGCTCT CCAAGAAATG CTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980  
CTGAGGAGA CCGGAAGAA CAATTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCA 2040  
75 AAAGGGGCC TGCATCGCTC AGTGCTTTGA

80 A159 Protein sequence:  
Gene name: ESTs  
Unigene number: Hs.29383  
Probeset Accession #: AW207206  
Protein Accession #: T43457  
Signal sequence: none found  
Transmembrane domains: 303-322  
Cellular Localization: not determined



```

1      11      21      31      41      51
5      |      |      |      |      |      |
MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPQAH S TLPLPQHRNT AINSSTRILGS 120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180
GFEVIAGRQV ATGCSPLPFP PSRAEMGRNP WDSFPCPARSL PQIAAVARPR ISSPMALSPH 240
MLGAQGIWTH SIQGSPLPAIW AATMTKGG S RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300
10     AHFPLSLGLG L TSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVVEGGP FPSRCGNSSE 360
LFWAKCGPSR QPQPC SAGDA DRTREEAMLS LGTCCSMCPK PSCFPDGP SG NHLSRASAPL 420
GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPKGKRGRLA GGSADTVRSP ADSLSMSSFFQ 480
SVKSISNSAN SQSKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGOARK 540
EKAESNAGA ACMGNSQHGG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELMNTNLLQ 600
15     TQELRHLKSL LEGSQRQPAQ PEEASFPRDQ EATHFPKYST KSLSKKCLSP PVAERAILFA 660
LKQTPKNFA ERQKRLQAMQ KRRLHRSVL

```

20 A160 DNA SEQUENCE  
 Gene name: LIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Probeset Accession #: U41060  
 Nucleic Acid Accession #: NM\_012319.2  
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
30     |      |      |      |      |      |
CTCGTGCCGA ATTCGGCAGC AGACCGCGTG TTGCGGCGCTG GTAGAGATT TCTCGAAGACA 60
CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCCTGGGA CAACGAGGCC 120
GCGGAGACGA AGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCCC 180
TCTCTGT CAC AATCCOCTT CATGAAC TAA AAGCAGCTCG TTTCCCCCAG ACCACTGAGA 240
AAATTAGTCC GAATTGGGAA TCTGGCATT A TGTGTACTT GGCAATTTC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360
35     TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCAAGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540
CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTCAG 600
40     GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTTC 780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACTAC AAAGAGCCGG GTGAGCCGGC 840
TGGCTGGTAG GAAAACAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
45     GAAACACAAA TGAAATCTCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960
GCATGGGCAT CCAGGTTCOG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
TCAACCAAA TGAATGCTGA TCTGTCTGA TTCATACAAG TGAAGAAGAG GCTGAAATCC 1080
CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
TCAAGTTCTCT GTCTCTGCTG GGGGTATCT TAGTGCTCT CATGAATCGG GTGTTTTC 1200
50     AATTTCCTCT GAGTTTCTCT GTGGCACTGG CGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
CAATGCAAA TGAAGAGAGA CCACTTTTCA GTCACTGTCT TTCTCAAAAC ATAGAAGAAA 1380
GTGCTTATTT TGATTCACAG TGAAGGGTCT TAACAGCTCT AGGAGGCCGT TATTTCTATG 1440
TTCTTGTGTA ACATGTCTCT ACATTTATTA AACAATTAA AGATAAGAAG AAAAAGAATC 1500
55     AGAAGAAAAC TGAAATGAT GATGATGTGG AGATTAAGAA CGAGTTGTCC AAGTATGAAT 1560
CTCAACTTTT ACAAATGAG GAGAAAGTAG ATACAGATGA TCGAAGTGA GGCTATTTC 1620
GAGCAGACTC GAAAGAGAGC TCCCACTTTG ATTCTCAGCA GCGTGCATCT TTGGAAGAAG 1680
AAGAGGTCTAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
GGTCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
60     TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCA AACCACCATC 1860
CTCAGCTGCA CAGCCAGCGC TACTCTGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT 1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAA TTT CAGCGATGGC CTAGCAATTG 1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGTCT GTGTTCTGTC 2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100
65     AGCAGGCTGT CCTTTATAAT GCATTGTGAG CCATGCTGGC GTATCTTGA ATGGCAACAG 2160
GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGT GATATTGTGA CTACTGCTG 2220
GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
GTTTGGAAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTC CGTATAAATT 2400
70     TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGTTCAT 2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATT 2520
TTGATTGAA TATTGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTTAAGT 2580
TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640
TAAACAAGAG ATTTGGCATG ACATGTTCTG TAGTGTTCAG GGAAAAATGT CTTTAATGCT 2700
75     TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG 2760
TGTTTAGGAA TAAGAAATGT CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
AGCAAGAGAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAAG 2940
CAGAATTAGT ATAGATACA TTCAATTAAC ATTTTGTCA GGATTATTTC CGGTAAAAAC 3000
80     GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTAAAC TTTGTATAAT ACAGAAATCT 3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120
TTGCGCGGGG TTATATACCA GATGAATACA GTGAGTAGTT TAGTATCAC CAGACTGGGT 3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGGTTC ACCTGGTTTA 3240
CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAGTAC ACCTAAGTA 3300
TCATTGTATT CGATTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATGTT 3360

```

GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420  
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

# 5 A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated  
Unigene number: Hs.79136  
Protein Accession #: NP\_036451  
Signal sequence: 1-21  
Pfam domain: Zip[591-743]  
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
MARKLSVILI LTFALSVTNP LHELKAAAPP QTTEKISFNW ESGINVDLAI STRQYHLQOL 60  
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHSDHS DHEHSDHER HSDHEHSDH 120  
EHHSDDHSDH HHNHAASGKN KRKALCPDHD SDSSGKDPN SQKGGAHRPE HASGRNVKD 180  
SVSASEVTST VYNTVSEGTG PLETIETPRP GKLFPKDVSS STPPSVTSKS RVSRLAGRKT 240  
NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGGMGIQV PLNATEFNYL CPAIINQIDA 300  
RSCLIHTSEK KAEIIPPKTYS LQIANVGGFI AISIISPLSL LGVILVPLMN RVFFKPLLSF 360  
LVALAVGTLG GDAFLHLLPH SHASHHSHS HEEPAMEMKR GLFSLHSSQ NIEESAYFDS 420  
TWKGLTALGG LYFMFLVEHV LTLIKQPKDK KKNQKKPEN DDDVEIKQL SKYESQLSTN 480  
EEKVDTDDRT EGYLRADSQE PSFDSQQA VLEEEVVMIA HAHPOEVYNE YVPRGCKNKC 540  
HSHFHTLQO SDDLIIHHHD YHHILHHHH QNHHPHSHS RYSREELKDA GVATLAWMVI 600  
MGDGLHNFSD GLAIGAAFE GLSSGLTSV AVFCHLPHE LGDFAVLLKA GMTVKQAVLY 660  
NALSAMLAYL GMATGIFIGH YAENVSMNIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720  
RWGYFFLQNA GMLLGGFIML LISIFEKIV FRINF

# 30 A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
CGCGGGCGCG GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGCAGAGA CCGCGGCGCT 60  
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120  
GTGAAGGAA AGGAAGATCA TTTCATGCCT TGTGTGATAA GGTCAGACT TCTGCTGATT 180  
CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300  
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360  
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
GACGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480  
GGTTCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG AACTCCCAT TCCTCATCAA 540  
AGAAAGATCA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600  
TGCCCTCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCCTTACTT 660  
ATATCTGTGA TCTGCTGTAG TTGCTCTTGT GTCCTTATCA TATTATTGTT TACTTCCGG 720  
TATAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780  
ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
TCAGGCTCCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900  
ATTGGAAGAG TCGCTATGCG GGAAGTTTGG ATGGGAAGT GGCCTGGCGA AAAGTAGTCT 960  
GTGAAGTGT TCTTACCAAC AGAGGAAGCC AGCTGGTCCA GAGAGACAGA AATATATCAG 1020  
ACAGTGTGA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080  
GGTCTCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTATGAT 1140  
TATCTGAAGT CCACACCTT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200  
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260  
CATCGAGATC TGAAGGATGA AAACATTCTG GTGAAGAAA ATGGAACTTG CTGTATTGCT 1320  
GACCTGGGCC TGGCTGTATA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
ACTCGAGTGG GCACCAAAAG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440  
AATCATTCCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTTGGGAG 1500  
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560  
CTAGTGGCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620  
CGCCCTCAT TCCCAACCG GTGGAGCAGT GATGAGTGTG TAAGGCAGAT GGGAAAACCTC 1680  
ATGACAGAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740  
ACACTTGCCA AAATGTGAGA GTCCCGAGAC ATTAACTCT GATAGGAGAG GAAAGTAAG 1800  
CATCTGTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
TAAGCATCCA CAGTACAGC CTTGAACATC GTCTGCTTC CCACTGGGTT CAGACCTCAC 1920  
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
TCTGTTTGA GCGGAGAAA CGTGGGTA ACTTGTTCAT GATATGATGC AT

# 75 A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.72472 / Hs.87223  
Probeset Accession #: AA250737 / U89326  
Protein Accession #: NP\_001194  
Signal sequence: 1-13  
Transmembrane domains: 128-144  
PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
 5 MLLRSAGKLN VGTKKEDGES TAPTTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60  
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCCTERN ECNKOLHPTL PPLKNRDFVD 120  
 GPIHHRALLI SVTVCSLLLV LIILPCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
 EQSQSSGSGS GLPLLQVORTI AKQIQMVKQI GKGRYGEVWM GKWRGEKAV VVFTTEEAS 240  
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 10 MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNIV KKNGTCCIAH LGLAVKFISD 360  
 TNEVDIPNPT RVGTKRYMPP EVLDESINRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420  
 EYQLFPYHDL VPSDPSYEDM REIVCIKKLR PSPFNRRSSD ECLRQMGKLM TECWAHPAS 480  
 RLTALRVKKT LAKMSSESQDI KL

A164 DNA sequence

15 Gene name: ESTs  
 Unigene number: Hs.157601  
 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 20 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 25 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60  
 TTTTATTGTC AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACTTC 120  
 OCTGGCGGTA GTTCTCCGA CCTCAGCCGG GTCCGGTGTG GCGGCCCTCT CCCAGGAGAG 180  
 ACAAACAGGT GTCCACGCTG SCAGCCGCGC CCCGGGCGCC OCTCCTGTGA TCCCGTAGCG 240  
 CCCCTGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300  
 TCGCGCTCTT CCTTCGCTTA TATCAACATG CCCCTTTCC TGTGTCTGGA GCGCGTCTGT 360  
 30 GTTTTCTCTG TTTCCAGAGT GCGCCCATCT CTCCCTTCCC AGGAAGTCCA TGTAAGCAAA 420  
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480  
 ATCATGTTTC TGTAGATGCG GTCTAACAGC GTCGGGAAGG GGAGCTTTGA AAGGTCCAAG 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CGAGAGGGGT CAGAGTGGGA 600  
 GCATTCAGT TCAGTTCAC TCCTCATCTG GAATTCCTCT TGGATTCATT TTCAACCCAA 660  
 35 CAGGAAGTGA AGGCAAGAA CTAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720  
 CTGTCTCTGA AATCCTTCT GCACAGAGGG TTGCTGGAG GCAGAAATGC TTCTGTGCC 780  
 CAGATCTCTA TCATCTCTAC TGATGGGAAG TCCAGGGGG ATGTGGCACT GCCATCCAAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGG TCAGGTTTCC CAGGTGGGAG 900  
 40 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGG TGCTGTGGC TGAGCAGGTG 960  
 GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCACGGGCC 1020  
 AGCCAGATCG GGAAGGTCTG GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080  
 GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GSATCGCGGC GSACCCCTGC GGTGCTGGCT 1140  
 GCACACTGCT CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGTC CACTGCTAC 1200  
 45 AGGACCACTT GCGGAGGCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260  
 CCAGAGGAC TGGAGCGGTA CCAATGCCTC TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320  
 TGTGCTCTGA AGTCTGACCT GGAATGCAGG GTGCACTCC TCTTCTGCT GGACAGCTCT 1380  
 GCGGGCACCA CTCTGGAAGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440  
 GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGAGCTG 1500  
 50 CTGGTGGCGG TGCTGTGGG GAGTACCCAG GATGTGCTGT ACCTGGTCTG GAGCTCGAT 1560  
 GGCATTCCTT TCGGTGGTGG CCCACCCCTG ACGGGCAGTG CCTTGCAGCA GCGCGCAGAG 1620  
 CGTGGCTTCG GAGGGCCCA CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGTTTGT 1680  
 CTCAGTGAAT CACACTCCGA GGATGAGGTT GCGGGCCAG CGCTCAAGC AAGGGCGCGA 1740  
 GAGCTGCTCC TGCTGGGTGT AGGCAGTGA GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800  
 55 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1860  
 GAGCTGCAAG GGAAGCTGTG CAGCCGCGAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1920  
 CTGCTCTTCA GTTTGACAC CTCTGCTCTA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980  
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGCGC 2040  
 CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCACCCG 2100  
 60 GCTGCGATGC TGGGGCCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160  
 ACGCCCTGTC TGACATCTTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGCCTGGT 2220  
 GCTGCCAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT 2280  
 GCGCAGAAC TGAGSAAACA TGGCATCTCT GTCTGTGTCG TGGCGTGGG GCCTGTCTTA 2340  
 AGTGAGGGTC TGCAGAGGCT TGCAGGTCCC CGGATTCCC TGATCCAGT GGCAGCTTAC 2400  
 65 CCGGACTGTC GGTACCAACA GGAAGTGTCT ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460  
 CCACTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCTG CTGTCAGAA 2520  
 GGGAGCTACC GCTGCAAGTG TCGGATGGC TGGGAGGGCC CCACTGCGA GAACCGTGAG 2580  
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGATTTC TTGAGAGGCC CTGAGGCAC 2640  
 ATGGCTCCCG TGCAGGAGG CAGCAGCCGT ACCCTCCCA GCACTACAG AGAAGGCCCTG 2700  
 70 GGCACTGAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760  
 TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 ATGCTGCTTA GAGCAAGAA AGCAGCTGAT GTCAACCACA AACGATGTTG TTGAAAAGTT 2880  
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940  
 CTGCCACCTT TCCCTTGAGG ATAAACRAGG GTCCTGAAG ACTTAAATTT AGCGCCTGA 3000  
 75 CGTTCCCTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060  
 AGGCCCTTAC TAGAGCATCC TTGGAAGCGC GAAGGCCACG GCCTTTCAAG ATGGAAGCA 3120  
 CAGCTTTTTC CACTTCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAGGGGG 3180  
 CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTGT GTGTGGAAGA GACTTGAAGA 3240  
 80 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGTGTGA TGATGGGGA GGGGCTGAGT 3300  
 TGTGATGGG CCCAGGCTCG GAGGGCCAG TAAATCGTT CTGAGTCTG AGCAGTGTCC 3360  
 ACCTGAAGG TCTTC

**A165 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPDLSFST QGEVKARIKR 120
MVFKGSRRTT ELALKYLLHR GLPGGRNASV PQILLIVTDG KSQGDVALPS KQLKERVTV 180
PAVGVRFPFW EELHALASEP RGQHVLLAQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSMK RVFLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVVKRFV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPIFRGGPT 420
LTGSALROAA ERGFSATRT GDPRFRVVV LLETSHSEDE VAGPARHARA RELLLLVGVS 480
EAVRALEEI TGSPKHMVMY GDPQDLFNOI PELQGLCSR QRPGCRTQAL DLVFMLDISA 540
SVGPENFAQM QSFVRSCALQ FEVNPVDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARF GVPKAVVLT GGRGAEDAAV PAQLRNNGI 660
SVLVVGVGV LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETFLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

```

**A166 DNA sequence**

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Probeset Accession #: AA011176  
 Nucleic Acid Accession #: AF272890  
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCCGC GCCCGGGCTT CTGGGGTGTG CCCCAACCAC GGCCAGCCG TGCCACACCC 60
CCCGCCCCCG GCTCTCCGAG CTCCGCGATGG GCGCGGGGGT GCTCGTCTGT GCGCGCTCCG 120
AGCCCGGTAA CCGTCTGCTCG GCGCGACCGC TCCCGGACGG CGCGGCCACC GCGCGCGCGC 180
TGCTGTGTCC CCGCTGCGCG GCGCGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGTCTA 240
CGCTGTCTCA GCAGTGAACA GCGGGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGTCTA 300
TGCTGTGTCC CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCGCGCG CTGCAGACGC 360
TCACCAACTC TTTCATCATG TCCCTGGCCA GCGCGGACCT GGTCTGTTGG CTGCTGTGTT 420
TGCGGTTCGG GCGCACCATC GTGCTGTGGG GCGCGTGGGA GTACGCTCC TTCTTCTGCG 480
AGCTGTGAC CTGAGTGAC GTGCTGTGGG TGACGGCCAG CATGAGACC CTGCTGTGTT 540
TTGCCCTGGA CCGCTACCTC GGCATCACCT CGCCCTTCGG CTACGAGAG CTGCTGAGCG 600
GCGCGCGCGC GCGCGGCTCT GTGTGACCGG TGTGGGCGAT CTGCGCCCTG GTGTCTCTTC 660
TGCCCATCCT CATGCACTGG TGGCGGGGCG AGAGCGAAGA GCGCGCGCGC TGCTACAAGC 720
ACCCCAAGTG CTGCACTTC GTCAACAACC GGGCCTAAGC CATCGCTCG TCCGTAGTCT 780
CCTTCTACGT CCGCTGTGTC ATCATGGCCT TCGTGTACCT GCGGTGTTTC GCGAGGCCCC 840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCTCGCGCGC CCAGCGCGGC 900
CGCCCTCGCC CTGCGCTCTG CCGCTCCCGG GCGCGCGCGC GCGCGCGCGA CCGCGCGGCT 960
GCGCGCGCGC GCGCGGCTCT GCGCGGCTGG CCAACGGGCG TGCGGGTAAG GCGCGGCTCT 1020
GCGCGCTGTG GCGCTCTGCG CCGCTCTTCC TGGCCACGTT GGTGAAGGCC TTCCACCGCG 1080
TCTTCAAGCT CTGCTGGCTG CCGCTCTTCC TGGCCACGTT GGTGAAGGCC TTCCACCGCG 1140
AGCTGTGTCC CGACCGCTCT TCGTCTTCT TCAACTGCT GCGCTACGCC AACTCGGCTCT 1200
TCAACCCCAT CATCTACTGC CGCAGCCCGG ACTTCCGCAA GGCCTTCCAG GCACTGTCTCT 1260
GCTGCGCGCG CAGGGCTGCC GCGCGGCGCC ACGGACCCA CGGAGACCGG CCGCGGCTCT 1320
GCGGCTGTCT GCGCGGCGCC GCGCGGCGCC CATGCGCGCG GCGCGGCTCT GCGGACGACG 1380
ACGACGATGT CGTGGGCGCC ACGCGGCGCG GCGCGGCTCT GCGGACGACG CCGCGGCTCT 1440
ACGCGGGGCG GCGCGGCGCG AGCGACTCGA GCGTGGACGA GCGGCTCTCG CCGCGGCTCT 1500
CCTCGGAATC CAAGGTGTAG GCGCGGCGCG GCGGCGCGCG CTGCGGCGCG GCGCTTCCAG 1560
GGGAACGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAAGTCTG AGCCCACAAT 1620
CCTGCTCTGA ATCATCCGAG GCAAGAGAGA AAGCCACGGA CCGTTCGACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGGAGAG TGGCTTCTG ATGTTCTCTG TGT

```

**A167 Protein sequence**

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Protein Accession #: AA011176  
 Signal sequence: none found  
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248  
 Pfam domain: 7tm\_1 [75-377]  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVIGA SEFGLNLSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG 60
MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMLGL VVFPGATIVV 120

```

WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLI TRARARGLVC 180  
 TVWALSALVS FLFILMHMWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240  
 AFVYLRVPRE AQKQVKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAATAP 300  
 LANRAGKRRL PSRLVALREQ KALKTLGIIM GVFTLCNLFP FLANVVKAFH RELVPDRLFV 360  
 FFWNLGYANS AFNPIIYCRS PDRKAFQGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420  
 PPSPGAASDD DDDDDVVGATP PARLLEPWAG CNGGAAADSD SSLDEPCRPC FASESKV

**A168 DNA sequence**

Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GCGTCCGCG CACACCTCC CGGCGCGCG CGGCCACCG CGCACTCCG CGGCTCTGC 60  
 CCGCAACCG TGAGCCATCC ATGGGGGTG CGGGCCGCA CCGTCCCGG GCGGCTGGG 120  
 CGGTGCTGCT GCTGCTGCTG CTGCTGCCG CACTGCTGCT GCTGGCGGG GCGTCCCGC 180  
 CGGGTCCGGG CCGTGCCTGG GGGCCGCGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240  
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGCAT CGATGAATGT GGAAATGAGC 360  
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGT 420  
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480  
 AGAACAAATG CGGCTGCCAG CATACCTGTG TCAACGTCT GGGAGCTAT GAGTGTGCT 540  
 GCAAGGAGGG GTTTTTCTG AGTGACAATC AGCACACCTG CATTACCGC TCGGAAGAGG 600  
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT TGTCGAAGAG GCCCAAGGG 660  
 GCAGCGTCCG CTGTGAGTGG AGGCCCTGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 TCTTGACCTG TAAOCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 GCGCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840  
 AGCGAGAGGA CACTGTCTGT GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900  
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG 960  
 ACCGCATCTG TAAAGATACT TCGACAGGTG TCCACTGCAG TTGTCTGTTT GGATTCACCTC 1020  
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAAGCCGCA AATGGAGGTT 1080  
 GTGATCATTT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA 1140  
 AATTATTAAAC AGATGAGAAG TCTTGCCAAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200  
 GTGACCAAGC CTGCAATCAAC CACCTTGGCA CATTGCTTTG TGCTTGCAAC CGAGGGTACA 1260  
 CCCTGTATGG CTTACCCAC TGTGAGAGCA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320  
 AGTCAGCGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAAGTCCAC CCTGGGTACA 1380  
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCTGCCCC ACAAGTGTGT 1440  
 CACCCCGTGT GTCCCTGCAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCTCAGAT 1500  
 GTCACTCTGG CATTCACTTC TCTTCAGATG TCACCAACAT CAGGCAAGT GTAACCTTTA 1560  
 AGCTAAATGA AGGCAAGTGT AGTTTGAATA ATGCTGAGCT GTTCCCGAG GGTCTGGAC 1620  
 CAGCACTACC AGAGAAGCA AGCTCAGTAA AAGAGAGCTT CCGTACGTA AACCTTACAT 1680  
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT 1740  
 TTATCACTGT TGAGTTTGG CTGAAAACCT ACCAAAAGGA GGTGACAGCT TCTTGTGACC 1800  
 TGAGCTGCTG CGTAAAGGCA ACCGAGAAGC GGCTCGTAA AGCCATCCG ACCTCAGAA 1860  
 AGGCGGTGCA CAGGAGAGAG TTTCACTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920  
 AAAAGCCTCC CAGAATCTT GAACGCCAGG CAGATGCTTG TGGAGTGGGC CAGGTCATG 1980  
 CAGAAAACCA ATGTGTGAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAAGCT 2040  
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACRAATGACT TGTGAACCAT 2100  
 GCGCAAGACC TGAATTTGGA AAAAAATAAT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2160  
 GTGGAGGTCT GTGTCAACTC GGTGAATATT CTGCAGATGG CTTTGCACTT TGCCAGCTCT 2220  
 GTGCCCTGGG CAGTGTCCAG CTTGAAGCTG GTGCAACTTC CTGCTTCCCC TGTGGAGGAG 2280  
 GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAACCC AGAGTTCAAT 2340  
 GTTCACTTGG ACATTTCTAC AACACCAACA CTCACCGATG TATTCGTTGC CCAGTGGGAA 2400  
 CATACCAAGC TGAATTTGGA AAAAAATAAT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460  
 ACTTTGATGG CTCACCAAC ATAAACCCAG GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520  
 GAGATTTCAC TGGGTACATT GAATCCCAA ACTACCCAGG CAATTACCCA GCCAACACOG 2580  
 AGTGTACGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCCTGAGA 2640  
 TCTTCTGCCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGOGGAAA ACCTCTTCAT 2700  
 CCAATTCTGT GACAAATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT 2760  
 CCAGGTCAAA GAAGCTGTGG ATTCACTTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT 2820  
 TCCAGTCCC ATACGTGACA TATGATGAG ACTACAGGA ACTCATTGAA GACATAGTTC 2880  
 GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAACTTA 2940  
 TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCGAG 3000  
 AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060  
 TTTTGAGACC TTACAAATGA CTCAGCCCACT GTGCCACTCA ATACAAATGT TCTGCTATAG 3120  
 GGTGTGTGGG ACAGAGCTGT CTTCTTCTG CATGTGAGCA CAGTCCGGTA TTGCTGCTC 3180  
 CGGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT 3240  
 GAACCTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300  
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGCTGGCT GAGCTGACT 3360  
 TTGCTCAGC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTCC TCAAGGAGTC 3420  
 TGTAGTGAA AGGAGGCCAC AGAATAAGCT GCTTATCTG AAACCTCAGC TTCTCTAGC 3480  
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540  
 CAAGAGGGGA GGGAGAGGAG CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG 3600  
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGAATC CAGGAACCTG 3660  
 AGTTCTAAGC AGTGCTCGTG AAAAAAATAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720  
 AGCACTTCTG GAGACAT

**A169 Protein sequence**

Gene name: CEGP1  
 Unigene number: Hs.222399

Probeset Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like\_domains [49-84,132-167,177-213,286-321,407-442] CUB\_domain [809-918]  
 Cellular Localization: may be secreted

10 1 11 21 31 41 51  
 | | | | |  
 MGVAGRRNRP AAMAVLLLLL LPPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60  
 LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNR CTCFDGFMIA 120  
 HDGHNCLDVO ECLENNNGCQ HTCYNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSOMNK 180  
 DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGCOHSCDD TADGPECSCH 240  
 15 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300  
 STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCOQVCVN 420  
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGSDGC FLRCHSGIHL 480  
 20 SSDVTIIRTS VTFKLNEGKC SLKNAELFPE GLRPALEPKH SSVKESFRYV NLTCSSGKQV 540  
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPRST ERQAESCQVG QGHAEQCVS CRAGTYIDGA RERCILCPNG 660  
 TFQNEBQMT CEPCEPRGNS GALKTPAEWN MSECGGLQCP GEYSADGFAP CQLCALGTFO 720  
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSFGHFY NTTHRCIRC PVGTQPEFG 780  
 25 KNCVSCFCFN TTTDFDGSIN ITQCKNRRCG GELGDFTYGI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPEIFLPIED DQGDYLVMRK TSSSNSVTY ETCQTYERPI AFTSRSKLW 900  
 IQFKNENGS ARGQVVPYV YDEYQELIE DIVRDGRLYA SENHQEILWD KKLIALFDV 960  
 LAHPQNYFKY TAQESREMP RSFIRLLRSK VSRFLRPYK

30 A170 DNA sequence  
 Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Nucleic Acid Accession #: AF007170  
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

35 1 11 21 31 41 51  
 | | | | |  
 AAGGAGGCGG CTTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60  
 CTGGACCACT GCATGACCGC CTTGGACCTC TTCTCACCAC ACCAGTTCTC AGAAGCACTC 120  
 40 AGCTACCTCA AGCCCAAGAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180  
 CTGGAGATGC AGGCCATGAT GACCTTTGAC CTTGAGGACA TCCTGCTTGC CGGCAACATG 240  
 ATGAAGGAGG CACAGATGCT GTGTGAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300  
 TTAGCAGCGT TGGTGAACCG CCCCACGCTG GGCCTAATTA CTGAAGAAGA AATCCACGCT 360  
 45 GAGGTCTGCT ATGCAGAGTG CTTGCTGCGC CGAGCAGCCC TGACCTTCTC GCAGGACGAG 420  
 AACATGGTGA GCTTCATCAA AGGCGGCATC AAAGTTGCGA ACAGCTACCA GACCTACAAG 480  
 GAGCTGGACA GCTTGTGTTCA GTCTCACAAC TACTGCAAGG GTGAGAACCA CCGCACTTT 540  
 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCG TTCAACCTGA CACTGTCCAT GCTTCCTACT 600  
 AGGATCTGGA GGTCTGTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660  
 50 CAGCTGAGAG AGGGAGCGTC AGGCGACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720  
 CTGTGCTACC ACACCTTCCT CACCTTCGTG CTCGGTACTG GGAACGTCAA CATCGAGGAG 780  
 GCGGAGAGC TCTTGAAGCC CTACCTGAAC CGGTACCCCTA AGGGTGCCAT CTCTCTGTT 840  
 TTTGAGGAGG GGATTAAGAT CATTAAGAGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900  
 GAGTGTCTGG AGGCCACGAG GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960  
 55 ATGTGTGCTC TCACCTACAA GGGCCAGTGG AAGATGTCTC ACTTCTACGC CGACCTGCTC 1020  
 AGCAAGGAGA ACTGCTGGTC CAAGGCCACC TACATTACA TGAAGGCCCG CTACCTCAGC 1080  
 ATGTTTGGGA AGGAGGACCA CAAGCCGTTT GGGGACGAGC AAGTGGAAAT ATTTGAGCT 1140  
 TGCCACAGGC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200  
 CGGAAGTCCC GGGCTACTCT CTCTCCAAC CCTATCTGCG TGCCAGTGCC TGCTCTGAA 1260  
 60 ATGATGTACA TCTGGAACGG CTACGCCGTG ATTGGGAAGC AGCCGAAACT CACGGATGGG 1320  
 ATACTTGAGA TTATCACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCCAGA GAACGAGTAC 1380  
 TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440  
 CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500  
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCTGCTGCTT TATGGAGCAA 1560  
 65 GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAACTA CAAGAATTAC 1620  
 TCCATGGAGT CAAGGACACA CTTTCGAATC CAGGCACCCA CACTCCAAGC CAAGTCTTCC 1680  
 CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCTT GTAGCTTTG TGCAGCAGTT 1740  
 CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCTT 1800  
 CCCCTGCCCC TGCCCTGCCT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860  
 70 TGTATCCGTG CAGAGCCGA GCTGGCATT TCAACAGTGT AGCCAAGGGC CTTTGCCAAG 1920  
 GGCAGAGCAG GTGAGOCCT CTGCCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980  
 TGATGTTTGA AGAGAATGTA TGAACAGTTT ACATTTTCTT TAGAAATACA TTGATGGGAT 2040  
 CACAGTTGGC TTTAAAAACC AACACATATC AACCACTGTG AAGTCTTTGT CTTCACCTAT 2100  
 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAAATG CTTTCAAAAT 2160  
 75 TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCCTCAGA GGACCTGAGG AATGCTGGG 2220  
 AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTTGGGC ATGAGGATGT ACACAGACAC 2280  
 CCCTACCTCT ACTACTCACA CTTCAATTCA CTCCTTTTGT AAAATTCCAA TTTAAAAATC 2340  
 AAGCAAGTCT TTTTAGTGAG ATAAAACTCT AGCTCTCTCT TAGAAAAATC AATCTCTACC 2400  
 AGTAGAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCGAG 2460  
 80 AAATTTGGGG GGCAGGAGGA GGTCTCTAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520  
 CTGAAACCAC TGGGAATAAT TTATGAAACA TAAAACTCTT CTGTACTTCA CTCCAAGGTA 2580  
 CATTGTCTTA CTGACAGCAT TTTTGTAAAA ACTGTTATTC TTGAAAAAAA AAAAAAAA 2640  
 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Protein Accession #: AAC39582  
 Signal sequence: none  
 Transmembrane domains: 210-226  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 10 MTALDLFLTN QFSEALSULK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMKEA 60  
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAECY AECLLQRAAL TFLQDENMVS 120  
 15 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHPEGV KLGVGAPNLT LSMLPTRLR 180  
 LLEFVGFSNG KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLTG NVNIEEAELK 240  
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECCQ AQQHWKQFHH MCYWELMWCF 300  
 TYKGQWQMSY PYADLLSKEN CWSKATYIYM KAAYLSMFGK EDHKPFGDDE VELFRAVPLG 360  
 KLKIAGKSLP TEKFAIRKSR RYFSSNPISL PVPALEMYI WNGYAVIGKQ PKLTDGILEI 420  
 20 ITKAEEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480  
 LIPNALLELA LLLMEQDRNE EAIKLESAS QNYKNYSMES RTHFRIQAAT LQAKSSLENS 540  
 SRSMVSSVSL

25 A172 DNA sequence  
 Gene name: EST  
 Unigene number: Hs.200102  
 Probeset Accession #: AL117406  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 30 ATGACTAGGA AGAGGACATA CTGGGTGCC AACTCTCTG GTGGCTCGT GAATCGTGGC 60  
 ATCGACATAG GCGATGACAT GGTTCAGGA CTTATTATATA AAACCTATAC TCTCCAAGAT 120  
 35 GGCCCTCGGA GTCAGACAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCCACCG 180  
 TGGGGGAAGT ATGATGCTGC CTTGAGAACC ATGATTCCCT TCCGTCCCAA GCCGAGGTTT 240  
 CTGCCCCCCC AGCCCTCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCCT GTCATGGCTC 300  
 ACCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACCCAT CCTCCACTG 360  
 40 TCAGTCCATG ATGCTCAGGA CAAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA 420  
 GTCTCAAGGC GAGGATGTA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480  
 ACAAGGTTGA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG 540  
 CCAATATTGA TTATACCAA GATCTGGGAA TATTACAGA AGCAGTTGGG GAATGTTGTC 600  
 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCGAAT GTGTGAAGTC TCTGAGTTTC 660  
 45 TCCTCCAGTT GGATCATCAA CCAACGCACA GCCATCAGGT TCCGAGCAGC TGTTCCTCC 720  
 TTTGCTTTG AGAAGCTCAT CCAATTAAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780  
 ATCAGCTTCT TCACCGGTGA TGTAACCTAC CTGTTGAAG GGGTGTGCTA TGGACCCCTA 840  
 GTACTGATCA CCTGCGATC GCTGGTCATC TGCAGCATT CTCTCTACTT CATTATTGGA 900  
 TACACTGCTA TTATTGCCAT CTTATGCTAT CTCTGGTTT TCCACTGGC GGTATTCTG 960  
 50 ACAGAATGG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT 1020  
 GTGACCACTG AAGTCTCTAC TTGCATTAA CTGATTAAAA TGTACACATC GGAGAAACCA 1080  
 TTTGCAAAA TCATTGAAGC TATGAAAGT CTGACTTTCT GCTCCAAACC TGGTGATGGC 1140  
 ATGGCTTCA GCATGCTGGC CTCTTGAAT CTCTTGGGC TGTGAGTGT CTTTGTGCTT 1200  
 ATTGCACTA AAGGTCTCAC GAATTCCAAG TCTGCAGTGA TGAGGTTCAA GAAGTTTTC 1260  
 55 CTCCAGGAGA GCCCTGTTTT CTATGTCAG ACATTACAAG ACCCCAGCAA AGCTCTGGTC 1320  
 TTTGAGGAGG CCACCTTGTC ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG 1380  
 GAGCTGATGA CAGCTGGGCA TGCTTCTGAG GGGATGACCA GGCCTAGAGA TGCCCTCGGG 1440  
 CCAAGAGGAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500  
 AAGGGGATGA TGTTAGGGGT CTGCGGCAAC ACGGGGAGT GTAAGAGCAG CCTGTTGTCA 1560  
 60 GCCATCTGG AGGAGATGCA CTTGCTGAG GGCTCGGTGG GGGTGCAGGG AAGCCTGGCC 1620  
 TATGTCCCC AGCAGGCTCG GATGCTCAGC GGAACATCA GGGAGAACAT CCTCATGGGA 1680  
 GGGCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740  
 CTGGAACCTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCTT CAACCTCTCT 1800  
 GGGGGGAGA AACAGAGGAT CAGCTGSCC CGCGCGCTT ATTCCGACCG TCAGATCTAC 1860  
 65 CTGCTGGAAG ACCCTCTGTC TGCTGTGGAC GCCCAGCTGG GGAAGCAGAT TTTTGAGGAG 1920  
 TGCAATTAAG AGACACTCAG GGGGAAGAGC GTGCTCTGG TGACCCACCA GCTGCAGTAC 1980  
 TTAGAATTTT GTGGCCAGAT CATTTTGTG GAAATGGGA AAATCTGTGA AAATGGAACT 2040  
 CACAGTGAGT TAATGCAGAA AAAGGGGAAA TATGCCAAC TTATCCAGAA GATGCACAAG 2100  
 GAAGCCACTT CGGACATGTT GCAGGACACA GCAAGATAG CAGAGAAGCC AAAGGTAGAA 2160  
 70 AGTCAGGCTC TGGCCACCTC CCTGGAAGAG TCTCTCAAG GAAATGCTGT GCGGAGCAT 2220  
 CAGCTCACAC AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCAACCAG 2280  
 TACATCCAGG CAGCTGGAGG TTACATGGTC TCTTGCATAA TTTTCTTCT CAGTGGCTG 2340  
 ATCGTCTTCT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGGTTGGA GCAGGGCTCG 2400  
 GGGACCAATA GCAGCCGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGACTAT 2460  
 75 AATCCTCAAC TGTCCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCCTGCT CCTCATCTGT 2520  
 GTGGGGGTCT GCTCTCAGG GATTTTCACC AAAGTCAAGA GGAAGGCATC CACGGCCCTG 2580  
 CACAACAAGC TCTTCAACAA GGTTTTCCGC TGCCCCATGA GTTCTTTGA CACCATCCCA 2640  
 ATAGGCGGCG TTTTGAAGCT CTTGCGAGGG GACTTGAAGC AGCTGGACCA GCTCTTGGCC 2700  
 ATCTTTTCTG AGCAGTTCTT GGTCTGTGTC TTAATGGTGA TGCGCTCTT GTTGATTGTC 2760  
 80 AGTGTGCTGT CTCCATATAT CTTGTTAATG GGAGCCATAA TCATGGTTAT TTGCTTCATT 2820  
 TATTATAGA TGTTCAGGAA GGCCATCGST GTGTTCAAGA GACTGGAGAA CTATAGCCCG 2880  
 TCTCTTTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT 2940  
 GGAAGAACTC AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000  
 CTGCTGTGTT TCTATCTTC CACACGATGG ATGGCATTGA GGCTGGAGAT CATGACCAAC 3060  
 CTTGTGACCT TGGCTGTGTC CTTGTTCTGT GCTTTTGGCA TTTCTCTCAC CCCCTACTCC 3120

	TTTAAAGTCA	TGGCTGTCAA	CATCGTGCTG	CAGCTGGCGT	CCAGCTTCCA	GGCCACTGCC	3180
	CGGATGTGCT	TGGAGACAGA	GGCAGATGTC	ACGGCTGTAG	AGAGGATACT	GCAGTACATG	3240
	AAGATGTGTG	TCTCGGAAGC	TCTTTACAC	ATGGAAGGCA	CAAGTTGTCC	CCAGGGGTGG	3300
5	CCACAGCATG	GGGAATCAT	ATTTCAGGAT	TATCACATGA	AATACAGAGA	CAACACACCC	3360
	ACCGTGTTC	ACGGCATCAA	CCTGACCATC	CGCGGCCACG	AAGTGGTGGG	CATCGTGGGA	3420
	AGGACGGGCT	CTGGGAAGTC	CTCCTGGGC	ATGGCTCTCT	TCCGCTTGGT	GGAGCCCATG	3480
	GCAGGCGGGA	TTCTCATTTA	CGGCTGGAC	ATTTGCAGCA	TCCGCTTGGG	GGAGCTTGGG	3540
	TCCAAGCTCT	CAGTGATCCC	TCAAGATCCA	GTGCTGCTCT	CAGGAACCAT	CAGATTCAAC	3600
10	CTAGATCCCT	TTGACCGTCA	CACTGACCAG	CAGATCTGGG	ATGCCTTGGG	GAGGACATTC	3660
	CTGACCAAGG	CCATCTCAAA	GTTCGCCAAA	AAGCTGCATA	CAGATGTGGT	GGAAAACGGT	3720
	GGAAACTTCT	CTGTGGGGGA	GAGGACGCTG	CTCTGCATTG	CCAGGGCTGT	GCTTCGCAAC	3780
	TCCAAGATCA	TCCTTATCGA	TGAAGCCACA	GCCTCCATTG	ACATGGAGAC	AGACACCTTG	3840
	ATCCAGCGCA	CAATCGGTGA	AGCCTTCCAG	GGCTGCACCG	TGCTGCTCAT	TGCCACCGCT	3900
15	GTCAACCACTG	TGCTGAACCTG	TGACCACATC	CTGGTTATGG	GCAATGGGAA	GGTGGTAGAA	3960
	TTTGATCGCG	CGGAGGTACT	GCGGAAGAAG	CCTGGGTTCAT	TGTTGCGAGC	CCTCATGGCC	4020
	ACAGCCACTT	CTTCACTGAG	ATAAGGAGAT	GTGGAGACTT	CATGGAGGCT	GGCAGCTGAG	4080
	CTCAGAGGTT	CACACAGGTT	CAGCTTCGAG	GCCACAGCTC	TGCGACCTTC	TTGTTTGGAG	4140
	ATGAGAGATT	CTCTGTGAAG	CAGGGGTAAA	TGTAGGGGGG	GTGGGGATTG	CTGGATTGAA	4200
20	ACCCTGGAAT	AGGCTACTTG	ATGGCTCTCA	AGACCTTAGA	ACCCAGAAC	CATCTAAGAC	4260
	ATGGGATTC	GTGATCATGT	GTTTCTCCTT	TTAACTTACA	TGCTGAATAA	TTTTATAATA	4320
	AGGTAAAGC	TTATAGTTT	CTGATCTGTG	TTAGAAGTGY	TGCAATGCT	GTACTGACTT	4380
	TGTAATATAT	AAACTAAGG	AAACTCAA	AAAAAAAA	AAAAAA		
25	<u>A173 Protein sequence</u>						
	Gene name:	EST					
	Unigene number:	Hs.200102					
	Probeset Accession #:	AL117406					
	Protein Accession #:	none found					
	Signal sequence:	none found					
30	Transmembrane domains:	169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034					
	PFAM domains:	ABC transporter [502-673], ABC membrane region [163-432, 771-1060]					
	ATP-binding domains:	[508-516, 1139-1147]					
35	Cellular Localization:	plasma membrane					
	1	11	21	31	41	51	
	MTRKRTYVWP	NSSGGLVNRG	IDIGDDMVSG	LIYKTYTLQD	GPWSQQRNP	EAPGRAAVPP	60
40	WGKYDAALRT	MIPFRPKPRF	PAPQPLDNAG	LPSYLTVSWL	TPLMIQSLRS	RIDENTIPPL	120
	SVHDASDKNV	QRLHRLWEE	VSRRIEKAS	VLLVLMRFQR	TRLIFDALLG	ICFCIASVLG	180
	PILITPKILE	YSEBQLGNV	HGVGLCFALF	LSECVKLSLF	SSSWINQRT	AIRFRAAVSS	240
	FAFEKLIQFK	SVIHITSGEA	ISFFTGDVNY	LFEGVCYGPL	VLITCASLVI	CSISSYFIIG	300
	YTAFTAILCY	LLVFPLAVFM	TRMAVKAQHH	TSEVSDQIRI	VTSEVLTCIK	LKMYTWKFP	360
45	FAKIEGME	LTPCKSPGDG	MAFSMLASIN	LLRLSVFFVP	IAVKGLTNSK	SAVMRFKCFP	420
	LQESPVFVQ	TLQDPSKALV	FEEATLSWQ	TCPGVINGAL	ELERNHASE	GMTRPRDALG	480
	PEEENSLGP	ELAKINLVVS	KGMMLGVCGN	TGSGKSSLLS	AILEEMHLE	GSVGVQSSLA	540
	YVPOQANIVS	GNIRENIMG	GAYDKARYLQ	VHCCSLNRD	LELLPFQDMT	EIGERGLNLS	600
	GQOKRIGLS	RAYVSDRQY	LLDDPLSAVD	AHVGHIPFEE	CIKTLRGKT	VVLVTHQLQY	660
50	LEFCQIILL	ENKICENG	HSELMQKKK	YAQLIQMHK	EATSDMLQDT	AKIAEKFKVE	720
	SQALATSL	SLNGNAVPEH	QLTQEEEMEE	GSLSWRVYHH	YIQAAGGYMV	SCIIFFFVVL	780
	IFVLTIFSEF	WLSYNLEQGS	GTNSSRESNG	TMADLGNIA	NPQLSFYQLV	YGLNALLLIC	840
	VGVCSSGIFT	KVTRKASTAL	HNKLFNKVFR	CPMSFFDTIP	IGRLNLCFAG	DLEQLDQLP	900
	IFSEQLPLV	LMVIALLLIV	SVLSPYILM	GAILMVICFI	YMMFKKAI	VFKRLNYSR	960
55	SPLFSLHLS	LQGLSSIHVY	GKTEDFISQF	KRLTDAQNNY	LLFLSSTRW	MALRLEIMTN	1020
	LVTALVALP	AFGISSTPYS	PKVMVAVNIV	QLASSFQATA	RIGLETEAQF	TAVERILQYM	1080
	KMCVSEAPLH	MEGTSQCPQW	PQHGEIIFQD	YHMYKRDNT	TVLHGINTL	RGHEVVGIVG	1140
	RTSGSKSLG	MALFRIVEPM	AGRILIDGVD	ICSIGLEDLR	SKLSVTPQDP	VLLSGTIRPN	1200
	LDPRFDRHTQ	QIMDALERTF	LTKAISKFPK	KLHTDQVVEG	GNFSVGERQL	LCIARAVLRN	1260
60	SKILIDEAT	ASIDMETDTL	IQRTIREAPQ	GCTVLVIAHR	VTVLNCQDI	LVMNGKVVVE	1320
	FDRPEVLRKK	PGSLFAALMA	TATSSLR				

	<u>A174 DNA sequence</u>						
	Gene name:	ESTs					
65	Unigene number:	Hs.128899					
	Probeset Accession #:	AA983251					
	Nucleic Acid Accession #:	AA983251					
	Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)					
70	1	11	21	31	41	51	
	ATGCTGTCTG	GCTTCTTGAT	GAGTCCCACT	ACCCAGCACA	GAGCACAGTA	CACTCCCGGA	60
	GGAAAGAAAC	TTCCGTGGGA	GGCTTCCATC	GGTGCGCACA	CCTCCCGAGG	GCGAGGCAGC	120
75	GACCGGGAGA	GGGAGAGCCG	GCCGGAGGCT	GCCGGGCTCC	TGTGGGACCG	CGCTGCAGCC	180
	GGGAGGCGG	AGAAGGGGAA	CCGGGGCGAG	CCGCCCGCCT	GGATCCGCGC	CCAGCAGCAG	240
	CGCGGGCCG	CGCCAGCTGG	GCAGGCTCCC	GGGACTGCGG	CTGGGGGCGC	GCAGGACCTT	300
	CGCTGTGCTG	CTGACGCTTC	CCGGGGGAGG	GTCCGGTTGC	CAGTGAAACC	TCCAGAGGCT	360
	TCCGAGGAC	AGCCCGGGGG	GCCTTCTGAC	TGCATCCCGA	GATTTCATC	AGCAGATGCA	420
80	ACTCATAAGG	CAGTCCCTAA	GGGACCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCTGGAC	CTAGGGCCCG	CGTCTGTGCG	CTCCTGGGCG	TCCGCGCAGA	GGGAGTGGC	540
	CGCGCGGAA	AGCCCGCGGG	GACAGTCAGT	GACGAGGCCG	GGGGGTGCGC	GGGGCCACGA	600
	CTTCTGGAG	ACCGTCTCTG	GCTCTCTGGA	GACGCGCTGT	CGCGCGCCAG	GGTGGTGCCA	660
	TGTGGGGCG	TGCGGCTCTG	TCCGTCTCCT	CATCCTGGAA	CGCGGCTCTG	CTCCTGCAGC	720
	TGCTGCTGCG	TGCGTGTGCTG	GCGCGGGGGG	CGAGGGCCCA	GCGCGAGTA	CTGCCACGCG	780



5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50

```

TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
GGCGAGCCCA CCATCTGCTG CGGCAGCTGC CGCTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
GGCGGCTTGG ACCAGGGCGG CTGGGACAAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
CGGCGCGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGCTTAG GGGTACCCAA 1020
GGAGACGGCG AGGGTGGCGC CCCACCGGTG AGGSGCTGGC AGCGGTGCTC CCCTGAAGGC 1080
TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TCCCGGGGCG TGCTGCCCGG TGCCAGACGC 1140
CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCG TGCAGCGGCC GCGCTTGCCC 1200
ATCTACGTGC CGTTCCTCAT TGTTGGCTCC GTGTTGTGCG CCTTATCAT CTTGGGGTCC 1260
CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCTTAAGC AGGATCCCCA GCAGAGCCGA 1320
GCCCGAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC 1380
CGGGGGTGGT CCTCAGGCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCAACTCC 1440
GGGGCCCGGG CGGCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG 1500
AACAACTGT ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACGTCA GCAGGCCACC 1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGTA CACGGTGCAG 1620
CAGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGS AGGCGCTGCA GCCTGGCTAC 1680
AGGCAGATT AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
ACTGTATAAC CGAGAGTCACT TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
GATTCTCGAG GTGGAAGTCC GCACATGTGC GTGTAATTTA TGGCAAGATT CCTTGGATG 1860
GCTTCATTTT CCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
CATCCAGGGT ATCAATGATT TATGATGGAA AACCGGCTCT AGCTGGAGAT GACTGTGATG 1980
TTGCTGATGG GTGCTAATAA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTCTTTT 2100
TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTT 2160
TTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220
TGGTGGGATC TGGGCTCAGT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCTGCTC 2280
AGCCTCCCA GGTGGCTGGG TTACAGGTGC CTGCCCAT GGCCTAATTT TTGATTTTT 2340
TGTAAGAGAT GGGTTTCACT ATGTTGGCTG GGTGGTCTC ACTCTCTGA CCTCAAGCAA 2400
TCTGCTGTC TCAGCTCTCC AAAGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGGCC 2460
TGAGCCTTTT TTTTTTCTA ATGCATCCAA GGTAAAGGG AAGACGCAA TAACAGGACT 2520
ATTCTAAAG GAAACCTGTT TGAATCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
GGCACACCTT AATTCTATTG TAAAAAGATA TATATATTT GTCTATTTT GTGCTTTTG 2640
GGGCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTACA 2700
TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCATT CATCCCTTC 2820
TTGATTGAT CTAAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATCTTTTT 2880
TATATTGAA GTCTTAACTA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCTTG 2940
TGGTTATGGT TTGGCGTTTC CTCTGTTTG GTTTTCAGAG CCCATGTCT ATATAGTCT 3000
GAGTGCAAGT ACTTACTATA CTTGTAAATG AAGATCAGTA TTCTGCTTA GATCTGATA 3060
AAAAATTTT TTGTCTTAGT TATAAAATT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
TAGCTCTCA GCCATAAACC GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTT 3180
GCAGATCATA AGGCTTTTGA TACTCTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
GATTGTAAAG AGAAAGCTT TTCAAGCAAG GATTGCCITT CTCTCCAC ACTGTCTCTG 3300
ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTC TGGCAATGT TCCAATAT 3360
CAAATTCAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAG 3420
ATGTGCAAGT ACATTTCCAA CTGTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480
GTATGGTATG GTCTTCTACA CATTATGTC TATAGATATC TATGATCAT CTTTCTATT 3540
TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAAAA AAAAAAAA AAAAAAAA
  
```

**A175 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MLGFLMSPS TOHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKGNRGE PPWIRAQQQ PRPPPAQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPEA 120  
 SGRQPRGSD CIPRFPASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEBSG 180  
 PRGKRRGTVS DEARGSPGPR LIGDRPALSG DALSAAPVVP CGALAARPS HPGTPLRSCS 240  
 CCLWRWRRG RGPSEYCHG WLDAGGVWRI GFQCPERFDG GDATICOCSG ALRYCCSSAE 300  
 ARLDQGCND DRQAGGEPG RADKDGPRRL GRASCLRGTO GDGEGAPPFV RAWQRCSPFG 360  
 SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420  
 LVAACCCRL RPKQDPQQR APGGNRLMET IFMIPSASTS RGSSSRQSST AASSSSSANS 480  
 GARAPPTRSQ TNCLPBGTM NNIVVNMPTN FSVLNCQQAT QIVPHQGYL HPFYVGYTVQ 540  
 HDSVPMTAVP PFMGLQPGY RQIQSPFHT NSEQRMYPV TV

**A176 DNA SEQUENCE**

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300  
 10 TGTGCCAGCC GGGCCCTGCC CCCGTCTCTC TCCGGGCCCC CCTGCCCTGC CCTGACGTCC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGCG TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAACTCG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCC CCAGGSCCAG CCTGGCACTC 600  
 15 AGCCCTTCGA GGGTGGGGCC CCCATCGCAC CCACCTCTCT TGGCTGGAGA CCCCCGGCAG 660  
 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCGGCC TTGCCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC GGTGTGTCCT CGCACCGAGC GCTTGACTCC GTTTKGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGAG CTACTACTGG CGCTGTCTAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCG TTTCCAGCG TGCCGCCCTG 900  
 20 GGTCCCATCT TCAGGGAAAG GCATGCCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
 AGAGGGCGAG AGTCCGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGAGGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTGCTC TGGCTGGGGA GCCCAGGGA TAGCGGTGG ACTTCAGGTT 1140  
 CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 25 GGCTTCATG TGCTTCCCA AGACCTGGGG GTGATGGCCT TCCCCCTCTT GGCCGGGACG 1260  
 TTGCCCCAGG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCACGTCC TAGGCAAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380  
 CTGGGGTCTG GGTCACCCCC CTTTGTCTCT ACGCCAGCC TGTCCCGAG TTTTCAGTGG 1440  
 GAGAGGCCAC CTCCTCTCAG CAAGGAAAGC GAGAACCCCC AGGTACAGG AGGAGGCTGG 1500  
 30 GGCAAGTCCC CTGGGTGTC ACTCCCTCAG CCCCCTGCCA GGCCCACTCC CGCTGGTGCT 1560  
 GGATGACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620  
 GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGCGCAG GGCCCTCGAT GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1740  
 CCGATGTCGG GGTCACTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACCTTGGT 1800  
 35 ACACGTGCCC ACAAGGCCAC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860  
 CCTTCCGAGG CCGGCTCCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGGCCA GCATGCAGCT 1980  
 GCCCTGCTG CTTGAGAGTG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCCTG 2040  
 ACCTCTGGG CAGGAAAGGG TGCAGTCTCT GAGGGCTGTG GCCCACAGC CCCAGCACCC 2100  
 40 AGGTGGAAGT CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160  
 GGCTGGGGTC TGCCCAACAG GGCCCTCCCA CGTCTGCCCT TGAGGGTGCC TGCCATGCC 2220  
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280  
 GGTGACTTCT TCAGAGAGAC GCCACATAG AGCTGGAGCC CGCAGCTGAA CGGGAATGT 2340  
 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTCCG TGCAAGGTGA 2400  
 45 AAAGAAATAG GTCCCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460  
 CACGAGGGGA GAATTTAAG GCGCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520  
 GCAGACCCCT GCTGAGGCT GCGCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580  
 GAGCAGCTGC CTGGGCTCT ATCGCGAGG TGCCAGTAGC GTGTGCAGT ACATACACGT 2640  
 GCGTGACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700  
 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCACACCA GGCCTCAGGA 2760  
 50 TTTTGTGTTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGGTGGT TGGTTACAGC 2820  
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAGAAAGAA AAAAAAGAG AAGAAATG AGAGATCCAG GTTTAAATAT 2940  
 TCATAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

## A177 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs. 2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51  
 | | | | |  
 GCGGAACACC GGGCCGCCGT CGCGGACGCT GCTTCAACCC TCTCTCTGCA GCCATGGGGC 60  
 TCCCTCGTGG ACCTCTCGCG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGCG 120  
 65 CTTCCGAGCC GTGCGGGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GGGGAGGGCG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCTT GGGCTGCCCT GGGCAAGAGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCAATCCAAA CGTATCTTAC 360  
 AAGACACAAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAGGGGTC 420  
 70 CTTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGCCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTGCTG GTAGAGAAGG 540  
 AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660  
 TCATCTGTAG CGACCAAGAT GACCAACAAG CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720  
 75 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
 ATGATGCCAT CTCACCTTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCNA 840  
 AGGACCCACA CGACTCATG TTCACATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900  
 CCAATGGCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
 80 TGGATGGGGA CGGCTCCACC ACCACGCGAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020  
 ACAATGCTCC CATGTTTGAC CCCCAGAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080  
 GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAOSC CCCCACCTCA CCAGCGTGGC 1140  
 GTGCCACCTA CTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200  
 CTGAGAGCAA CCAGGGCATC CTGACAAACA GGAAGGGTTT GGATTTTGAG GCCAAAACCC 1260  
 AGCACACCTC GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTTCCCAACT 1320  
 CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCACC 1380

CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440  
 CTGCAGAAGA CCTCTGACAG GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500  
 CAGGGTGTCT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 5 ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740  
 ACGTGTCTGA CATCAGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTTC CAGGCCAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTGTCCCTT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACACTT TCTCTGTCTG 1920  
 10 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGGAAGC CTGCCCTGGA CCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CCTCTACTG CAGAAGATG ACACCGTGA CAACGCTCTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 15 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCGCG CCTACGACAC CCTCTTGGTG TTGACTATG 2400  
 AGGCGAGCGG CTCGACGCG GGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520  
 20 ACGTGGCGG GGAGGAAGAG TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580  
 CACAGAGCAT CTGCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTC 2640  
 GGAAGTGGCC GTAGCAACTT GGCAGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCTT TCCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC ATGGGTGCTT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 25 TGCTCAACCC TGTGTCTCTG GCTTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940  
 TCAGAAAGTT AGAGAAAGTT CTCAAAAGT GCAGCCCAAG GCTGCTGGGC CCACTGGCG 3000  
 TCTGTCAATT CTGTTTCCCA GACCCCAATG CTTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 30 ATACTGAGTG TGCTTAGGTT GCCCTTATT TTTTATTTTC CTGTGTGCGT TGCTATAGAT 3120  
 GAAGGTGAG GACATCGTG TATATGTACT AGAAGTTTTT TATTAAGAA A

**A178 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51  
 45 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLA GGAQEPGQA LGKVFMGCPG 60  
 QEPALPSTDN DDPFVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDWV VAPISVPENG 120  
 KGFPFQRLNQ LKSNKORDTK IFYSITGPGA DSPPEGVFAV EKETGMLLIN KPLDREELAK 180  
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKPTQDTF RGSVLEGLVP GTSVMQVTAT 240  
 50 DEDDAIYTYN GVVAVSIHQ EPKDPHDLME TTHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSGST TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVORLT VTDLDAFNPS 360  
 AWRATYLMG GDDGDHFTIT THPESNGGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKUVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLANDP DSGQVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540  
 55 VMDHGFVPEP RQITICNQSP VRHVLNITDK DLSPTSPFPQ AQLTDSDDIY WTAEVNEEGD 600  
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFL LVLALLVRKK RKIKEPLLLP EDDTRDNVFP YGEEGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIIIE NLKAANTDPT APPYDTLLVF 780  
 DYEAGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKLA DMYGGGEDD

**A179 DNA SEQUENCE**

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 70 CTCTTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAGCACA TGGACTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120  
 GGAAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCTCTGT TATTTTTTTT 180  
 TCTAATCTTC TGGTCAATGC GGCAGTGATC AAAAAACAGAA AATTTTCATT CCCCCTCTAC 240  
 75 TACCTGTGGG CTAATTTAGC TGCTGCGGAT TTCTTCTGCTG GAATTGCCCTA TGTATTCTCTG 300  
 ATGTTTAAAC CAGGCCCACT TTCAAAAACCT TTGACTGTCA ACCGCTGGIT TCTCCGTGAC 360  
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420  
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480  
 CTGCTCATTT TGCTGTCTCT GGCCATCGCC ATTTTATATG GGGCGGTCCC CACACTGGGC 540  
 80 TGGAAATGCC TCTGCACAT CTCTGCGTGC TCTTCCCTGG CCCCCTTTTA CAGCAGGAGT 600  
 TACCTTGTTT TCTGGACAGT GTCCAACTTC ATGGCCTTCC TCATCATGGT TGTGGGTGAC 660  
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAAGCTCT TGTCTCCGCA TACAAGTGGG 720  
 TCCATCAGCC GCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

5 GCCTTTGTGG TATGCTGGAC CCCGGGCGCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840  
 AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900  
 GTCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960  
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020  
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080  
 GTCTGCAATA AAAGCATCTC CTAAACTCTG GATGCCTCTC GGCCACCCA GGTGATGACT 1140  
 GTCTTAGG

10 A180 Protein sequence:  
 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Protein Accession #: NP\_036284  
 15 Signal sequence: none found  
 Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51  
 MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60  
 FHPPFYLLA NLAAADFFAG IAYVPLMFNT GPVSKTLTVN RWPLRQGLLD SSLTASLTNL 120  
 25 LVIAVERHMS IMRMVRHSNL TKKRVLLIL LVWAIATFMG AVPTLWNCNL CNISACSSLA 180  
 PIYSRSYLVF WTVSNLMAFL IMVVYLRIY VYVKRKTNVL SPHTSGSISR RRTFMKLMKT 240  
 VMTVLGAFVV CWTPLGLVLL LDGLNCRQCG VQHVKRWFL LALINSVVNP IYYSYKDEDM 300  
 YGTMKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

30 A181 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.162859  
 Probeset Accession #: AA569531  
 Nucleic Acid Accession #: AA569531  
 35 Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGACCTACA GTTACTCAIT TTTCAAGCCT GAGITGATCG TTAATCATCT TAATTATGTT 60  
 40 CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACTTTAT TGCTCTGCTC TTCATTCTCT 120  
 GATGAAACCT CTGGAGTAAG CACACATCTT CCTTGTATTAT CTCTCTCAAA GGAGTGTGGA 180  
 GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240  
 CAGCTATACC TGTGGGACAT GGGTGGTTTT ACAATATTTA AGAACCCTGTG GATGAGCCTC 300  
 ATACCCAGAG GGAACAAACG CTCGCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360  
 45 AAGCAGAAGC AAGTTCAAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420  
 CTCTCTTCAT TCTGGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTGGGGCA 480  
 GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTCTTCA 540  
 GCTACGTTGT CCCAGCACTT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600  
 AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTATC TACTGAGCTG CTACCATATC 660  
 50 CCAGCTACTC CTGCAATGTT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720  
 TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTCTT GCCAAACATC 780  
 ACATGAGGAT GAACAATGAA ACCGATTGTA AACCAAGATT GTCTGATTCC AACATCTCTG 840  
 GGTCTCTTTT CACTCTGATA TGCTGCAATT AAAAGCCAT TTCTAAGACT GT

55 A182 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.162859  
 Probeset Accession #: AA569531  
 Protein Accession #: none found  
 60 Signal sequence: 1-46  
 Transmembrane domains: none found  
 Cellular Localization: not determined

65 1 11 21 31 41 51  
 MTYSYSFFRP ELIVNHLNVV HSEANRRXT KTLLSLLSFL DETSGLSTHL PCLSLSKECG 60  
 VLHLDIHGKK EDMRITQSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF 120  
 70 KQKQSSKIQE ERRRESAGPN LSSFWFVGNA GRGDRPQIWA GSKQPSG

75 A183 DNA SEQUENCE  
 Gene name: ESTs  
 Unigene number: Hs.179809  
 Probeset Accession #: N95796  
 Nucleic Acid Accession #: XM\_050197  
 Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCCGGGTGAC 60  
 AGCCGCGGCG CTGCGCCAGG ATCTGAGTGA TGAGACGTGT CCCCACTGAG GTGCCCCACA 120  
 GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAGGGCT GGCAGAAATG 180  
 GGCGCTGGC TGATTCTTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCG CAGCTTCTGG 240  
 AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCTGAGC CCTACCGGCC 300

5 TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCGCCTGC TGGCGCACCG GAAAGCCCAG 360  
 CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCGC AGGCATCACC 420  
 TATGTGCCCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGCTG 480  
 GGCATTGGTC CAGTGTCTGG CCTGGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCAC 540  
 TGGCGTGGAG GCTATGGCCG CCGCCGGCCC TTCATCTGGG CACTGTCCTT GGGCATCCTG 600  
 CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCGGATCCC 660  
 AGGCCCTGG AGCTGGCACT GCTCATCTG GCGCTGGGGC TGCTGGACTT CTGTGGCCAG 720  
 GTGTGCTTCA CTCCTACTGA GGCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780  
 CGCCAGGCTT ACTCTGTCTA TGCCTTCATG ATCAGTCTTG GGGCTGCCT GGGTACCTC 840  
 10 CTGCTGCCA TTGACTGGGA CACCAGTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900  
 TGCCTCTTTG GCCTGCTCAC CCTCATCTTC CTCACCTGGC TAGCAGCCAC ACTGTGGTG 960  
 GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTCCGC CCCCTCCTTG 1020  
 TCGCCCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080  
 15 CCGCGCTGC ACCAGCTGTG CTGCGCATG CCGCGCACCC TGGCGCGCT CTCTGTGGCT 1140  
 GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCAGCTGT TTTACACGSA TTTGTTGGGC 1200  
 GAGGGGCTGT ACCAGGGCTG GCCCAGAGCT GAGCGGGGCA CCGAGGCCCC GAGACACTAT 1260  
 GATGAAGGGT TTGGATGGG CAGCCTGGGG CTGTTCCTGC AGTGCCCAT CTCCCTGGTC 1320  
 TTCTCTCTGG TCACTGACCG GCTGGTGCA CGATTCCGCA CTCGAGCAGT CTATTGGCC 1380  
 20 AGTGTGGCAG CTTTCCCTGT GGCTGCCGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440  
 GTGACAGCTT CAGCGGCTTC CACCGGGTTC ACCTTCTCAG CCTCGCAGAT CTGCCCCATC 1500  
 ACACCTGGCT CCCTTACCA CCGGAGAGA CAGGTGTTC TGGCCAAATA CCGAGGGGAC 1560  
 ACTGGAGGTG CTAGCAGTGA GGACAGCCTG ATGACCACTG TCCTGCCAGG CCTAAGCCT 1620  
 GGAGCTCCCT TCCCTAATG ACACTGGGT GCTGGAGGCA GTGGCTGCT CCCACCTCCA 1680  
 25 CCGCGCTCT GCGGGGCTC TGCCTGTGAT GTCTCCGTAC GTGTGGTGT GGTGAGGCC 1740  
 ACGAGGCCA GGGTGGTTC GGGCGGGGC ATCTGCCTGG ACCTGCCAT CCTGGATAGT 1800  
 GCCTTCTGCT TGTCCAGGT GCGCCCATCC CTGTTTATGG GCTCCATTG CCAGCTCAGC 1860  
 CAGTCTGTCA CTGCTATAT GGTGTCTGCC GCAGGCTGG GTCTGTGCGC CATTACTTT 1920  
 GCTACACAGG AGGCCAGAG GGTCCATGC ACTGGAATG GGGGACTCT CAGGTGGATT 1980  
 30 AGCACATTGG GGTGAGGGC CTGCTCACT GGTCCACG TCCCGCTCC TGTAGCCCC 2040  
 ATGGGGCTGC CCGGCTGGCC GCCAGTTTCT GTTGTGCCA AAGTAATGT GCTCTCTGCT 2100  
 GCCACCTGT GCTGCTAGG TGCCTAGCT CACAGCTGGG GGCTGGGGC TCCTCTCTCT 2160  
 CTCTCCCGAG TCTTAGGGC TGCCTGACTG GAGGCTTCC AAGGGGTTT CAGTCTGGAC 2220  
 TTATACAGG AGGCCAGAG GGTCCATGC ACTGGAATG GGGGACTCT CAGGTGGATT 2280  
 35 ACCAGGCTC AGGGTAAAC GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTT 2340  
 GGGAGCTGAA TAAACTCAGT CACCTGGTT CCCATCTCTA AGCCCCITAA CCTGCAGCTT 2400  
 CGTTTAATGT AGCTCTTGA TGGGAGTTTC TAGGATGAAA CACTCTCTCA TGGGATTGTA 2460  
 ACATATGAAA GTTATTGTGA GGGGAAGAGT CCTGAGGGG AACACACAAG AACAGGTCC 2520  
 40 CCTCAGCCCC ACAGGCACGT GTCTTTTTC CTNGANTCCA CCCCCCCT CTTTACCCTT 2580  
 TT

**A184 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.179809  
 45 Probeset Accession #: N95796  
 Protein Accession #: XP\_050197  
 Signal sequence: none  
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401  
 50 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 55 MVQRLVWSRL LRHRKAQLLL VNLITFGLV CLAAGITYVP PLLLEVGVVEE KPMIMVLGIG 60  
 PVLGLVCPVL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGMLA GLLCPDFRPL 120  
 ELALLILGV LLDPCGQVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGCLGYLLPA 180  
 IDWDSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTPEAE GLSAPLSLPH 240  
 CPCRARLAF RNLGALLPRL HQLCCRPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL 300  
 60 YQGVPRAEFG TEARRHYDEG VRMSLGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360  
 AFPVAAGATC LSHSVAVVTA SAALTGFTEF ALQILPYTLA SLYHREKQVE LFKYRGDTGS 420  
 ASSEDSLMTS FLPGPKPGAP FPNHVGAGG SGLPPPPAL CGASACDVSV RVVVGEPTER 480  
 RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSTVQLSQSV TAYMVSAGL GLVAIYPATQ 540  
 VVFDKSDLAK YSA

**A185 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.11260  
 70 Probeset Accession #: R73640  
 Nucleic Acid Accession #: AK002126  
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 75 ATGGTTCCGC GGGGGCTGCT TGCCTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60  
 TGCTGTGCTA TCTCTGTCT GTACATGTTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG 120  
 CTGGCACTGC CCAGGGCCAA CAGCCCAACG GGAAGGAGG GGTACCAGGC CGTCTCTCAG 180  
 GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCAGAGCTC 240  
 80 AAGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300  
 GCTGCTGGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCTGGGCC 360  
 TTCTGCACT CGCAGGTGGA CAAGCAGAG GTGAATGCTG GGTCAAGCT GGCCACAGAG 420  
 TATGACAGC TGCCTTTTGA TAGCTTTACT CTACAGAGG TGTACCAGCT GGAGACTGGC 480  
 CTTACCGCC ACCCCAGAGA GAAGCCTGTG AGGAAGGACA AGCGGATGA GTTGGTGGAA 540  
 GCCATTGAAT CAGCCTTGA GACCTGAAC AATCTCTGAG AGAACAGCCC CAATCACCGT 600

CCTTACACGG CCTCTGATT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660  
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAACGGCT CATCTTATTT 720  
 CGACCATTCG GCCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780  
 ATCAATGTTA TCGTGCTCT AGCAAAAAGG GTGGACAAGT TCGGCAGTT CATGCAGAA 840  
 TTCAGGGAGA TGTGCTATGA GCAGGATGGG AGAGTCCATC TCACTGTGT TTACTTTGGG 900  
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTTGAAAACA CTTCCAAAGC TGCCAACTTC 960  
 AGGAACCTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT 1020  
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTTCTCTTT TCTGTGATGT GGACATCTAC 1080  
 TTCACATCTG AATTCTCTAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140  
 TATCCAGTTC TTTTCAGTCA GTACATCTCT GGCATAATAT ACGGCCACCA TGATGCACTC 1200  
 CCTCCCTTGG AACACGAGCT GGTCAATAAG AAGGAACTG GATTTTGGAG AGACTTTGGA 1260  
 TTGGGATGA CGTGTGAGT TCGGTGAGC TTCATCAATA TAGTGGGTT TGATCTGGAC 1320  
 ATCAAAGGT GGGGCGGAGA GGATGTGAC CTTTATCGCA AGTATCTCCA CAGCAACCTC 1380  
 ATAGTGGTAC GGACGCTGT GCGAGGACTC TTCACCTCT GGCATGAGAA GCGCTGCATG 1440  
 GACGAGCTGA CCCCAGAGCA GTACAAGATG TGCATGAGT CCAAGGCCAT GAACGAGGCA 1500  
 TCCACGGCC AGCTGGGCT GCTGTGTTT AGGCACGAGA TAGAGGTCTA CCTTCGCAAA 1560  
 CAGAACAGA AGACAAGTAG CAAAAAACA TGA

20 A186 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.11260  
 Probeset Accession #: R73640  
 Protein Accession #: NP\_060841  
 25 Signal sequence: 1-26  
 Transmembrane domains: none found  
 Cellular Localization: not determined

30 1 11 21 31 41 51  
 MVRRLAWI SRVVLLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60  
 EWEQHRNYV SSLKRIQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTQADLLA 120  
 FLHSQVKAEE VNAGVKLATE YAAVPFDSFT LQKVYQLEGT LTRHPEEKPV RKDKRDELVE 180  
 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILE 240  
 35 RPFGRIMKVK NEKLNMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300  
 KEEINEVKGI LENTSKAANF RNFTFIQLNG EFSRGKGLDV GARFWKGSNV LLFFCDVDYI 360  
 FTSEFLNTRC LNTQPGKVPF YPVLFSQYNP GIIYGHDAV PPLEQQLVIK KETGFWRDFG 420  
 FMGTQYRSLD FNIQGGFLD IKGWGGEDVH LYRKVLYHSL IIVRTPVRGL FHLWHEKRCM 480  
 40 DELTPEQYKM CMQSKAMNEA SHQQLGMLVF RHEIEAHLRK QKQKTSKKT

45 A187 DNA SEQUENCE  
 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCCTCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTCAATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTAA 240  
 55 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGCGCCA 360  
 CCAGAAATGCC ATTTGTGTGG TGAAGGAAAA TTGGAGCATA CACTGCCCGC AGACTTGGTT 420  
 CCAGGTGATA CAGTTTGGCT TCTGTGTTGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480  
 60 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540  
 AAGGTGACAG CTCTCAGGCC AGCTGCAACT AATGGAGATC TTGCATCSAG AAGTAACATT 600  
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAGCRAAAG GTGTTGTCTAT TGGAACAGGA 660  
 GAAATTTCTG AATTGGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780  
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAG ATATCCTGGA AATGTTTACT 840  
 65 ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTGT GGTCAACATG 900  
 AOGCTAGCTC TTGGTGTATT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960  
 ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTCGG AACACTGACG 1020  
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080  
 GGAGTTGGCT ATATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTCT 1140  
 70 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TCGTGTAA 1200  
 AGAAACAATA CTCTAATGGG GAAGCCAAAC GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260  
 ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320  
 GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
 75 TGTTTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500  
 ATGGGCTCAG CGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGTAACT GGGACAGCTG 1560  
 ACATTTCTTG GCTTGGTGGG AATCAATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620  
 ACACAAAGT TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTG ACAGGAGACT 1680  
 80 GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAA CTTCCAGTCT AGTCTCAGGA 1740  
 GAAGAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAA GGTTCAGTA 1800  
 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860  
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCGA TTGCTCTGAA GGCTGCAGAC 1920  
 ATTGGAGTTG GATGGGCGCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980  
 CTAGTGGATG ATGATTTTCA AACCAATATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT 2040

5 AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100  
 ATCTCATTTG CTACATTAAAT GAACCTTTCT ATCTCTCTCA ATGCCATGCA GATTTTGTGG 2160  
 ATCAATATTA TTATGGATGG ACCCCAGCTT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220  
 GATGTCATTC GTAAACCTCC TCGCACTGG AAGACAGCA TTTTGACTAA AAACCTTGATA 2280  
 CTTAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTCTGGCGT 2340  
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400  
 TTTTGTGACA TGTTCAATGC ACTAAGTTCC AGATCCCGA CCAAGTCTGT GTTTGAGATT 2460  
 GGACTCTGCA GTAATAGAAT GTTTGTCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520  
 10 CTAGTTAATT ACTTCTCCCT GCITCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
 GATCTGTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640  
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700  
 CTGAAGTAT GA

# A188 Protein sequence:

15 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 20 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

25 1 11 21 31 41 51  
 MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKYKI 60  
 SQFKNPLIML LLASAVISVL HQFDDAVSI TVAILIVTV AFVQYRSEK SLEELSKLVP 120  
 30 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDSLIDES SLTGETTPCS 180  
 KVTAPOPAAT NGDLASRSNI AFMGTILVRG KAKGVVITG ENSEFGEVFK MMQAEAPKT 240  
 PLQKMDLLG KQLSPYSFGI IGIIMLVGWL LGRDILEMFT ISVSLAVAAI PEGPLIVTV 300  
 TLALGVNRMV KRAIVYKLP IVETLGCNCV ICSDRKTFLT KNEMTVTHIF TSDGLHAEVT 360  
 GVGVNQFGEV IVDGDVHGF YNPVSRIVE AGVCNDVAI RNNTLMGKPT EGALIALAMK 420  
 35 MGLDGLQDY IRKAEYFPSS EQKMAVKCV HRTQQRPEI CFMKGAYEQV IKYCTTYQSK 480  
 GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASPELQQL TFLGLVGIID PPRTVKKEAV 540  
 TLLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEDAMDVQQ LSQIVPKVAV 600  
 FYRASPRHQM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGTGT DVCKEADMI 660  
 LVDDDFQTIM SAIEEGKIY NNKNFVRFP LSTSLAALTL ISLATLMNFP NPLNAMQILW 720  
 40 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFW 780  
 ELRDNVITPR DTTMTFTCFV FFDMPNALSS RSQTSKVFEE GLCSNRMFCY AVLGSIMGQL 840  
 LVIYFPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIK KVERSREKIQ KHSVSTSSSF 900  
 LEV

# A189 DNA SEQUENCE

45 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 50 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 55 ATGGGCTACC AGAGGCAGGA GCCGTGCATC CCGCCGCGA GAGGATTGCC TTATTCAATG 60  
 AAGCAAGCTG GGTTCCTTT GGAATATATG CTTTATTCT GGGTTTCATA TGTACAGAC 120  
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180  
 TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTT TCAGTTTTTG 240  
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300  
 60 TTCAAAGATA TCCAGGAGT TGATCCTGAA AACGTGTTA TTGGTCGCCA CTTCAATTAT 360  
 GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACGAAATAT AGCAAAGCTT 420  
 GGAAGGCTCT CCTCATCTC TACAGGTTTA ACACTCTGA TTCTTGGAA TGTAAATGGA 480  
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540  
 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTCAT TTATTGCCA CCATAACTCC 600  
 65 TTCTTAGTIT ACAGTTCTCT AGAAGAACC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660  
 ATGTCCATCG TGATTCTCTG ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720  
 TTTACTGGCT TCACCAAGG GGACTTATTT GAAATTAAT GCAGAAATGA TGACCTGGTA 780  
 ACATTGTGAA GATTTTGTGA TGGTGTCACT GTCAATTTGA CATACCTAT GGAATGCTTT 840  
 GTGACAAGAG AGSTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900  
 70 ATTGTGTAA CAGTGATGCT CATCACTGTA GCCACGCTTG TGTCAATGCT GATTGATTGC 960  
 CTCGGGATAG TCTAGAACT CAATGGTGTG CTCGTGSCAA CTCCTTCAT TTTTATCATT 1020  
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080  
 TCTTGTGACA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTGCT CATGGCTATT 1140  
 ACAAATACTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTC TGACAATTC 1200  
 75 TCTCTCACA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260  
 ATTAGTATCT TCAACTCGA GTAA

# A190 Protein sequence:

80 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 | | | | | |  
 MGYQRQEPVI PPQRGLPYSM KQAGFPILGIL LLFWVSIVTD FSLVLLIKGG ALSGTDITYQS 60  
 LVNKTGFGPG YLLLSVLQFL YPFIAMISYN IAGDTLSKV QRIPGVDPE NVFIGRHFII 120  
 GLSTVTFTLP LSLYRNIAKL GKVSILSTGL TTLILGIVMA RAISLGHPIH KTEDAWVFAK 180  
 PNAIQAVGVM SFAPICHHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240  
 10 FTGFTQGLDF ENYCRNDDL VTFGRFCYGV TILTYPMECF VTREIVANVF PGNLSSVVFH 300  
 IIVTVMVITV ATLVSLILDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360  
 SCVMLPIGAV VMVGFVMAI TNTQDCTHGQ EMFYCFDFNF SLTNTSESHV QQTQLSTLN 420  
 ISIFQLE

**A191 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | | |  
 25 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CGCCGCGAGT TTTCCCTTGT TTTATTGATA 60  
 AAAGGAGGGG CCTCTCTCGG AACAGATACC TACCACTCTT TGGTCAATAA AACITTCGGC 120  
 TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180  
 AGTTACAATA TAATAGCTGG AGATACITTTG AGCAAAGTTT TCAAAGAAT CCCAGGAGTT 240  
 30 GATCCTGAAA ACGTGTITAT TGGTCGCCAC TTCATTATTG GACTTTCCAC AGTTACCTTT 300  
 ACTCTGCCCT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360  
 ACAGGTTTAA CAATCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420  
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTGCAAAGC CCAATGCCAT TCAAGCGGTC 480  
 GGGGTTATGT CTTTTCGATT TATTGCCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540  
 35 GAAGAACCAC CAGTAGCTAA GTGGTCCGCG CTTATCCATA TGTCCATCGT GATTTCGTGA 600  
 TTTATCTGTA TATCTTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660  
 GACTTATTGG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTGTGTTAT 720  
 GGTGTCACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAGAGA GGTAAATGCC 780  
 AATGTGTTTT TTGCTGGGAA TCCTTCATCG GTTTTCCACA TTGTGTAAAC AGTATGGTTC 840  
 ATCACTGTAG CCACGCTTGT GTCACTGCTG ATTGATTGCC TCGGGATAGT TCTAGAAGTC 900  
 40 AATGGTGTGC TCTGTGCAAC TCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
 CTGTCTGAAG AACCAAGGAC ACACTCCGAT AAGATTATGT CTGTGTGTCAT GCTTCCCAT 1020  
 GGTGCTGTGG TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
 CATGGGCAGG AAATGTTCTA CTGCTTTTCT GACAATTTCT CTCTACAAA TACCTCAGAG 1140  
 45 TCTCATGTTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200  
 TAA

**A192 Protein sequence:**

Gene name: ESTs  
 50 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: 1-26  
 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351  
 55 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | | |  
 60 MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLSVL QFLYPFIAMI 60  
 SYNIAGDTL SKVFQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLLS 120  
 TGLTTLILGI VMARISLGP HIKPTEDAVV FAKENAIQAV GVMSFAPICH HNSFLVYSSL 180  
 EEPTVAKWSR LIHMSIVISV PICIFFATCG YLTPTGFTQG DLFFENYCRND DLVTFGRFCY 240  
 65 GVTVILTYPM ECFVTREVIA NVFPGNLLSS VFHIVTVMV ITVATLVSLI IDCIGIVLEL 300  
 NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVGFV MAITNTQDCT 360  
 HGQEMFYCFP DNFLNTNSE SHVQQTQLS TLNISIFQLE

**A193 DNA SEQUENCE**

Gene name: ESTs  
 70 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | | |  
 75 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CGCCGCGAGG TCAATAAAAC TTTCCGCTTT 60  
 CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120  
 80 TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180  
 CCGAATAACG GTTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240  
 CTGCTTTTAT CCTGTAGCCG AAATATAGCA AAGCTTGGAA AGGCTCCCT CATCTCTACA 300  
 GGTTTAAACA CTCTGATTCT TGAATTGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360  
 ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGTCCGGG 420



5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70

```

GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
ATCTGTATAT TCITTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA GCTTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCAT CAGCCTGITA TCTGAACTG 900
TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGCTT GTGTCATGCT TCCCATTGGT 960
GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTTCTACTG CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTTCAG AGACAACACA ACTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

```

**A194 Protein sequence:**

Gene name: ESTs  
Unigene number: Hs.293185  
Probeset Accession #: N62096  
Protein Accession #: none found  
Signal sequence: none found  
Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
MGYQRQEPVI PPQVNKTGFG PGVLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIGVD 60  
PENVFIGHRF IIGLSTVTFT LPLSLYRNIA KLKGVSLIST GLITLILGIV MARAISLGP 120  
IPKTEDAWVF AKENAIQAVG VMSFAPICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVP 180  
ICIFATCGY LFTFTGTQGD LFENYCRNDD LVTFRFCYGY VTVILTYPM ECFVTREVIAN 240  
VFEGNLSSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCAATPLIF IIPSACYLKL 300  
SEEPRTSDSK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360  
HVQQTQLST LNISIFQLE

**A195 DNA SEQUENCE:**

Gene name: ESTs  
Unigene number: Hs.293185  
Probeset Accession #: N62096  
Nucleic Acid Accession #: N62096  
Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

45  
50  
55  
60  
65  
70

```

ATGGGCTACC AGAGGCAGGA GCGTGTATC CCGCCGAGA GAGATTAGA TGACAGAGAA 60
ACCCCTGTTT CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180
GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGSTTTTCA ATGTTACAGA CTTTTCCTTT 240
GTTTATTGTA TAAAGAGAGG GGCCCTCTCT GGAACAGATA CCTACCAATC TTGGTCAAT 300
AAAACCTTCG GCTTTCAGG GTATCTGCTC CTCTCTGTTT TTAGATTGTT GTATCCTTTT 360
ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAAG TTTTCAAGA 420
ATCCAGGAG TTGATCCTGA AAACGCTGTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480
ACAGTTACCT TTAATCTGCC TTTATCCTTG TACCGAAATA TAGCAAAAGCT TGGAAAGGTC 540
TCCTCATCT CTACAGGTTT AACAACCTCT ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600
TCACTGGGTC CACACATACC AAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC 660
ATTCAAGCGG TCGGGTTTAT GTCITTTGCA TTTATTTGCC ACCATAACTC CTCTTAGTT 720
TACAGTTCTC TAGAAGAAC CACAGTAGCT AAGTGGTCCC GCCTATCCA TATGTCATC 780
GTGATTTCTG TATTATCTG TATATTCTT GCTACATGTC GATACCTGAC ATTTACTGGC 840
TTCAACCAAG GGGACTTATT TGAAATATC TGCAGAAATG ATGACCTGGT AACATTGGGA 900
AGATTTTGT ATGGTGTGAC TGTCAATTTG ACATACCCTA TGGAAATGCT TGTGACAAGA 960
GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTTCA CGGTTTCCA CATTGTTGTA 1020
ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATGATTG CCTCGGGATA 1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
ATGCTTCCA TGGTGTCTGT GGTGATGGTT TTTGGATTG TCATGGCTAT TACAAATACT 1260
CAAGACTGCA CCCATGGGCA GGAATGTTC TACTGCTTTC CTGACAATT CTCTCTACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA

```

**A196 Protein sequence:**

Gene name: ESTs  
Unigene number: Hs.293185  
Probeset Accession #: N62096  
Protein Accession #: none found  
Signal sequence: none found  
Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415  
Cellular Localization: plasma membrane

1 11 21 31 41 51  
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60

5  
 10  
 15

GFPLGILLLF WVSVYTFPSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYFP 120  
 IAMISYNIIA GDTLSKVQFR IPGVDPENVF IGRHFIIIGLS TVTFTLPLSL YRNIKLGKV 180  
 SLISTGLTTL ILGLVMARAI SLGPHIPKTE DAWVFAKPNA IQAVGVMSFA FICHNSFLV 240  
 YSSLEETPA KMSRLIHMSI VISVPICIFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFG 300  
 RFCYGVTVIL TYMECFVTR EVIANVFPG NLSSVFHIV TVMVITVATL VSLIDLGLI 360  
 VLELNGVLCA TPLIFIIPSA CYLKLSEEP THSDKIMSCV MLPIGAVMV FGFVMAITNT 420  
 QDCTHGQEMF YCFPDNPSLT NTSSEHVQQT TQLSTLNISI FQ

**A197 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Nucleic Acid Accession #: NM\_017636  
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

ATGAGGAGTG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCACG 60  
 GAGAAGCCCA CCGATGCGTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACACG 120  
 AATTTCCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTCAACACG 180  
 ACATGGGGCT TCGGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGGCCC 240  
 GTCTTCCAGA CTGTGGCTGA GGACCTGCTG CGTCTGGGGC TGGTGGGGC TGCCACAGAG 300  
 ACAGAGAGCT GGATTGTAC TGGGGGTCTG CACACGGGCA TCGGCCGCA TGTGTGTGTG 360  
 GCTGTACGGG ACCATCAGAT GGGCAGACT GGGGGCACCA AGGTGTGTGG CATGGGTGTG 420  
 GCGCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCCAAGGG CTCGTTCCCT 480  
 GCGAGGTACC GGTGGCGCGG TGACCCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAAC 540  
 TACTCGGCTC TCTTCTGTGT GGAAGACGGC ACACACGGCT GCCTGGGGGG CGAGAACCGG 600  
 TTCCGCTTGC GCCTGGAGTC CTACATCTCA CAGCAGAAGA CCGCGGTGGG AGGCACTGGA 660  
 ATTGACATCC CTGTCTCTGT CCTCTGTATT GATGGTGTAT AGAAGATGTT GACGCGAATA 720  
 GAGAAGCCCA CCGAGGGCTCA GCTCCCATGT CTCTCGTGG CTGGCTCAGG GGGAGCTGGG 780  
 GACTGCTGGC CGGAGACCTT GGAAGACACT CTGGCCCCAG GGAGTGGGGG AGCCAGGCAA 840  
 GCGCAAGCCC GAGATGGAAT CAGGCGTTTC TTTCCCAAAG GGCACCTTGA GGTCTGCAG 900  
 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTGA CAGTCTATT TCTGAGGAT 960  
 GGGTCTGAGG AATTCTGAGC CATAGTTTTC AAGGCCCTTG TGAAGGCTTG TGGGAGCTCG 1020  
 GAGGCTCAG CTTACCTGGA TGAGCTGCGT TTGGCTGTGG CTGGGAACCG CGTGGACATT 1080  
 GCCCAGGATG AACTCTTTTC GGGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140  
 CTCATGGAG CCTTCTGTAA TGACCGGCTT GAGTTCGTGC GCTTGTCTAT TTCCCAAGGC 1200  
 CTCAGCCTGG GCCACTTCTT GACCCCGATG CGCTGGCCCC AACTCTACAG CGCGGCGCCC 1260  
 TCCAACCTGC TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACAGCGCAGG CACCAAGGCC 1320  
 CCAGCCCTAA AAGGGGGAGC TGCGGAGCTC CGGCCCTCTG ACGTGGGCA TGTGTGTAGG 1380  
 ATGCTGCTGG GGAAGATGTG CGCGCCGAGG TACCCCTCCG GGGGGCGCTG GGACCTCAC 1440  
 CCAGGCCAGG GCTTCGAGG GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTCGCGCTC 1500  
 TCGCTGGATG GTCGCTCGG GCAGGCCCCC TGGAGCGACC TGCTTCTTTG GCACTGTGTG 1560  
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620  
 GCTCTTGGGG CCTTCTTCTT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGTGAGGAG 1680  
 GCAGCAGGGA GGAAGAGACT GGCCTTCAAG TTTGAGGGGA TGGGCGTGA CCTCTTTGGC 1740  
 GAGTGTCTAT GCGACAGTGA GGTGAGGGCT GCGCCCTCC TCCTCGTCTG CTGCGCGCTC 1800  
 TGGGGGATG CCACTTGCCCT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTCTTTTGCC 1860  
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920  
 CCCATCTGGG CCTTCTTCTT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGCCTCTATC 1980  
 ACCTTCAGGA AATCAGAAGA GGAGCCACA CCGGAGGAGC TAGAGTTTGA CATGATAGT 2040  
 GTCATTAAAT GGGAAAGGCC GTTCGGGACG GCGGACCCAG CCGAGAAGAC GCCGCTGGGG 2100  
 GTCCCGGCC AGTCGGGCGG TCCGGGTTGC TGGGGGGGCC GCTGCGGGG GCGCGGGTGC 2160  
 CTACCGCGCT GGTTCACATT CTGGGGCGCG CGGGTGACCA TCTTCATGGG CAACGTGGTC 2220  
 AGCTACCTGC TGTTCCTGCT GCTTTTCTG CGGGTGTGTC TCGTGGATT TCAGCGGGG 2280  
 CCGCCCGGCT CCTCGAGCT GCTGCTCTAT TTCTGGGCTT TCACTGCTCT GTGCGAGGAA 2340  
 CTGCGCAGG GCTCAGCGG AGGCGGGGCG AGCCTCGCCA GCGGGGGCCC GGGGCTGGC 2400  
 CATGCTCAC TGAGCCAGCG CTTGCGCCTC TACCTCGCG ACAGCTGGA CCAGTGGAC 2460  
 CTAGTGGCTC TCACCTGCTT CCTCTTGGG GTGGGCTGCC GGTGACCCC GGGTTTGTAC 2520  
 CACCTGGGCC GCACTGTCTT CTGCATCGAC TTCATGGTT TCACGTGGG GCTGCTTAC 2580  
 ATCTTCAGG TCACAAACA GCTGGGGCCC AAGATCGTCA TCGTAGCAA GATGATGAAG 2640  
 GAGCTGTCTT TCTTCTCTT CTTCCTCGG GTGTGGCTGG TAGCCTATGG CGTGGCCAG 2700  
 GAGGGGCTCC TGAGGCCAGG GGACAGTGAC TTCCCAAGTA TCCTGCGCG CGTCTTCTAC 2760  
 CGTCCCTACC TGCAGATCTT CGGGCAGATT CCCCAGGAG ACATGAGAGT GGCCCTCATG 2820  
 GAGCACAGCA ACTGCTCGTC GGAGCCCGGC TTCTGGGCAC ACCCTCTTGG GGGCCAGGCG 2880  
 GGCACCTGGC TCTCCAGTA TGCCACTGG CTGGTGGTGC TGCTCTCTGT CATCTTCTG 2940  
 CTGTGGCCA ACATCTCTCT GTTCAACTTG CTCAATGCCA TGTTCAGTTA CACATTGGC 3000  
 AAAGTACAGG GCAACAGCGA TCTTACTG AAGCGCAGC GTTACCGCT CATCCGGAA 3060  
 TTCACTCTC GGGCCGGCTT GGGCCCGGCC TTTATCGTCA TCTCCACTT GCGCCTCTG 3120  
 CTCAGGCAAT TGTGCAAGCG ACCCCGAGC CCCCAGCGT CCTCCCGGC CCGAGCAT 3180  
 TTCGGGTTT ACCTTCTTAA GGAAGCCGAG CGGAAGCTGC TAAAGTGGGA ATCGGTGCAT 3240  
 AAGGAGAAT TCTCTCTGCG ACGGCTAGG GACAAGCGG AGAGCGACT CGAGCGTCTG 3300  
 AAGCGCAGT CCAGAAAGGT GGAATGGCA CTGAACAGC TGGGACACAT CCGGAGTAC 3360  
 GAACAGCGCC TGAAGTGTCT GGAGCGGAG GTCCAGCAGT GTAGCCCGT CCTGGGGTGG 3420  
 GTGGCGAGG CCTGAGCGG CTCTGCTTG CTGCCCCAG GTGGGCGGCC ACCCCCTGAC 3480  
 CTGCTGGGT CCAAGACTG A

**A198 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Protein Accession #: none found

Signal sequence: none found  
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995  
 Cellular Localization: plasma membrane

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

1      11      21      31      41      51
|      |      |      |      |      |
MEDAFGAADV TVWDSADHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
TWGFRAPNLV VSVLGGSGGP VLQTLQDLL RRGIVRAAQS TGAWIVTGGL HTGIGRHHGV 120
AVRDHQMAST GGTKVAMGV APWGVVRNRD TLINPKGSFP ARYRWGRDPE DGVQFPPLDYN 180
YSAFPLVDDG THGCLGGENR FRLRLSYIS QKRTGVGGTG IDIPVLLLI DGDERMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLASTLEDT LAPGSGGARQ GEARDRIIRF FPKGLLEVLO 300
AQVERIMTRK ELLTVYSSD GSEEFETIVL KALVKACGSS EASAYLDEL RAVAWNRVDI 360
AQSELFRTDI QWRSFHLEAS LMDALLNDRP EFVRLISHG LSLGHFLTPM RLAQLYSAAP 420
SNSLRNLDD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQGFSGSMY LLSDKATSPL SLDAGLGQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540
ALGACLLLRV MARLEPDARE AARRKDLAFK FEGMGVDLFG ECTRSSEVRA ARLLLRRCPL 600
WGDATCLQLA MQADARAFPA QDGVQSLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI 660
TFRKSEETP RELEFDMDS VINGEGPVT ADPAEKTPLG VPRQSGRPGC CGGRCCGRRC 720
LRRWFHFWGA PVTIPMGNVV SYLLFLLLS RVLVDFQPA PPSLELLLY FWAFTLLCEE 780
LRQGLSGGSG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLFG VGCRLTPGLY 840
HLGRTVLCID FMVPTVRLHL IFTVNKQLGP QIVIVSKMMK DVFFFLFPLG VWLVAYGVAT 900
EGLLRPRDSD FPSILRRVFP RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPGGAQA 960
GTCVSYANW LVVLLVIFL LVANILVNL LIAMFSYTFG KVQNSDLYW KAQRYRLIRE 1020
FHSRPAALFP FIVISHLRL LRQLCRPRS PQSSPALEH FRVYLSKEAE RKLLTWESVH 1080
KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQCSRVLGW 1140
VAEALSRSAL LPPGPPPPD LPGSKD
  
```

**A199 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Nucleic Acid Accession #: AA054237  
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCTGTG CTCCCTGGGG 60
CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CGACCCCGG CGGCCACAAG 120
GAGAGCTGCG AGCCGACCGG CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CGGCTGATG 180
CGCTGTGCGC ACTTGCCTCG GCGGGACTCG CCCCCTGGGG GCGCGCGGCT GCTCCCGGGC 240
GCGCGCGGGG GCGCGGACCC CGAGTCTCTG CGCTCGCTCC TGGGCTCGG CGGGCTGGAC 300
GCCGAGTGGG GCGCGGCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCATCG ACCCGGACAT CGACACCCTC ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCAGG ACATTCTTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGAATCTCGT ATGATTGAA CCGGCTCCCA 660
TGCACCATTT CCTCTGTGAC TTATGCCGCG AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCTGACC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCTGGTGCTA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA
  
```

**A200 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Protein Accession #: none found  
 Signal sequence: 1-18  
 Transmembrane domains: 179-201, 209-231, 257-279  
 Cellular Localization: plasma membrane

65  
 70  
 75  
 80

```

1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
PLSHLPLRDS PPLGRRLLP GPGRADPESW RSLGLGLLD AECGRPLFAT YSGLWRKCYF 120
LGIDRDIDTL ILKGIAQRCT AIKYHPSQPI RLRLNIPENLT KTIQDEWBL LHLRRTAGF 180
LGMVAVLLC GCIVATVSFP WEESLTQHVA GLLPLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV
  
```

**A201 DNA SEQUENCE**

Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

80

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCGAC TGAATCGGAA AAAAAGCTTA AGTTTGGTAA AAGAGTTGGA TGCCITTCGG 60
AAGGTTCTCG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
  
```

5 TTTACAATA TGGCTTTATT AACATAATG GAATTCCTCAG TATATCAAGA TACATGGATG 180  
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT 240  
 ACTGTTGCCA TGAAGTGTC AATATGTTGGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300  
 GTTGCACTCG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360  
 10 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420  
 CAAGATGTGA TATTTAAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480  
 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATAAAA 540  
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600  
 CATTGGCAG CACITGTCAA CCATGAATCT TACAATTTT CTCTAGAAT AGATCATTG 660  
 15 TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAAGTGA AAAAATTGCT 720  
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAAACAA ACTACATACA 780  
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840  
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTTCTCTT 900  
 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGCCAGT TTTTGTAGG ACTCTGTGGT 960  
 20 ATGTTTGGAG GAATCTTTTC AACACAGGC ATGTTACATG GAATGGAAA ATTTATAGTT 1020  
 GAAATAATTT GCTGTGCTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCTTTT 1080  
 GAGGATGGCC ACACAGACAA CCACTTACCT CTTTTAGAAA ATAATACACA TTGA

20 **A202 Protein sequence:**  
 Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Protein Accession #: NP\_057654  
 25 Signal sequence: none found  
 Transmembrane domains: none found  
 Cellular Localization: nuclear

30 1 11 21 31 41 51  
 | | | | | |  
 MRLNRKKTLLVSKELDAFPKVPESYVETSASGGTVSLIAFTTMALLTIM EFSVYQDTWM 60  
 KYEYEVDRDFSSKLRLINIDI TVAMKQYVGVADVLDAETM VASADGLVYE PTVFDLSPQQ 120  
 35 KEWQRLQLI QSRLEQEHSL QDVIFKSAFK STSTALPPRE DSSSQSPNAC RIHGHLYVNK 180  
 VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGLVPAII NPLDGTEKIA 240  
 IDHNMQFYF ITVVPKLTHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300  
 MVTVTEHIMP FWQFFVRLCG IVGGIFSTTG MLHGIGKFIV EIICRFRLG SYKFPVNSVPP 360  
 EDGHTDNLHP LLENNTH

40 **A203 DNA SEQUENCE:**  
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 Probeset Accession #: S79876  
 45 Nucleic Acid Accession #: NM\_001935.1  
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 | | | | | |  
 CGCGCGTCTCG CGCGCGCCGCG GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC 60  
 GAGGAGACGCG CGACGATGAA GACACCGTGG AAGATTCCTC TGGGACTGCT GGGTGCTGCT 120  
 CGCGCTTGTC CCACTCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180  
 55 ACAGCTGACA GTGCAAAAC TTACACTCTA ACTGATTACT TAAAAATAC TTATAGACTG 240  
 AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAT 300  
 ATCTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360  
 GATGAGTTTG GACATTCAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420  
 TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTTAT 480  
 60 GATTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540  
 ACATGGTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGGG ACAATGACAT TTATGTTAAA 600  
 ATTGAACCAA ATTTACCAAG TTACAGAATC ACATGGACGG GGAAGAAGA TATAATATAT 660  
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCCACTC TGCTCTGTGG 720  
 TGGTCTCCAA ACGGCACTTT TTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780  
 65 ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA 840  
 TATCCAAAGG CAGGAGCTGT GAATCCAACT GTAAAGTTCT TTGTTGTAAT TACAGACTCT 900  
 CTGAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGCTTTC TATGTTGATA 960  
 GGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTC TTTCAGTGG 1020  
 CTGAGGAGA TTCAGAACTA TTCGGTCATG GATATTGTG ACTATGATGA ATCCAGTGG 1080  
 70 AGATGGAAC GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140  
 AGATTTAGGC CTTCAGAAC TCATTTTACC CTGATGGTA ATAGCTTCTA CAAGATCATC 1200  
 AGCAATGAAG AAGGTTACAG ACACATTGCG TATTTCACAA TAGATAAAAA AGACTGCACA 1260  
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACAGG TGATTATCTA 1320  
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAATCCAA 1380  
 75 CTTATTGACT ATACAAAAGT GACATGCTCT AGTTGTGAGC TGAATCCOGA AAGGTGTCAG 1440  
 TACTATTCTG TGTCAATTCAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCGGTCTCT 1500  
 GGTCTGCCCC TCTATCTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCTTGGAA 1560  
 GACAAATCAG CTTCGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAACTGGGAC 1620  
 TCAATTATT TGAATGAAAC AAAATTTTGG TATCAGATGA TCTTGCTTCC TCAATTTGAT 1680  
 80 AAATCCAGA AATATCTCT ACTATTAGAT GTGTATGACG GCCCATGTAG TCAAAAAGCA 1740  
 GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800  
 GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860  
 AGAAGACTTG GAACATTGGA AGTTGAAGAT CAAATTTAAG CAGCCAGACA ATTTTCAAAA 1920  
 ATGGGATTTG TGGACAAACA ACGAATTGCA ATTTGGGGCT GGTCAATAGG AGGGTACGTA 1980  
 ACCTCAATGG TCTTGGGATC GGAAGTGGC GTGTTCAAGT GTGGAATAGC CGTGGGCGCT 2040

5 GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100  
 CCAGAAGACA ACCCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAAAAATTTT 2160  
 AAACAGTTTG AGTACCTCCT TATTATGGA ACAGCAGATG ATAAACGTTCA CTTTCAGCAG 2220  
 TCAGCTCAGA TCTCCAAGC CCGTGTGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280  
 ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340  
 AGCCACTTCA TAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400  
 AAGCTTATTA AAACCTATT TTGTTTTCAT TATCTCAAAA CTGCACGTGC AAGATGATGA 2460  
 TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520  
 10 ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCAACA GATTATTACC TTACAGAAAT 2580  
 TTGAATTATC CGGTCGGGTT TATTGTTTAA AAATCATTTC TGCATCAGCT GCTGAAACAA 2640  
 CAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700  
 TTTCTAATCG GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760  
 AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGATTAG GGAGAGAAGA TAGCAGGGCA 2820  
 TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCCCTCGG 2880  
 15 AGAAGAGCTG TTCACACAGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT 2940  
 CAGGAATACA AATATCGAAA GCCTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000  
 AAAGAAATGT AAGGGAATCT GCCAGCAACG CAGCCCCCAG GTGCCAGTTA TGGCTATAGG 3060  
 TGCTACAAAA ACAGCACAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATAA 3120  
 20 TACTGATGTT CCTAGTGAAG GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180  
 CTGTTAAAG ATGAAATAT TTGTATCACA AATCTTAACT TGAAGGAGTC CTGTCATCAA 3240  
 TTTTCTTAT TTCAATTTCT TGAGTGTCTT AATTAAAGA ATATTTTAACT TTCCTGGAC 3300  
 TCATTTTAAA AAATGGAACA TAAATACAA TGTATGTAT TATTATTCCT ATCTACATA 3360  
 CTATGGAATT TCTCCAGTC ATTTAATAAA TGTGCCTCA TTTTTC

25 A204 Protein sequence:  
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 30 Probeset Accession #: S79876  
 Protein Accession #: NP\_001926.1  
 Signal sequence: none found  
 Transmembrane domains: 6-28  
 DPPIV\_N\_term domain: 43-557  
 35 Peptidase\_S9 domain: 558-635  
 Cellular Localization: plasma membrane

40 1 11 21 31 41 51  
 MKTPWKILLG LLGAAALVTI ITVPVLLNKK GTDDATADSR KTYTLTDYLK NTRYRLKLYSL 60  
 RWISDHEYLY KQENNILVFN AEYGNSSVPL ENSTFDEFHG SINDYSISPD GQFILLEYN 120  
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVINSFP GHKLAYVMNN DIYVKIEPNL 180  
 PSYRITWTGK EDIYNGITD WYEEEVFSA YSALWWSFNG TFLAYAQFND TEVPLIEYSP 240  
 45 YSDESLLQYPK TURVPYKPK AVNPTVKPFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300  
 CDVTWATQER ISLQWLRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360  
 EPHFTLDGNS FYKIIISNEEG YRHICYFQID KKDCTPITKG TWEVIGIEAL TSDYLYIYSN 420  
 EYKMPGGGRN LYKLIQIDYT KVTCLSCSELN PERCQYYSVS FSKEAKYQQL RCGSPGLPLY 480  
 TLHSSVNDRG LRVLNENSL DKMLQNVQMP SKKLDPIILN ETKFWYQML PHFEDKSKKY 540  
 50 PLLLDVYAGP CSQKADTVFR LHWATYLAST ENIIVASFDG RSGGYQGDKI MHAINRRLGT 600  
 FEVEDQIEAA RQFSKMGFVD NKRIAINGWS YGGYVTSMLV GSGSGVFKOG IAVAPVSRWB 660  
 YYDSVYTERY MGLPTPEDNL DEYRNSTVMS RAENFKQVEY LLINGTADDN VHFQQAQIS 720  
 KALVDVGVDV QAMWYTDHGH GIASSTAHQH IYTHMSHFPIK QCPSLP

55 A205 DNA SEQUENCE  
 Gene name: predicted exon  
 Unigene number: none found  
 Probeset Accession #: none found  
 Nucleic Acid Accession #: none found  
 60 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51  
 ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAATGACA ATGCCATCAG AGTTGACAAC 60  
 AGAAGTGTA TTAAGTGCG TGCTAACCG TGTTCCTGCG ATGAGGCAGA AAGTGAATCC 120  
 AGAAACCCCTC AGGAGCTCTG GATGGGCTCG CTCCTCTGA TGGGGGTCTC AGAAGCATGT 180  
 GTGGAAATGA GGCCTCTGTC AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240  
 CAGCCACAC TGGATGTCTA A

70 A206 Protein sequence:  
 Gene name: predicted exon  
 Unigene number: none found  
 75 Probeset Accession #: none found  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 46-68  
 Cellular Localization: not determined

80 1 11 21 31 41 51  
 MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHEAESES RNPQELWMGL LLLMGVLEAC 60  
 VEMRPLSVWS LRDDKEQSPH QPTLDV

**A207 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.222886  
 Probeset Accession #: AI672225  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

```

10      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTGGAAGCA GTAAATGTTT AAAAACTGCT 60
      CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
      ATTGATGTAT CTTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
      ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
      TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTATGTGGG ATTCCAGAA 300
      AACCTGACTA ATGGTGCCGC TGCTGGCAAT GGTGATGATG GATTAATTCC TCCAAGGAAG 360
      AGCAGAACAC CTGAAGGCCA GCAATTTCTT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
      GTCAAAGATC AGATAGTTGT AGATATGCGG OGTTATTTCT GA
  
```

**A208 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.222886  
 Probeset Accession #: AI672225  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 16-38  
 Cellular Localization: not determined

```

30      1      11      21      31      41      51
      |      |      |      |      |      |
      MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLLEQN IDVSSQDLDR RPESMLFLVI 60
      IMWTSFVEDN LSMGWGKLED FMAIEEEMKK HGSTHVGFPE NLITNGAAAGN GDDGLIPPRK 120
      SRTPEQQQFP DTENEYHRF VKDQIVVDMR RYF
  
```

**A209 DNA SEQUENCE**

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1  
 Unigene number: Hs.23796  
 Probeset Accession #: NM\_014253  
 Nucleic Acid Accession #: NM\_014253  
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

```

45      1      11      21      31      41      51
      |      |      |      |      |      |
      GACTGCTTGC ATTAAAGGAC TTCCCTCATCC TTTTITTCAT GAAACTGAGC TTGCTTAATC 60
      AGAGATGGAG CAAACTGACT GCAAACCCCTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT 120
      GGATCTAGCT TACACCAGTT CTTCTGATGA GAGTGAAGAT GGAAGAAAC CAAGACAGTC 180
      ATACAACCTCC AGGGAGACCC TGACAGAGTA TAACCAGGAG CTGAGGATGA ATTACAATAG 240
      CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAAC 300
      CTCTCAGCTC CTGTGCTCTG GCTACCAAAAC AGACATGCAC AGCGTTTCTC GGCATGGGCTA 360
      CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
      TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCTGTGT TGTCAGCCG 480
      GGCCAACCTCT GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
      TGGTTTCAAA TTCTCTCTGT TTTGTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
      TGTGACAGAG AGCCACACAC ACCAGTTTCA CTTGAGACCC CTCCACCGC CACCTCCGCC 660
      TCCTCATGCC TGCACTGTG CCAGGAAGCC ACCCCTGCA GGGGACTCTC TTCAGAGGAG 720
      ATCAATGACT ACCCGCAGCC AGCCAGCCC AGCTGTCCA GCTCCCCAA CCAGCACGCA 780
      GGATTCAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCA 840
      GCATTCCCTG TTCAACATG GATCTGGTTC CTCTGCGATC TTGACTGCGC CCAGTCAGAA 900
      CTACCCCTCTG ACATCCAATA CCGTGTACTC GCCCCTTCCC AGGCCTCTTC CTCGAAGCAC 960
      CTTTTCOCGA CCGCTCTTTA CCTTTAACAA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
      AGCATTGAGC GCCACTGCAA TCACAGTGAC TTTGGCCTTG TTAAGTCCCT ATGTGATTGC 1080
      AGTGCAATTG TTCGGCCTGA CTTGGCAGTT GCAACCAATT GAAGGAGAGC TGTATGCAAA 1140
      TGGAGTTAGC AAAGGGAACA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
      AGGAAAGATT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGGACGGG CGATAGACAC 1260
      TGGAGAAATT GACATTGGTG CACAGGTTCAT GCAGACCATT CCACCTGGTT TATTCTGGCG 1320
      TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTTCIT TAGCCAAGGA 1380
      CTCTCTGCTG GGAATTTATG GCAGAAGAAA CATTCACCT ACACATACTC AGTTTGATT 1440
      TGTAAAACCTA ATGGATGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC 1500
      ACAGCACTCC CCTCGAACC TGATCTTAAC TTGCTTCAG GAGACAGTT TCATAGAGTA 1560
      TATGATCAAA GGCCTCTGCT ATCTGGCGTT TTACAATGAT GGAAGAAAGA TGGAGCAAGT 1620
      ATTCTGTGTA ACTACAGCAA TTGAATAAT GGATGACTGT TCAACCAATT GCAATGGAAA 1680
      TGGAGAGTGT ATCTCTGGCC ATTGTCAATG TTTCCAGGA TTCCTTGGAC CTGACTGTGC 1740
      TAGAGATTCC TGCCCTGTGC TGTGTGGTGG GAATGGAGAA TACGAGAAAG GACTGTGT 1800
      CTGCGGCGAT GGTGGAAGG GGCCAGAGTG TGACGTTCCG GAAGAACAAAT GCATTGATCC 1860
      AACATGCTTT GGCACGGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920
      AGGAGAAATA TGGGAGGAG AGGACTGCCT AGACCCAATG TGTTCCAACC ATGGCATCTG 1980
      TGTAAAAGGA GAATGTCACT GTTCTACTGG CTGGGGAGGA GTTAAGTGTG AAACCCACT 2040
      TCCTGTATGT CAAGAGCAGT GCTCAGGACA CGGAACITTT CTCTGGAGC CTGGAGTATG 2100
      CAGCTGTGAT CCCAAGTGA CAGGATCTGA CTGCTCAACA GAGCTGTGTA CCATGGAGATC 2160
      TGGTAGCCAT GGAAGTCTGT CAAGAGGAAT TTGCCAGTGT GAAGAAAGCT GGTAGGAGG 2220
      AACATGTGAG GAACGCTCCT GTCATTCTCA TTGACTGAG CATGGCCAAT GCAAAGATGG 2280
  
```

	AAAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
	AAATGGTTGG	CAGTGTGTGT	GTCAAGGTGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTGAT	2460
5	GGAAATGCTT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTTAACCG	ACTGTGTGGA	2520
	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCCT	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCAITTCAGC	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAATTC	TCATTGGCAA	GGACAGTACT	CATGTCAITC	CTCCTGAGGT	2700
	GTCAITTCAG	AGCAGGCGTG	CCGTGTGTAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAA	2760
10	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCAAGT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAGCTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCATCC	CTTTTCCTGC	CTGAGAAGAG	AACACTCTGG	TTGCCTTGGG	ATCAGTTTAT	2940
	TGTGTAGAG	AAAGTCACCA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCTC	GGATATCTC	3000
	CAACTTTATC	AGCCCAAAAC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
15	CTGTCCAGAG	AGGGGAACCTA	TTGTTCTGTA	GCTGCAGGTT	GTACAGGAGG	AAATTTCCCAT	3120
	TCCTCCAGC	TTTGTGAGGC	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAAACCT	3180
	GCTACGGAT	CTTCTGACAC	ATTCAAGAT	TCCCGTAGGC	ATGATAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GGCCCAATTA	ATCTTGCTA	3300
	CACATTGTCT	TGGAACAAGA	CCGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
20	TTTGGTATCT	TGCGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTCTCT	GGGAGCAAG	3420
	GACAGTCGTT	TTACAGGTTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAAGCATCAC	ATTTTGAATC	CTCAAAGTGG	AATCATACT	AAAGGGAATG	GAGAAAAAT	3540
	GTTCATTTCC	CAGCAGCCCC	CAGTCATATC	AACATAATG	GGTAATGGAC	ACCAAAGGAG	3600
	TGTAGCTCTG	ACCAACTGCA	ATGGCCGAGC	CCACAACAC	AAACTCTTTG	CTCCTGTGCG	3660
25	CTTAGCTTCT	GGCCCTGATG	GCAGTGTGTA	TGTTGGGAC	TTCAATTTTG	TAAGGAGAA	3720
	ATTTCCCTCG	GGAAACCTCG	TTAGTATTTT	GGAAATTAAG	ACAAGTCTGT	CTCACAATA	3780
	CTATCTGGCT	ATGAGCCCTG	TGCTGGAATC	ACTCTATCTA	TCAGACACCA	ATACTGCAA	3840
	AGTCTACAAG	TTGAAATCTC	TTTGGAGAC	GAAAGATCTG	TCCAAGAAAT	TTGAAAGTGT	3900
	GGCAGGAAGT	GGTGATCAGT	GCCTTCCCTT	TGACCAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
30	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTGATAGGCG	ATGGATTAT	4020
	TTACTTTGTG	GATGGGACTA	TGATTCGCAA	AATGATGAG	AATGCTGTGA	TCACAACGT	4080
	AATCGGCTCA	AATGGCTGTA	CTTCCACACA	ACCACTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CAGTCAGGTC	CGATTAGAGT	GGCCAACAGA	CCTTGCAGTA	AATCTATGAG	ACAATTCATT	4200
	GTATGCTCTG	GATAACAACA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTGGATCAT	4260
35	CGCAGGACGC	CCCAATCACT	GCCAGGTGCC	AGGCATCGAT	CATTTCCTGG	TCAGCAAGGT	4320
	AGCAATGCT	TCCACTCTAG	AGTCAGOGAG	GGCCATCAGT	GTCTCCCA	CGGGGCTGCT	4380
	CTTCATAGCT	GAACACAGAG	AGAGGAAAGT	AAACCGCATT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATGCTG	GTGCCCCAC	TGACTGTGAC	TGCAAAATG	ATCCAAACCTG	4500
	TGACTGTCTT	TCAGGTGATG	GTGGCTATGC	CAAAGATGCA	AAGATGAAG	CCCTTCTCTC	4560
40	CTTAGCAGTG	TGCGCTGATG	GAACCTCTA	TGTGGCAGAC	CTCGGAATG	TTGGAATTCG	4620
	TACCATCAGC	AGGAACCAAG	CCCACTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACGTGTTT	ATAACTTCAC	CTACAATCT	GAGGTGACT	TGGCGCGAT	4740
	GATAACAAGG	GACTATGTTT	ATAACTTCAC	CTACAATCT	GAGGTGACT	TGGCGCGAT	4800
	TACCAAGCAG	AATGGCAATT	CAGTGCACAT	TGCGCGTGAT	GCAGGCGGAA	TGCCGCTATG	4860
45	GCCTGTGGTG	CCTGGGGGAC	AAGTATACCT	GCTGACTATA	AGCAGCAATG	GAGTCTGAA	4920
	AAGAGTGTC	GCCCAAGGCT	ATAATCCGGC	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCTGGCTACC	AAAGATTAAG	AAATGGATG	GACAAACGTT	TATGAGTATG	ACCCGAGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTGACG	AGCTTCCACA	GTGACCTGGA	5100
	GAAGCTGACA	AAAGTGGAGC	TAGATACTTC	CAACCGTGAA	AATGTCTCTA	TGTCAACCAA	5160
50	CTTGAACGCA	ACTAGTACCA	TATATATTTT	AAACCAAGAA	AATACTCAAA	GTACCTATCG	5220
	GGTGAATCCA	GATGGTTCCC	TGCGTGTAC	TTTTGCCAGC	GGGATGAGAA	TCGGCCCTCAG	5280
	CTCAGAGCCC	CACATCTAGC	CAGGGGCGAGT	CAACCTTACC	CTGGGCAAT	GCAACATCTC	5340
	ATTGCCCGGA	GAGCACAATG	CAAACTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
	AGGCAATGTT	TGCGCTTTTG	AAAGGAGGCT	GAGGGCCAC	AACAGAAACC	TACTCTCCAT	5460
55	AGATTTTGAT	CATATAACCC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AATTCACCTT	5520
	TGCAATTTCT	TATGACGACA	CTGGGCGACC	CATTCTGTGG	TCTCTGTGAA	GCAGATATA	5580
	TGAAGTGAAC	ATCATAAT	CACCTTCGGG	ATTGGTGACG	TTTATTCAAA	GAGGAAAGTG	5640
	GAATGAAAA	ATGGAATATG	ACCAGAGTGG	GAAATTAAT	TCAAGAACTT	GGGCTGATGG	5700
	GAAATTTTGG	AGCTATACCT	ACTTAGAAAA	ATCTGTGATG	CTTCTCTTAC	ACAGCCAGCG	5760
60	GGTTACATC	TTTGAGTATG	ACCAATCAGA	TTGCCCTGCT	TCAGTTACCA	TGCCATGAT	5820
	GGTGGGCCAC	AGCTTACAAA	CCATGCTTTC	AGTGGGCTAC	TACGTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAAG	CTATAGTCGA	GATGGCCGAT	TGCTACAGAC	5940
	CCTGCATCTG	GGGACAGGGC	GCAGAGTCTT	ATACAAGTAC	ACCAAGCAAG	CAAGGCTTTC	6000
	TGAGGTTCTC	TATGATACCA	CTCAGGTCAC	ATTAACATAT	GAAGAGTCTT	CTGAGTGAT	6060
65	TAAGACAATA	CACCTGATGC	ATGACGGATT	CATCTGCACA	ATCAGATACA	GGCAACAGG	6120
	ACCTCTTAT	GGAGCCGAGA	TTTTAGATT	CAGTGAAGAA	GGCTTGTGTA	ATGCAGCGTT	6180
	CGACTACAGC	TACACAAT	TCCGAGTCAC	AAGCATGCAA	GCTGTAATCA	ATGAAACCCC	6240
	TTTGCTTATA	GATCTTTTACC	GATATGTTGA	TGCTCTGGC	AGAACAGAGC	AGTTTGGAAA	6300
	ATTCAAGTGA	ATTAAATACG	ATTAAATCA	GGTCATAACT	ACTACAGTGA	TGAAACACAC	6360
70	CAAAATCTTC	AGTGCCAAATG	GACAAGTCAT	TGAAGTCCAA	TATGAATCC	TAAAGGCAAT	6420
	TGCCACTGCG	ATGACCAATC	AATATGATAA	TGTGGGCCGA	CATGGTAATA	TGTGCATAG	6480
	GGTAGGAGTA	GATGCCAATA	TAAACAGGTA	CTTCTATGAA	TACGATGCTG	ATGGGCAACT	6540
	TCAGACTGTT	TCTGTAATG	ACAAACCCCA	GTGGCGTTAT	AGTTACGATC	TGAATGGAGA	6600
	CATCAACCTC	TTAAGCCATG	GGAAGAGTGC	TGCTCTTACT	CCTCTCGAT	ATGACCTCG	6660
75	AGACCGCATC	ACCAGATTAG	GAGAAATTC	GTATAAAATG	GATGAAGATG	GCTTTCTGAG	6720
	GCAGAGGGGA	AATGATATTT	TTGAATATAA	TTCTAATGGC	CTGCTGCAGA	AAGCCTACAA	6780
	TAAGGCTTCT	GGCTGGAGCT	TGCAGTATTA	CTATGATGGG	CTTGGGCGAC	GTGTCGGGAG	6840
	TAAGTCCAGC	CTAGGGCAGC	ACCTTCAGTT	CTTTGTGAC	GCGACCGCGA	ACCCCATAG	6900
	AGTTACTCAT	TTGTACAACC	ACCAAGGCTC	GGAGATTACA	TCTCTGTATT	ATGATCTCCA	6960
80	AGGTCACTT	ATTGCCATGG	AGTTAAGCAG	TGGTGAAGAA	TATTATGTAG	CCTGTGATA	7020
	TACAGGTACC	CCACTAGCTG	TGTTAGCAG	CCGAGGTGAG	GTCAATAAAG	AGATACTATA	7080
	CACACCTTAT	GGGATATCT	ATCATGACAC	TTACCTGAC	TTTCAGGTCA	TAATTGTTT	7140
	TCATGGAGGA	CTCTATGATT	TCCTTACTAA	ATTAGTGCAC	CTGGGGCAA	GGGATTATGA	7200
	TGTTGTGCT	GGCAGATGGA	CAAGGGCCTA	TCATCACA	TGGAACAGT	TGAACCTCT	7260
	TCCTAAACCA	TTCAACCTCT	ACTCCTTTGA	AAATACTAC	CCAGTTGGCA	AAATTCAGA	7320

	TGTTGCAAG	TATACCACAG	ACATCAGAAG	TTGTTGGAG	CTATTTGGTT	TCCAATTACA	7380
	CAATGTACTA	CCTGGATTTT	CCAAACCTGA	ATTAGAAAAT	TTAGAAATTA	CTTACGAGCT	7440
	TCTACGGCTT	CAGACAAAAC	CTCAAGAGTG	GGATCCTGGA	AAGACTATCC	TGGGCATTCA	7500
5	GTGTGAACCT	CAGAAACAGC	TCAGGAATTT	CATTTCCTTG	GACCAACTAC	CTATGACTCC	7560
	CCGATACAA	GATGGACGGT	GCCTTGAAGG	AGGGAAGCAA	CCAAGTTTGG	CTGCTGTCCC	7620
	TTCTGTTTTT	GGAAAGGTA	TAAAATTTGC	CATCAAGGAT	GGCATAGTAA	CAGCTGATAT	7680
	TATAGGAGTA	GCCATGAAG	ATAGCAGGCG	GCTTGCTGCC	ATTCTCAATA	ATGCCCATTA	7740
	CCTGGAAAAC	CTACATTTTA	CCATAGAGGG	GAGGGACACT	CACACTTCA	TTAAGCTTGG	7800
10	GTCTCTGGAG	GAGACCTGG	TGCTCATCGG	TAACACTGGG	GGGAGGCGGA	TTCTGGAGAA	7860
	TGGTGTCAAT	GTCACTGTGT	CCCAGATGAC	TTCTCTGTTG	AATGGGAGGA	CTAGACGGTT	7920
	TGCAGATATT	CAGCTCCAGC	ATGGAGCCCT	GTGCTTCAAC	ATCCGGTATG	GGACAACCTG	7980
	CGAAGAGGAA	AGAATACACG	TGTTGGAGAT	TGCCAGACAG	CGCGCAGTGG	CCCAGGCCCTG	8040
	GACTAAGGAA	CAAGAAGGC	TGCAAGAGGG	GSAAGAGGGG	ATTAGGGCAT	GGACAGAAGG	8100
15	GGAAAAGCAG	CAGCTTTTGA	GCACCTGGCG	GGTACAAGGT	TACGATGGGT	ATTTTGTITT	8160
	GTCTGTTGAG	CAGTATTTAG	AACTTTCTGA	CAGTGCCAAT	AATATTCAC	TTATGAGACA	8220
	GAGCGAAATA	GGCAGGAGGT	AACAAAAATA	TCTCTGCCCT	TGCGTCACCA	AAGACTGCCT	8280
	GTTTTTAAAA	CATAAAATGG	TTTATTGTAT	TGGTTTTCTA	GATCAGAACT	CTGTATATGT	8340
	AAATATGGAG	GA AAAACATA	TCCAACCTGC	TTTCAATGTG	ACGGAAGATG	GTATTTTAAT	8400
20	ATTGTTTGT	TAAACTCTTT	AAGAAATGAC	AGAGATTTT	AGTTCITGTG	TGGCAGTATT	8460
	CAAAATAACA	CAAGTAGAAC	TCAACAGCT	AAAAACAGTT	TTAGAAAAGC	ACCACCTTCA	8520
	ATTGCGGAG	CCATGCATAT	GTTCATAT	CCAGAAAGAA	CCCAAGGTTT	TCTATCTCTA	8580
	TTGTGAGAAG	CAGTTTCATC	CTTAACCTGT	GGCAGAACTT	ACGGGCTATT	TGAATAGGTG	8640
	GTGCAATAGT	ATCTGAACT	TGCCCTTTCG	AAGACTGCCA	GCCCTTTGAC	GTTTCCAGA	8700
25	TCGTGTATAG	GAAACTTAAA	AACAGGTGTA	AAATGCTTTC	AGCCACCATC	TCTTAGAGTG	8760
	AGGACCCAAT	TGCCCTTCTC	TCCTGATTAT	TCCTCCTTGC	TTGTTAAAGT	AAATGCCATA	8820
	TTGTTGTGCT	GTGTTTGGCG	GTGTGGTGGC	TGGGTTCTGT	CTACCATGCT	TCCTGTGGGG	8880
	TGTGTAAACC	AGACTGTATA	GCCGCTATTT	GCTCGTGTGT	ACATGATACC	AAAGCAGCTG	8940
	GCCAGCGTGA	CCTCTCTCAC	ACGACCTGTT	TTGACTCAAT	TTTTTACTAA	AAGTGTGTTA	9000
30	GCTGTATTGG	TATCATGTAA	ACATAGCTTT	TATTAACCTG	GGTAGGAATT	TCTCATTTAT	9060
	ATATAGGATG	TGTTTTGGTG	ATAGTTTCAC	ATTAGTGATT	CAGTATCTAT	ACACTGACCC	9120
	AATGGTTTTG	TGCACATGAA	CGGTAATTTA	CTTAAAGTA	TGATTTCTGG	ACAAAAACAA	9180
	ACAAAGGCTT	TAGCAGGCAT	ACGTGTCTGG	GATGCCGATA	CATACATTAA	CTACTACTGC	9240
	AGAAATTCAT	AAGAGCCAAA	ACCTTAAAAA	AATAGACCTG	GTACTTAAAT	GAAAGTACTA	9300
35	AAGGGAAGAC	CAGACCAAAC	ATCACAGCAG	TTGCTGCCAC	ATTGTTTCAG	CCCACCTAGA	9360
	TTTATCTTTC	AAATGTACAA	TTCTGTATTG	AACATCTCCC	AGCCATCTTC	AGGAAATOGA	9420
	ATCAAGTAA	TCCTTTCCAA	COGAAAACAT	TTCAACTAAC	TATAGAGAGG	CAGACTCAT	9480
	TTTACTAAAA	TAAATTTATC	AGTTAGTTAT	TTTGTCTCTC	CGTACTTACC	CATTATCTTT	9540
	TATTTAATCG	TCTCTACTGC	CTAGGAAAAT	AACATTTTTC	CAGGACGGGT	TATTTGTCT	9600
40	GCGATCATTT	AAAATTTGGA	GAAAGGTCAG	GATTAGTGT	AATATCAGCT	GCAGTTTCTC	9660
	AATCTCTAGG	AATCCTCGAG	TAAAACAAGC	CCCTTGGTGA	GCTGGAAGAT	TTGTGCCCAG	9720
	TGACAAAGAG	TGATTTTGTG	AAATGCTGTG	TAAATGTAA	TTACACACAA	TGAAAATACA	9780
	TGACAGCACA	ATGTGGCCCG	TAGAAAATTC	CCCTGAGCCA	GCTTCTGCAC	TTTCATCACC	9840
	GAATCTGAAC	ATTGCTATG	TCTGAAGSCA	AATTTATGAT	GSAATGTTAG	TTTGGATTCT	9900
45	TTCCAGATGC	TACCTAAATG	CAGTGTGGGG	TCATTGCCCT	GCTTTGCGAT	GACAGTTTCT	9960
	TTGAAAATAT	GCAAAGTCAT	AAGCTCATGT	TAAGGTTTTT	CAAGAGTCTG	CCTCCTACTA	10020
	CACAAAGGAA	AGCAAGGGA	AGGAAATGAC	CCTGGCAAA	AGTAGGGAAG	GGTGTATTCA	10080
	AACATTTTAT	TTTCAAAACC	TTGGGGTTAG	AATACCACTT	ACACATGTAT	TCTGAGAGAC	10140
	AGAATTCATG	AGGAACTCAT	CTCTCTTTAT	AACCTGGAAC	ACACCAGCTT	GATATATTGC	10200
50	TAAATCCATC	TAAATTCATA	TTATTGGGTT	TTTTCTGAAT	CAGGCTGTGA	TTAATGGTAC	10260
	AGTATTTATT	CAGAATGGAA	TTCTAAATTT	ACTAACCAAC	TTGTTGAAAA	TTTGAATACC	10320
	TTCAACACCA	CTTAAATAGT	GACCTTAAAT	TCTTAGAAC	TCTGATGTTT	TTTTAAATTA	10380
	ATGGAATAAT	AATTTGTGAA	CTGTATATAG	AGAGTGCAAT	CATAAATGTG	ATTATGTATT	10440
	TTATCACAAA	TCCAAATATG	CAATATTAGA	GTCTATTTTG	CTTATATTTT	AAGCAATTAT	10500
55	ACGTTTTTGC	AATTCATTGA	TGATGTATCA	TTTTCAAAC	GCTTTAAATA	TCCATTAGAA	10560
	ACAAATATT	GAAGCTTTTA	CTTAATAGTG	ATTACCTTGA	ACTGTGCATT	TCTAGTTTGT	10620
	AATAAGTATT	TGTTGGTTTC	GTGCTTTAG	TTTGTAAAG	TTACATTTTG	ATTATATTCA	10680
	GSAAATGAC	TTTTTATTAC	TTACAGCTGT	GGTTTTAATA	CTGCTTGA	CTATTATTAT	10740
	TCTTTTTACA	ACTCCTAAAG	CTTGAGGAG	GAAAGAAAAA	AAAAACAAAA	CTACTAATCA	10800
60	GTAGTAAATC	GAAGAGAAAC	ATTTGGGCAT	TTCTTAAGAA	GAAGATGGAG	ATATTGAGTA	10860
	TATCACTTCC	TATTCAGCTG	AATAGAAAGA	ATGCCCTCAT	TGACTTCGAG	TTCTGCGATT	10920
	TAAATATTG	AAAGAACAAT	TGTTTGCAT	TTCTGTATGA	AAGTAAAGC	ATTTTTCAGA	10980
	GAAACATATG	AATTTCTCAT	ACCCAGCAGA	CAGATGGCTG	ACACTGCACA	GCCACACACC	11040
	ATTGAGTAA	GTTAAAGTGA	GAGCATAGTA	GTTGGACTCT	CCTATGAAGA	ACATTCCTGG	11100
65	CTGGAGGCG	GGAATACTCC	ATGGTTGTTT	CTTTTCTCTA	CTTAAGCCCA	TTTTGTTTGT	11160
	GCTTTTCTGT	TTTGTTTTGT	TTTCACTCTT	GCATACAGT	CTAGAGATCC	AAATGAACCTG	11220
	AAAAGTTCAA	AGTTTAAAC	ATTTAAATAT	GTTTACTTTT	AGTTGTCAAT	CTAATCGTTA	11280
	TTGATTAGAA	GCATGACTCC	TGAAGGAAAG	GGAAATAAAT	CTCAATTCAT	ACTAATCTGC	11340
70	AACAAAAAC	TTTTACCATA	TAAATAAGTA	TATGATTTAT	TTTTAACCCA	AAAAATGTAT	11400
	AAAAATAAGT	TGTCCTTTAC	TGTCAATTTA	TCGAGAAGAT	CTATAATATA	TAGACTACAT	11460
	ATATATAATA	TATACACAT	AGCCAAATGT	ATGAAAACCT	GACAATGTAT	AATTTTGAAT	11520
	TCACATGCTA	CCTATGTAGA	CAGGTATGAA	ATTAAGTTAT	AATTTTCATG	AGACATTTTC	11580
	ATCACTGTGT	ACACAGTTTC	AAGGCATTC	ATCATGTTAT	TTTGACTCTT	TTTCTTTTTT	11640
	TTTTCTTTAA	AAATATATTT	TTAAGTAGAC	CAGGCCCCAC	TATAATATCA	CTTAAGAGAG	11700
75	TCAGGGCAAA	GTTTTTGCAT	TTATGAAGAT	GTGTTCAATG	AAGGGTGATT	GTAATGGAGT	11760
	TCATTGGTAA	TAGAAGCAAA	AGTACAGTAA	CGAAGTATTG	AAAAGAAAAA	TTTGGAGACA	11820
	TTGGAGCAT	TATATATAG	CTTGTGGAAA	GACATAAGGC	TACAGATGGA	ATGGAACATT	11880
	CCTGTTTTCT	TGAAGAAAT	CACATACACA	TAGCTGACCT	GACTAGTACT	TCAGCTCTTC	11940
	CACAGCCTTC	TATAAAGGTT	CTTTCTCTG	CAAAGAAAA	AAAAACAAAC	AAAAACAAAC	12000
80	AAAAAAAAC	AAAAAAGCG	CAAAAAACAA	AAAAACAAA	AAAAGCAAG	TAAATTTTAA	12060
	AAATACAGAA	AAACAACAC	AAAAAAGAA	TCAACCATAA	ATAGTGACTA	TTATTTTCAG	12120
	TGTTGCTTTC	ATGTGAAGC	TATTAAGGAC	CAATATACT	ACTGTTTATA	AGAAGAAATT	12180
	ACTTTCTAAA	CAGTAACTGA	AAATACTTAG	AGTTAAACTT	GCTGTGGATT	TTGCTTGGC	12240
	AGTTGTCTAT	TTACATTATT	TGTCAAAGGA	AATGTGTTG	GCAATTAAAA	ATCTTCTCTT	12300
	AGATTTAGTG	TGGACCTTTA	ACCTCTTAAA	TAAATGTTAG	TATATCAGAT	TGTTGCTCTG	12360



AAAAATATT TACTTGATG AATCATGACA ACGTCTAAAT CTTTACTATT CTCTCGCAA 12420  
 AAGCATCAGT AAGAAAGAG GCGAAAAAGA GAAGTATAGC CTTTATGTCA GAAAAACATT 12480  
 CTTTGTAGCT GCTTACTTTC TCATGAAAAG TAAAGATGTT TACAGTGTAT GCCAAGTTTT 12540  
 CAGTTTCTGT ATAACAACAG GTAGAGGTTT TAATCATATT GAAATTTGTT TTATAATGGT 12600  
 CTGAGCCATG TTGCTAGGAA ACAATAGGTT CCAATTTTGT ATTCTGCTC TCCTGTGCTG 12660  
 AAAAGTGACT GGATACTGTA CAGGTTTCATG TTCTCTGGCT GCAGTTAAAT GGTCTTTTGC 12720  
 ATTTTGCTCT GGCTTTCAGG CCAGAAGCAT GCATTTTCTT ACAAGAGCAT CACAACAACA 12780  
 TCGTGTAAAT ATTTAAAGTT AAACATTATG TGTGTATATT TGAAAGAAAA GTACTTTGAA 12840  
 TATTTTCATT TTTAAAAATA AAATTGCCAA TGAAAAAATA

**A210 Protein sequence:**

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1  
 Unigene number: Hs.23796  
 Probeset Accession #: NM\_014253  
 Protein Accession #: NP\_055068  
 Signal sequence: none found  
 Transmembrane domains: 318-340  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MEQTDCKPQ PLPKVKHEMD LAYTSSSDS EDGRKPRQSY NSRETLHEYN QELRMNYSQ 60  
 SRKRKEVEKS TQEMEFCEST HTLCSTGYQD MHSVSRHGYQ LEMGSDVDTE TEGAASPDHA 120  
 LRMWIRGMS EHSSCLSSRA NSALS LTDITD HERKSDGENG FKPSPVCCDM EAQAGSTQDV 180  
 QSSPHNQFTF RPLPPPPPPP HACTCARKPP PAADSLQRRS MTRSQSPSPA APAPPTSTQD 240  
 VSHLHNSWVL NSNIPLETRH SLFKHSGSGS AIFSAASQNY PLTSNTVYSP PPRPLPRSTF 300  
 SRPAPTFNKP YRCNCWKCTA LSATAITVTL ALLLAYVIAV HLFGLTQWLQ FVEGELYANG 360  
 VSKGNRGTES MDTTYSPIGG KVSDEKSEKV FQKGRADITG EVDIGAQVMQ TIPPGLFWRP 420  
 QITIHPIYL KFNISLAKDS LLGIYGRNNI PPTHTQFDFV KLMDGKQLVK QDSKSGDDTQ 480  
 HSPRNLILTS LQETGFIEYM DQGPWYLAFY NDGKMEQVFP VLTIAEIMD DCSTNCGNG 540  
 ECISGHCCHF PGFLGPPDCAR DSCPVLCCGN GEYKGGHCV C RHGKGGPECV VPVEQCIDPT 600  
 CFHGHTCIMG VCICVPVYKG EICEEEDCLD PMCSNHGICV KGECHCSTGW GGVNCEPLP 660  
 VCQEQCSHG TFLDAGVCS CDPKHTGSDC STELCTMECG SHGVCSSGIC QCEEGWVGT 720  
 CEERSCHSHC TEHGCKDGGK CECSPGWEGD HCTIAHYLDA VRDGCPLGCF GNGRCTLQDN 780  
 GWHCVQGVG SGTGCNVVME MLCGDNLDND GDGLTDCVDP DCCQSQNCYI SPLCQSGPDP 840  
 LDLIQSQSTL FSQITSLRFP DRIKFLIGKO STHVIPPEVS FDSRRACVIR GQVVAIDGTP 900  
 LVGVNVSLFL HSDYGFITSR QDGSFDLVAI GGISVILIFD RSPFLPEKRT LMLPWNQPIV 960  
 VEKVTMRVV SDPPSCDISN FISPNPIVLP SPLTSFGGSC PERGTIVPEL QVVQEIPIP 1020  
 SSFVRLSYLS STPGYKTLR RILLTHSTIP VGMKIVHLTV AVEGRLTQKV FPAAINLVYT 1080  
 FAWNKTDIYG QKVGLEALAE VSVGEYETC PDFILWEQRT VVLQGFEMDA SNLGDWSLWK 1140  
 HHILNPQSGI IHKNGENRST ISQPPVIST IMNGEQRSV ACTNCGPAH NNKLFAPVAL 1200  
 ASGPDGVSIV GDFNFVRRIE PSGNSVSILE LSTSPAHKYY LAMPVSESL YLSDTNTRKV 1260  
 YKLKSLVETK DLSKNFEVVA GTCDQCLPFD QSHCGDGGRA SEASLNSPRG ITVDRHGPYI 1320  
 FVDGTMIRKI DENAVITTVI GSNGLTSTQP LSCDSGMDIT QVRLEWPTDL AVNPMNLSLY 1380  
 VLDNINVLQI SENRRVRIIA GRPIHCQVPG IDHFLVSKVA IHSSTLESARA ISVSHSGLLF 1440  
 IAEEDERKVN RQQTITNGE IYIAGAPTD CCKIDPNCD CFSGDGGYAK DARMKAPSSL 1500  
 AVSPDGLTYV ADLGNVRIET ISRNQAHLD MNIYEIASPA DQELYQFTVN GTHLHTLNL 1560  
 TRDYVYNFTY NSEGLDGAIT SSNGNSVHIR RDAGGMPLWL VVPGQVWYL TISSNGVLKR 1620  
 VSAQGNPAL MTPYNGTGLL ATKSNEGWT TVYEYDPEGH LTNATPFTGE VSSFHSDLEK 1680  
 LTKVELDTSN RENVLMSTNL TATSTIYILK QENTQSTYRV NPDGSLRVTF ASGMEIGLSS 1740  
 EPHILAGAVN PTLGKNISL PGEHNNALIE WRQRKEQNGK NVSAFERLR AHNRLNLSID 1800  
 PDHITRTGKI YDHRKFTLR ILYDQTGRPI LWSFVSRYNE VNITYSPSGL VTFIQRGTWN 1860  
 EKMEYDQSGK IISRTWADGK IWSYTYLEKS VMLLHSQRR YIFEYDQSDC LLSVTMPMSV 1920  
 RHLQTLMLSV GYRNRYITPP DSSTSPFIQDY SRDGRLLQTL HLGTRRVLY KYTKQARLSE 1980  
 VLYDTTQVTL TYEESGVIK TIHLMDHDFI CTIRYRQTGP LIGRQIFRPS EELGVNARFD 2040  
 YSYNNFRVTS MQAVINETPL PIDLYRYVDV SGRTEQFGKF SVINYDLNQV ITTVMKHTK 2100  
 IFSANGVIE VQYELKALIA YWMTIQYDNV GRGNMCIHV GVDANITRYF YEYDADQLQ 2160  
 TVSVNDKTQW RYSYDINGDI NLLSHGKSAR LTPLYDLRD RITRLGEIQY KMDGDFLRQ 2220  
 RGNDFEYNS NGLLQKAYNK ASGWTQVYYY DGLGRVASK SSLQQLHQQF VDATANPIRV 2280  
 THLYNHTSSE ITSPLYDLQG HLIAMELSSG EEEYVACDNT GTPLAVFSSR GQVIKEILYT 2340  
 PYGDIYHDY PDEFVIGFHF GGLYDFLTKL VHLGQRDYDV VAGRWTAYH HIWKQLNLLP 2400  
 KPNLYSPEN NYPVGIQDV AKYTTDIRSW LELPGFQLHN VLPGFPPKPEL ENLELYTELL 2460  
 RLQTKQEWFD KDGIVTADII GVANEDSRRL AAILNAHYL ENLHFTIEGR DTHYFIKLS 2520  
 VFGKGIKFAI KDGIVTADII GVANEDSRRL AAILNAHYL ENLHFTIEGR DTHYFIKLS 2580  
 LEEDLVLIQN TGGRRILENG VNVTVSQMTS LLNGRTRRFA DIQLQHGLC FNIRYGTIVE 2640  
 EEKNHVLLEA RQRAVAQAWT KEQRRLEQEG EGIRAWTEGE KQQLLSTGRV QYDGYFVLS 2700  
 VEQYLELSDS ANNIHFMRQS EIGRR

**A211 DNA SEQUENCE:**

Gene name: Solute carrier family 26, member 4  
 Unigene number: Hs.159275  
 Probeset Accession #: AF030880  
 Nucleic Acid Accession #: NM\_000441  
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTCAGCCTTC CCGGTTCCGG AAAGGGAAG AATGCAGGAG GGGTAGGATT TCTTCTCTGA 60  
 TAGGATCGGT TGGGAAAGAC CGCAGCCTGT GTGTGTCTTT CCGTTCGACC AAGGTGCTG 120  
 TTGCTCCGTA AATAAAGCT CCCACTGCCT TCTGAGAGCG CATATAAGGC AGCGGAAGGG 180  
 TAGTCCGCGG GGCATTCCGG CGGGGGCGCG AGCAGAGACA GGTCTATGCA GCGCCAGGCG 240  
 GCAGGTGCGA CGCCGCGCAG CTCCCGAGT ACAGCTGCAG CTACATGTGT TCGCGGCGCG 300  
 TCTACAGCGA GCTCGCTTTC CAGCAACAGC ACGAGCGGCG CCGTGCAGAG CGCAAGAGCG 360

5 TGCGGGAGAG CCTGGCCAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCTTT GGTGTGCTAA 420  
 AGACTCTTGT GCCATCTTGT GAGTGGCTCC CCAAAATACCG AGTCAAGGAA TTGGTGCTTA 480  
 GTGAGCTCAT TTGGGGAGTT AGTACTGGGC TAGTGGCCAC GCTCAAGGG ATGGCATATG 540  
 CCTACTAGC TGCACTTCT GTGCGATATG GTCTCTACTC TGCTTTTTC CCTATCCTGA 600  
 CATACTTTAT CTTTGGAAAC TCAAGACATA TCTCAGTTGG ACCTTTTCCA GTGGTGAGTT 660  
 TAATGGTGGG ATCTGTGTGT CTGAGCATGG CCCCCGACGA ACACTTTCTC GTATCCAGCA 720  
 GCAATGGAACT GTATTAAAT ACTACTATGA TAGACACTGC AGCTAGAGAT ACAGCTAGAG 780  
 TCCTGATTGC CAGTGCCCTG ACTCTGCTGG TTGGAATTAT ACAGTTGATA TTTGGTGGCT 840  
 10 TGCAGATTGG ATTCAATATG AGGTACTTGG CAGATCCTTT GGTGTGGTGG TCAACACAG 900  
 CTGCTGCCCT CCAAGTGCTG GTCTCAGCAG TAAAGATTGT CCTCAATGTT TCAACCAAAA 960  
 ACTACAATGG AGTTCTCTCT ATTATCTATA CGCTGGTTGA GATTTTTCAT AATATTGGTG 1020  
 ATACCAATCT TGCTGATTTC ACTGCTGGAT TGCTCACCAT TGCTGCTGT ATGGCAGTTA 1080  
 AGGAATTAAT TGATCGTTT AGACACAAAA TCCAGTCCC TATTCTATA GAAGTAATTG 1140  
 15 TGACGATAAT TGCTACTGCC ATTTCAATATG GAGCCAACT GGAATAAAT TACAATGCTG 1200  
 GCATTGTAA ATCCATCCCA AGGGGGTTTT TGCTCCTGA ACTTCCACCT GTGAGCTTGT 1260  
 TCTGGGAGG AGTTGCTGCA TCATTTTCCA TCGCTGTGGT GGCTTATGCT ATTGCAAGTT 1320  
 CAGTAGGAAA AGTATATGCC ACCAAGTATG ATTACACCAT CGATGGGAAC CAGGAATTCA 1380  
 TTGCTTTGGG GATCAGCAAC ATCTTCTCAG GATTTCTTC TTGTTTGTG GCCCACTG 1440  
 20 CTCTTTCCCG CAGGCGCGTC CAGGAGAGCA CTGGAGGAAA GACACAGGTT GCTGGCATCA 1500  
 TCTCTGTGTC GATTGTGATG ATCGCCATTC TTGCCCTGGG GAAGCTTCTG GAACCTTTCG 1560  
 AGAAGTCGGT GTTGGCAGCT GTTGAATTG CCAACCTGAA AGGGATGTTT ATGCAGCTGT 1620  
 GTGACATTCC TGCTGTGTTG AGACAGAATA AGATTGATGC TGTATCTGG GTGTTTACGT 1680  
 GTATAGTGTG CATCACTTCT GGGCTGGATC TCGGTTTACT AGCTGGCCTT ATATTGGAC 1740  
 25 TGTGACTGT GGTCTGTAGA GTTCAGTTTC CTCTTGGA TGCCCTTGA AGCATCCCTA 1800  
 GCACAGATAT CTACAAAGT ACCAAGAATT ACAAAAACAT TGAAGAACCT CAAGGAGTGA 1860  
 AGATTCTTAG ATTTTCCAGT CCTATTTCT ATGGCAATGT CGATGGTTT AAAAAATGTA 1920  
 TCAAGTCCAG AGTTGAGTTT GATGCCATTA GAGTATATAA TAAGAGGCTG AAAGCGCTGA 1980  
 GGAATAACA GAAACTAAT AAAAAAGTGGAC AATTAAGAGC AACAAGAAT GGCATCATAA 2040  
 30 GTGATGCTGT TTCAACAAAT AATGCTTTTG AGCTGTATGA GGATATTGAA GATCTGGAGG 2100  
 AACTTGATAT CCCAACCAAG GAAATAGAGA TTCAAGTGGG TTGGAACCTC GAGCTTCCAG 2160  
 TCAAGTGAA CGTTCCCAAA GTGCCAATCC ATAGCCTTGT GCTTGACTGT GGAGCTATAT 2220  
 CTCTCTGGA CGTTGTGGA GTGAGATCAC TGCGGGTGTG TGTCAAGAA TTCCAAAGAA 2280  
 TTGATGTGAA TGTGATTTT GCATCACTTC AAGATTATGT GATAGAAAAG CTGAGCAAT 2340  
 35 GCGGGTCTT TGACGACAC ATTAGAAAG ACACATTCTT TTGACGGTC CATGATGCTA 2400  
 TACTCTATCT ACAGAACCA GTGAAATCTC AAGAGGGTCA AGGTTCCATT TTAGAAACGA 2460  
 TCACCTCTAT TCAGGATTGT AAAGATACCC TTGAATTAAT AGAAACAGAG CTGACGGGAG 2520  
 AAGAATCTGA TGTCAGGAT GAGCTATGC GTACACTTGC ATCCTGAAG TGGGTTCCGG 2580  
 AGGTCTCTAT GAGCAAGGAA TACAGACAA AACTTCTCA ATGCATTGAC TATTCTTCA 2640  
 40 GACTCAAAAC ACTCATCTT TTTTCTATTA AGCCATTGAA AGAGAAGCAC TAAGACTGCT 2700  
 TCTAGGCTTT ATTTATAAAA TAAACACCTT ATCCCTAACA TGGGCAAAAT GGCTAGAATT 2760  
 ATTCAGACGA TTGGCAGGTC TCCAGGGTAA GCTGGTGTTA TAATACGCTG CTGATCTACA 2820  
 TCACAGATT GCTAATATG TTCAAGTGGG CCTGGGCATA TCTCTGTCA GTTAGAGTGA 2880  
 GTGCTGACCC ACAGGCTCT GTGGTCAAGC GAGTCAOGAA TGATTATCA TAAAGAAAAA 2940  
 45 TCAGTTTTG ACTGACCTGG ATATCCATGA GCTGCACCTA TCACCATGTA AGGTACACTT 3000  
 TAGTAATATG TGAAATAAA TGATTATATG ATTTATCAAT AAAAGCCTTT GAAAATACTT 3060  
 TGGATAATAA ATTTGAGTTT TAAAAATGCA AATTGTGCTA GTATCTAATA ATGAAGTGT 3120  
 ATTACATATA GCGGGAATTG AGGATCTCTT TGATCCTGGA AATGTTTAC CTAAAAGCTA 3180  
 CAGAACCAAG CAAATATATT TTGAAATATT GATGCAGACA AATGAAATAA TAAAGAGATT 3240  
 50 TTCATGTTTT ATAAAAATCT TTTTGTATAT GATAATAATC ATGATCAACA CTGAGATCAA 3300  
 AAAAAATATG GACAGATTAT TTGTTTAAA AATGCACTTT TAATTATCTT AGCTATATGA 3360  
 AATGATCATT GATGGAGGCT ATGTATAGGT ATGATCTGTG TAAATCTGA CATAAAAAACA 3420  
 GTGCTATTCT GATGAAAAAT TTTTGTGATG TGCTTACATA ACCATGGTGA TTAATATGAG 3480  
 TTTATATTTT TTCTCAAAA TTTTAGCAGT GTGTAAAGTA AGTAATCTTT AACTGAACTC 3540  
 55 TGACCACTTA AAAAAAATC TAAAAATTGA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600  
 ATTTTAAAG ACAAGCATT CTAAATGAAC TCAATATAAA AACATTCAAT TGGAAATGTAC 3660  
 ATACTGAAA ATACAGGTTT TTTGACCAA AAGTTTTTAT ATCTTTTCTT TTTATTTATT 3720  
 TTTTCTCTAA GTGCCAACAA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTTGGG 3780  
 GACTTTTCCC ATATATTTCA CACTGGAGTG AATGAAGTTG TACTTCAATT CTAGAGAAAA 3840  
 60 GTTATACCCA GGTCCCAAT TGAGATGTC TTGCTTGATT GAAAACGACA TCATCCCTTG 3900  
 GTATACTCCA GGGATTGGTT TCAGGACCCC TGCAATTACC AAAATTGTG CACACTCAAG 3960  
 TCTCGACGTC ACCCTGCCT AAAGATAGAA TGGCTTCTCT GTTTTCTTC TGAATACAA 4020  
 CCAGAACCAA TGTGCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTTAAT 4080  
 CCTGAATCTT GGTGTGAAAT CTGGTTACAG CATACTAGG ATTATAATGC TGCCTCAATT 4140  
 65 TCACAGCACT ACTTGCTTAT ATTGACAACA AATCATCTCG CTAAGAGTGA AATGTAGGCC 4200  
 AGGCGCGGTG GCTCATGCCT GTAATCCAG CACTTTGGGA GCGGAGGCG GGTGGATCAC 4260  
 GAGGTACAGA GATCGAGACC ATCTGGCTA ACATGGTAAA ACCCGTCTC TACTAAAAAT 4320  
 AGAAAAAAG AAATTAGCCT AGCGTGGTGG CTGCGGGCG CCTGTAGTCC CAGCTATTG 4380  
 GGAGGCTAAG GCAGGAGAAAT GCGGTGAACC CGGAGGCGG AGCTTGCACT GAGCCGAGGT 4440  
 70 CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATA 4500  
 AAAAAAATA AGAGTGAATG TAATAGTCTT GCAGAAATG AATGAATACC TTTGTTCAAT 4560  
 AAAGGAATA TGCACTGCTC ACTTTTGA AGGAAATGCC AAAGTTACGT TTTACAACA 4620  
 GGCTAGAGTT TGTAAATCT GGGTTCAATT GTGATGACAT AAGTCAGCAA ACTGCGGGAA 4680  
 TACTGTCTCT TCTATGTAAT TTGTGAATAG TAAGCATAAT TTTAGTTTGT TATTATCAAT 4740  
 75 GAAAAATTC CTGAAATTA AAGCTGCCCT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800  
 TCCAGTATTG TATATGAGT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAATA 4860  
 TTTGCACACA TTTAAAAATA AATGTAAAGT TGTCTTTTAA ACTACTCGGA TGTGCTCTT 4920  
 CTGAACAAAA

**A212 Protein sequence:**

Gene name: Solute carrier family 26, member 4  
 Unigene number: Hs.159275  
 Probeset Accession #: AF030880  
 Protein Accession #: O43511  
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,  
347-369, 386-408, 420-442, 448-470, 486-508  
Cellular Localization: plasma membrane

5  
10  
15  
20

1	11	21	31	41	51	
MAAPGGRSEP	PQLPEYSCSY	MVSRPVYSEL	AFQQQHERRL	QERKTLRESL	AKCCSCSRKR	60
AFGLVKTLPV	ILEWLPKYRV	KEWLLSDVIS	GVSTGLVATL	QGMAYALLAA	VPVGYGLYSA	120
FFPILTYTIF	GTSRHISVGP	FPVVSIMVGS	VVLSMAPDEH	FLVSSSNGTV	LNTMTIDTAA	180
RDTRVLIAS	ALTLVLVGIQ	LIFGGLQIGF	IVRYLADPLV	GGPTTAAAFQ	VLVSQKLKIVL	240
NVSTKNYNGV	LSIIYTLVEI	FQNIQDNLIA	DFTAGLLTIV	VCMAVKELND	RFRHKIPVPI	300
PIEVITVIAI	TAISYGANLE	KNYNAGIVKS	IPRGFLPPEL	PPVSLFSEML	AASPSIAVVA	360
YAIASVGVKV	YATKYDYTID	GNQEFIAFGI	SNIFSGFFSC	FVATTALSRT	AVQESTGGKT	420
QVAGIISAAI	VMAILALGK	LLEPLQKSVL	AAVVIANLKG	MFMLCDIPR	LWRQNKIDAV	480
IWVFTCIWSI	ILGLDLGLLA	GLIFGLLTIV	LRVQFPWNG	LGSIPSTDIY	KSTKNYKNIE	540
EPQGVKILRF	SSPIFYGNVD	GPKKCIKSTV	GFDAIRVYNK	RLKALRKIQK	LKSGQLRAT	600
KNGIISDAVS	TNNAFEPDED	IEDLEELDIP	TKIEIQVDW	NSELPVKVNV	PKVPIHSLVL	660
DCGAIISFLDV	VGVRSLRVIV	KEFQRIDVNV	YFASLQDYVI	EKLEQCGFPD	DNIRKDTFFL	720
TVHDAILYLQ	NQVKSQEGQG	SILETITLIQ	DKDITLELIE	TELTEELDV	QDEAMRTLAS	780

25  
30

**A213 DNA SEQUENCE:**  
 Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
 Unigene number: Hs.98280  
 Probeset Accession #: AA418000  
 Nucleic Acid Accession #: NM\_021614  
 Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

35  
40  
45  
50  
55  
60  
65  
70  
75

1	11	21	31	41	51	
CGGCGGCAGC	AGCCCATGCC	TCCGGTGCAA	CAGCTGCGCC	TCCTCCGCTG	CCCCGGCGGC	60
GGGCGCGGGA	GATAACCTGT	CCCTGCTGCT	CCGCACTCC	TCGCCCGCGC	GCGCCTTCOG	120
GACCCGCAAC	TCCTCGCGCG	TGTGCGGCTC	GTCCTGCTGC	TGCTGCTGCT	GCTCGTCCGG	180
CCGCGGCAGC	CAGCTCAATG	TGAGCGAGCT	GACGCGGTCC	AGCCATGCCA	GTGCGCTCCG	240
GCAGCAGTAC	GCGCAGCAGT	CCGCGCAGCA	GTCGCGGTCC	GCCTCCCACT	ACCAACCATG	300
CCACAGCTCG	CAGCCCGCGC	CCAGCCCCAC	GGGCACTCTC	GGCAGTCTGG	GCTCCGCGCC	360
CCCGCTCTCG	CACCAACACC	ACCAACCCCA	CCCGGCGCAC	CACCAAGACC	ACCAGCCCCA	420
GGCGGCGCGC	GAGAGCAACC	CCTTCAACGA	AATAGCCATG	AGCAGCTGCA	GGTACAACGG	480
GGGCGTCAAT	CGCGCGCTCA	GCAACTTGAG	CGCGTCCCGC	CGGAACCTCC	ACGAGATGGA	540
CTCAGAGGCG	CAGCCCCCTG	AGCCCCCGCG	GTCTGTCCGA	GGAGGTGGCG	GCGCGTCTCT	600
CCCGTCTGGC	GACGCTGCGC	CCGCGCGCGC	TGTTTCTGTC	TCAGCCCCCG	AGATCGTGCT	660
GTCTAAGCCC	GAGCACAACA	ACTCCAACAA	CCTGGGCGTC	TATGGAACCG	GCGCGGAGAG	720
CAGCACTGGA	GAGAGCGGCG	GCGGTGGAGG	GAGCGGCGAC	GGCAGCAGCA	GTGGCACCAG	780
GTCCAGCAAA	AAGAAAAACC	AGAACATCGG	CTACAAGCTG	GGCCACCGGC	GCGCCCTGTT	840
CGAAAAGCGC	AAGCGGCTCA	GCGACTAGCG	GCTCATCTTC	GGCATGTTCC	GCATCGTGCT	900
CATGCTCATC	GCTGATGAGG	TGTGCTGGGG	CGCCTACGAC	AAGGCGTCCG	TGTATTCCCT	960
AGCTCTGAAA	TGCCCTATCA	GTCTCTCCAC	GATCATCTCG	CTCGGTCTGA	TCATCGTGTA	1020
CCAOGCCAGG	GAAATACAGT	TGTTTCTGCT	GGACATGGA	GCAGATGACT	GGAGAATAGC	1080
CATGACTTAT	GAGCGTATTT	TCTTCTATCT	CTTGGAAATA	CTGGTGTGTG	CTATTCTATC	1140
CATACCTGGG	AATTATACAT	TCACATGGAC	GGCCCGGCTT	GCCTTCTCCT	ATGCCCATCC	1200
CACAACCAAC	GCTGATGTTG	ATATTATTTT	ATCTATACCA	ATGTTCTTAA	GACTCTATCT	1260
GATTGCCAGA	GTCATGCTTT	TACATAGCAA	ACTTTTCACT	GATGCTCTCT	CTAGAAGCAT	1320
TGGAGCACTT	AATAGATATA	ACTTCAATAC	ACGTTTGTGT	ATGAAGACTT	TAATGACTAT	1380
ATGCCCAGGA	ACTGTACTCT	TGGTTTTTAG	TATCTCATTA	TGGATAATTG	CCGCATGGAC	1440
TGTCCGAGCT	TGTGAAAGGT	ACCATGATCA	ACAGGATGTT	ACTAGCAACT	TCCTTGGAGC	1500
GATGTGGTTG	ATATCAATAA	CTTTTCTCTC	CATTGGTTAT	GGTGACATGG	TACCTAACAC	1560
ATACTGTGGA	AAAGGAGTCT	GCTTACTTAC	TGGAATTATG	GGTGTGTTT	GCACAGCCCT	1620
GGTGGTAGCT	GTAGTGGCAA	GGAAGCTAGA	ACTTACCAAA	GCAGAAAAAC	ACGTGCACAA	1680
TTTCATGATG	GATACTCAGC	TGACTAAAAG	AGTAAAAAAT	GCAGCTGCCA	ATGTACTCAG	1740
GGAAACATGG	CTAATTTACA	AAAATACAAA	GCTAGTGAAA	AAGATAGATC	ATGCAAAAGT	1800
AAGAAAAACAT	CAACGAAAAT	TCCTGCAAGC	TATTCATCAA	TTAAGAAAGT	TAAAAATGGA	1860
GCAGAGGAAA	CTGAATGACC	AAGCAACAC	TTTGGTGGAC	TTGGCAAAGA	CCCAGAACAT	1920
CATGTATGAT	ATGATTTCTG	ACTTAAACGA	AAGGAGTGAA	GACTTCGAGA	AGAGGATTGT	1980
TACCTTGGAA	ACAAAACCTAG	AGACTTTGAT	TGGTAGCATC	CACGCCCTCC	CTGGGCTCAT	2040
AAGCCAGACC	ATCAGGCAGC	AGCAGAGAGA	TTTCATTGAG	GCTCAGATGG	AGAGCTACGA	2100
CAAGCACGTC	ACTTACAATG	CTGAGCGGTC	COGCTCCTCG	TCCAGGAGGC	GGCGGTCTCT	2160
TTCCACAGCA	CCACCAACTT	CATCAGAGAG	TAGCTAGAAG	AGAATAAGTT	AACCACAAAA	2220
TAAGACTTTT	TGCGATCATAT	TTTAGCTTTT	ATTGTAAAGC	CCCTATGGTT	2280	
CTAATCAGCG	TTATCCGGGT	TCTGATGTCA	GAATCCTGGG	AACCTGAACA	CTAAGTTTTA	2340
GGCCAAAATG	AGTGAAAAC	CTTTTTTTTT	CTTTCAGATG	CACAGGGAAT	GCACCTATTA	2400
TTGCTATATA	GATTGTTCTC	CCTGTAATTT	CACCTAATTT	TTATTCATGC	ACTTCAAAAC	2460
AACTTTACTA	CTACATTATA	TGATATATAA	TAAAAAAGT	TAATTCGGA		

80

**A214 Protein sequence:**  
 Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
 Unigene number: Hs.98280  
 Probeset Accession #: AA418000  
 Protein Accession #: NP\_067627  
 Signal sequence: none found  
 Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488  
Cellular Localization: plasma membrane

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      M S S C R Y N G G V M R P L S N L S A S R R N L H E M D S E A Q P L Q P P A S V G G G G A S S P S A D A A A A A A V S 60
      S S A P E I V V S K P E H N N S N N L A L Y G T G G G G S T G G G G G G G S G H G S S S G T K S S K K Q N Q N I G Y K 120
      I G H R R A L P E K R K R L S D Y A L I P G M F G I V M V I E T E L S W G A Y D K A S L Y S L A L K C L I S L S T I I 180
10     L L G L I I V Y H A R E I Q L P M V D N G A D D W R I A M T Y E R I F F I C L E I L V C A I H P I P G N Y T F T W T A R 240
      L A F S Y A P S T T A D V D I I L S I P M F L R L Y L L A R V M L L H S K L F T D A S S R S I G A L N K I N F N T R P 300
      V M K T L M T I C P G T V L L V F S I S L W I I A A W T V R A C E R Y H D Q Q D V T S N F L G A M W L I S I T F L S I G 360
      Y G D M V P N T Y C K G K V C L L T G I M G A G C T A L V V A V V A R K L E L T K A E K H V H N F M M D T Q L T K R V K 420
      N A A A N V L R E T W L I Y K N T K L V K K I D H A K V R K H Q R K F L Q A I H Q L R S V K M B Q R K L N D Q A N T L V 480
15     D L A R T Q N I M Y D M I S D L N E R S E D F E K R I V T L E T K L E T L I G S I H A L P G L I S Q T I R Q Q Q R D F I 540
      E A Q M E S Y D K H V T Y N A E R S R S S S R R R R S S S T A P P T S S E S S

```

A215 DNA SEQUENCE:

Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Nucleic Acid Accession #: NM\_016029  
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

```

25     1      11      21      31      41      51
      |      |      |      |      |      |
      C T G C G A T C C C G C A G G C C A G C G A C G C G A C T C T G T G C G G G C G T C T T C T T C C C C C G A G C T 60
      G G G C G T G C G C G C C G C C A A T G A A C T G G G A G C T G C T G C T G T G C T G T G C G C G C C T G T G C G C G C 120
30     T G C T C T C T C T C T T G T G T C A G C T G C G C G T T C C T G A G G G C T G A C G G C G A C C T G A C G C T A C 180
      T A T G G G C C G A G T G G C A G G G A C G A C G C C C A G A A T G G G A G C T G A C T G A T A T G T G G T G T G G G 240
      T G A C T G G A G C C T G C A G T G G A A T T G G T G A G G A G C T G G C T T A C C A G T T G T C T A A C A T A G G A G 300
      T T T C T C T T G T G C T G T C A G C C A G A A G A G T G C A T G A G C T G G A A A G G G T G A A A A G A A G A T G C C 360
      T A G A G A A T G G C A A T T T A A A A G A A A A G A T A C T T G T T T T G C C C C T T G A C C T G A C G A C A 420
35     C T G G T T C C C A T G A A G C G G C T A C C A A A G C T G T T C C C A G G A G T T T G G T A G A A T C G A C A T T C 480
      T G G T C A A C A A T G G T G G A A T G T C C A G C G T T C T G T G C A T G G A T A C C A G C T G G A T G T C T 540
      A C A G A A A G C T A A T A G A G C T A A C T A C T T A G G A C G G T G T C C T T G A C A A A A T G T G T T C T G C 600
      C T C A C A T G A T C G A G A G A A G C A A G A A A G A T T G T T A C T G T G A A T A G A T C A C T C T G G T A T C A 660
40     C T C A C A T G A T C G A G A G A A G C A A G A A A G A T T G T T A C T G T G A A T A G A T C A C T C T G G T A T C A 720
      T A T C T G T A C C T C T T T C C A T T G G A T A C C A G T A T A A T A G T T C T A A C A T T T G C C C A G 780
      A T G C C T T C G A A C A G A A C T T G C C A C A T A C C A G T A T A A T A G T T C T A A C A T T T G C C C A G 840
      G A C C T G T G C A A T C A A A T A T T G T G G A G A A T C C C T A G C T G G A A G A G T C A C A A G A C T A T A G 900
      G C A A T A A T G C A G A C C A G T C C A C A A G A T G A C A A C C A G T C G T T G T G T G C G G C T G A T G T T A A 960
45     T C A G C A T G G C C A A T G A T T T A A A G A A G T T T G G A T C T C A G A C A A C C T T T C T G T T A G T A A 1020
      C A T A T T T G T G C A A T A C A T G C C A A C C T G G G C C T G G T G G A T A A C C A C A A G A T G G G A A G A 1080
      A A A G G A T T G A G A A C T T T A A G A G T G T G T G A T G C A G A C T C T C T T A T T T A A A A C T T T T A 1140
      A G A C A A A C A T G A C T G A A A A G A C A C C T G T A C T T T C A A G C C A C T G G A G G A G A A A T G G A 1200
      A A A C A T G A A A A C A G C A A T C T T C T A T G C T T C T G A A T A A T C A A A G A C T A A T T T G T G A T T T 1260
      A C T T T T T A A T A G A T A T G A C T T T G C T T C C A A C A T G G A A T G A A A T A A A A A A T A A T A A T A A A
50     A G A T T G C C A T G A A T C T T G C A A A

```

A216 Protein sequence:

Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Protein Accession #: NP\_057113  
Signal sequence: 1-26  
Transmembrane domains: 183-206, 221-243  
Cellular Localization: plasma membrane

```

65     1      11      21      31      41      51
      |      |      |      |      |      |
      M N W E L L L W L L V L C A L L L L L V Q L L R F L R A D G D L T L L W A E W Q G R R P E W E L T D M V V V T G A S S 60
      G I G E L A Y Q L S K L G V S L V L S A R R V H E L E R V K R R C L E N G N L K E K D I L V L P L D L T D T G S H E A 120
      A T K A V L Q E F G R I D I L V N N G G M S Q R S L C M D T S L D V Y R K L I E L N Y L G T V S L T K C V L P H M I E R 180
      K Q G K I V T V N S I L G I I S V P L S I G Y C A S K H A L R G F F N G L R T E L A T Y P G I I V S N I C P G P V Q S N 240
      I V E N S L A G E V T T I G N N G D Q S H K M T T S R C V R L M L I S M A N D L K E V W I S E Q P F L L V T Y L W Q Y 300
70     M P T W A W I T N K M G K K R I E N F K S G V D A D S S Y F K I F K T K H D

```

A217 DNA SEQUENCE:

Gene name: Homo sapiens mRNA; cDNA DKFPZp56401763 (from clone DKFPZp56401763)  
Unigene number: Hs.27373  
Probeset Accession #: F13036  
Nucleic Acid Accession #: AC012478  
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

```

80     1      11      21      31      41      51
      |      |      |      |      |      |
      A T G G G G G G C G T G C G C T G C C G C C C G C T C T G C C G C T G C T G C T G C G C T C T G G C C 60
      G C T C C G C G C C C C G C G C C A G C A G C G A G T C C G T C T C G C G C G T G C C G A A C C C G A G 120
      C G G A G T C G C G C C A C C G C C C G G C C G G G A A C C A C C C G G T T G G G T C T G G C 180
      G G G G G G G G C G A C G C G C A G C T C C A C A G C A G T G C G A C G C C T T G G T A C C G C C 240

```

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCGTTGGCC 300  
 TTTACACCCC TCCTCATCGC CTGCCTGCTG CTGCGCGTCT TCAGGTCGGG AAAGAGGTTA 360  
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGA AATGGCGCCA 420  
 CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TOSACATCAA ATACAGAGTG 480  
 TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540  
 GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGAGTGG AAGGCGCTGAT 600  
 GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660  
 TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGGT CGGAGGTGTT 720  
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGGTGTG AGGCATCTGC 780  
 TCAGACTGTG ACTGGCAAGC TOGTTTCCAC GTCACCAAA TGGAGTTGCT TCTGCCACCC 840  
 TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900  
 CTGAATCTCA TGAAGAACT GGAATCTCT GCCTTAAGCA GAAACACCG GGCCTCATCT 960  
 GCCAGGTGCT TGCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020  
 CCTTGGTGGC ACTTCAGGCG CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAAACCATG 1080  
 AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGCCAGC GGGGCACCTT TTGTGAAGAC 1140  
 AGAGCAGTAC CTTAGGTTCT CCAGGTTAGC TCTTTCTCCA AACAGCTGGC CTGGAAGCCA 1200  
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260  
 ACCCATCTGT TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320  
 AGGGTGTTC GGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380  
 TGCCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTGTACAAA 1440  
 ATCTGCTACC CTTGCTGTGC GTTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500  
 GTCTTGGCGT CATTTGAGCA GAGCCACAA AAGCGAGCTG CTGCCACGG GGAGCCTGTC 1560  
 AAACGAGGGC CCACTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620  
 GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCACTGA GGATGTCACT 1680  
 CACCTGGAG GAGACTTGA TGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740  
 GATGGCAGAT GCCAGAAAGT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800  
 TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860  
 TCCCCCGCAC AGCCCTGTGT TCTGTCCAGG CCTTGA

# A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)  
 Unigene number: Hs.27373  
 Probeset Accession #: F13036  
 Protein Accession #: FGENESH predicted  
 Signal sequence: 1-27  
 Transmembrane domains: 94-115, 448-469  
 Cellular Localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPNPEPE RESRPPPGPG PGNTRFRSGG 60  
 AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF A FTLLIACLL LRVFRSGKRL 120  
 KKTRYDIIT TPAERVEMAP LNEEDEDED STVPDIKYRV SLPAALRRQL PGQQTLLTVP 180  
 VPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240  
 ETKINVMYKT PAPSCVSGIC SDCHMQARFH VTMELLPLP FGHFPKVPPT STPHGFRQLQ 300  
 LNLMEKLSS ALRNRTRAPS ARCLPLVLAE MAAESDLPN PWHFSAATGS PIKTLTYOTM 360  
 STLGLDVFQ AGQRTGFCED RAVTKVLQGS SPSQLRWPK ALESQGFPHL RLLRECPPLS 420  
 THEPVLARS DARGQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDFYK 480  
 ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAAGPEPV KRGPSSQLTR HTCPGWIITH 540  
 ANLQITIPDQ GQEGPREVDY HPGGDLGVA NFYLEEBGFQ DGRQCKMVLN SEEGPPSLTG 600  
 CERLTGSHHF SSSKSWSEFL SPRQPLFLSR P

# A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGG 60  
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATATG 120  
 CAGCAAGAGT ACACACACCT GGTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180  
 TCCATATTGA GCTATTACCC AAGTATTATC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240  
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300  
 GAACCCAAACA ATAGGCAAAA AGATGAGGAC TGGCTGGAGA TCTACATCAA GAGAGAAAAA 360  
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAAT TGTGAAGTGT 540  
 ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAACTTC 600  
 AGCTACAAAT CTTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCAAT GTATGTCTCT TGGAGAATGG AGTGTCTCTA TTCCAGCCTG CAATGTGGTT 720  
 GAGTGTGTA CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTCGGA 780  
 AGCTTCCCAT GGAACACAAC CTGTACATT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840  
 GCGCAGAGCC TTCACTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 CCTGTGACAT GCAGGGCGGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
 CTTGCTGGAG AGTTCACTT CAAATCATCC TGCAACTTCA CTTGTGAGGA AGGCTTCATG 1020  
 TTGCAAGGAC CAGCCAGGT TGAATGCACC ACTCAAGGAC AGTGGACACA GCAAAATCCA 1080  
 GTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATGTG 1140  
 CTTCTAGTGT CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200  
 GGTTTTGTGT TGAAGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGA GTGGGACAC 1260

5 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320  
 GTGAGGTGTG CTCATTCCTC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCTTTCAGC 1380  
 TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440  
 TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAAAATGTT CAAGCCTGGC AGTTCCGGGA 1500  
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTGT 1560  
 CCTGAAGGAT GGAGCGCTCA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620  
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
 CTTTCTGCTG CTGGACTCTC CCTCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740  
 TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAGCCT TGAATCAGAC 1800  
 10 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

#### A220 Protein sequence:

15 Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 20 Transmembrane domains: 555-573  
 C-lectin domain: 23-139  
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 MIAEQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYYTHLVAI QNKEEIEYLN 60  
 SILSYSPSYW WIGIRKNNVW VVVVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120  
 DVGMMNDERC SKKILALCYT AACTNTSCSG HGECEVETINN YTCKCDPGFS GLKCEQIVNC 180  
 30 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
 ECDAVTNPAN GFVECFQNPQ SPPHNTTCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPAQVECT TQGWQTQIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGFTGEWDN 420  
 EKPTCEAVRC DAVHQPPKGL VRCASHPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480  
 35 WTEEVPSQOV VKCSSLAVPG KINMSCSGEP VFGTVCKPAC PEGWTLNGSA ARTCGATGHW 540  
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKAIKFVP ASSCQSLESQ 600  
 GSYQKPSYIL

#### Taxol Prostate

40 A221 DNA SEQUENCE  
 Gene name: ESTs; Liprin A2  
 Unigene number: Hs.306480  
 Probeset Accession #: N51002  
 Nucleic Acid Accession #: N51002  
 45 Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60  
 50 CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120  
 GAAAGGGATC GTCTTCTAGA CACCCTTCGG GAGACCCAGG AAAGCCCTCT ACCTGCCCTG 180  
 CAAAGACTTC AGGATGTCAAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGACGC 240  
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300  
 COGGAATTGT CTGCACGTGAC AAAAGAATTA AATGCCTGCA GGGAAACAACT TCTAGAAAAG 360  
 55 GAAGAAGAAA TCTCTGAATC TAAAGCTGAA AGAAACRACA CAAGACTATT ACTGGAGCAT 420  
 TTGGAGTGCC TTGTGTACAG ACATGAAAGA TCACCTAAGAA TGACGGTGGT AAAACGSCAA 480  
 GCGCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCAGT GAAATCTTTG 540  
 TTTGAGCACC ACAAGGCCCTT GGAATGAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600  
 AGAGTCTCTG CACTGGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCTTGCGT 660  
 60 GAACAAAATG TTCATATACA AAGAAAATG GCATCARGCG AGGGATCCAC AGAGTCAGAA 720  
 CATCTTGAGG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTC CAATGGTTCT 780  
 ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAACCTAC AAGAATTGCT TGAAAAGCAA 840  
 AACTATGAAA TGGCCAGAT GAAAGAACGT TTAGCAGCCC TTTCTTCCC AGTGGGAGAG 900  
 GTGGAACAGG AAGCAGAGAC AGCAAGAAAAG GATCTCATT AACAGAGAAG AATGAACACC 960  
 65 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAAGAAAT 1020  
 ACAACCCCTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080  
 AATGATAAAC TAGAAAATGA GTTAGCAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140  
 AAAAAAGAGC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200  
 AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAACCTG CTCAGAGAA TGCAGCCCTA 1260  
 70 ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAAGCTA TGAGACATTT AGAGGGTCAA 1320  
 CTTGAAGAGA AGAATCAAGA ACTTCAAAGA GCTAGGCAAA GAGAGAAAAT GAATGAGGAG 1380  
 CATAACAAGA GATTATCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCCTA 1440  
 CAACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA 1500  
 TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAGG ATTAGCAGAA 1560  
 75 GAAATGAAA AGCTGAGATC TGAACCTGAC CAATTGAAA TGAGAACTGG CTCITTAATT 1620  
 GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680  
 TCCTTAGTGG ACAGCCAGTG TGATTACAGA ACAAATAAG TAATAAGAG ACCAAGGAGA 1740  
 GGGCGCATGG GTGTGCGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800  
 AATGAACCTC AACAGATTGG AGTACTAAGC AGCCACCCCT TTGAAGTGA CACTGAAATG 1860  
 80 TCTGATATTG ATGATGATGA CAGAGAAAAC ATTTTATGCT CAATGGATCT TCTCTCTCCA 1920  
 AGTGGTCATT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGATGCCATC 1980  
 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040  
 ATTGAAAATA GAGTGGCTAG TGTGAGCCTC GAAGGCCCTG ATTTGGCAAG GGTCCACCCA 2100

5  
10  
15  
20  
25  
30

```

GGTACCTCCA TTAATGCCTC TGTTACAGCT TCATCGCTGG CCAGTTTCATC TCCCCCAGT 2160
GGACACTCAA CTCCAAAGCT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220
GTCATGACAC TGCCAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCAGT TGTGGAAGAA 2280
GATGGTCCGAG AGGACAAAGC AACAAATTAA TGTGAAACTT CTCCTCCTCC TACCCTTAGA 2340
GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400
TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTGTGTAAGT CCAACAGCAG CCAAGACTCT 2460
CTTCACAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGAAGTTT GTTTGGTAAA 2520
AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCCTTTATG AGACTGAAGC TGCAGCTCAG 2580
GAGTCCCTGG GGTTAGGCCA ACTCGGAAC CAAGCTGAGA AGGATCGAAG ACTAAAGAAA 2640
AAGCATGAAC TTCTGAAGA AGCTCGGAGA AAGGATTAC CTTTGGCCCA GTGGGATGGG 2700
CCAAGTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG 2820
AGAGAAATGG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTGATTAGC AATCCAGGAG 2880
ATGGTTTCCC TAACAAGTCC TTCAGCTCCT CCAACATCTC GAACTCCTTC AGGCAACGTT 2940
TGGGTGACTC TCGAAGAAAT GGAATAATCT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000
GAAGGAAGCT GGGCCAGTG TCCGGTTTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060
CATGAGTGGG TTGGAATAGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
TTTATGGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCGGT 3180
GTCCATTAA AAATGGTGGG TAGTTTCCAT CGAACAAAGT TACAATATGG AATTATGTGC 3240
TTAAGAGAGT TGAATTATGA CAGAAAGAA CTAGAAGAA GACGGGAAGC AAGCCAACAT 3300
GAAATAAAG ACGTGTGGT GTGGAGCAAT GACCGAATTA TTGCTGGAT ACAAGCAATT 3360
GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATAT TACAGATTCC AACACAGAAC 3480
ACCCAGGCAA AGCAGATTCT TGAAGAGAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540
AGGCGACTGG ATGAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAGGCAG 3600
TTTCTCTCTC TGGAAGTACA TGGAAATCAG ATGATGCTCG GGTCTCAGA AACATTACCA 3660
GCTGGATTTA GGTAAACCAC AACCTCTGGG CAATCAAGAA AAATGACAA AGATGTTGCT 3720
TCATCAAGAC TGCAGAGGTT AGACAATCC ACTGTTCCGA CATACTCATG TCTCGAGTAA 3780
GCGGCGCTT TAA

```

**A222 Protein sequence:**

Gene name: ESTs; Liprin A2  
 Unigene number: Hs.306480  
 Probeset Accession #: N51002  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: none found  
 AAA domain: 286-539  
 SAM domains: 895-964, 1017-1084, 1105-1177  
 Cellular Localization: not determined

45  
50  
55  
60  
65

```

1 11 21 31 41 51
| | | | |
MMCEVMPPTN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDLTL ETQESLSLAQ 60
QLRQDIYDRL DSIQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEL NACREQLLEK 120
EEEISELKAE RNNTLRLLLEH LECLVSRHER SLRMTVVVKRQ AQSPSGVSSE VEVLKALKSL 180
FEHHKALDEK VRERLRVSLR RVSALEBELA AANQEIVALR EQNVHIQRKM ASSEGSTESE 240
HLEGMEPGQK VHEKRLSNGS IDSTDTSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300
VEQEAEATARK DLIKTEEMNT KYQDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360
NDKLENELAN KEAILRQME EKNRQLQERLE LAEQKLQOTM RKAETLPEVE AELAQRILAAL 420
TKAERHGNH EERMRHLEQ LEEKNQELQR ARQREKQNEE HNKRLSDTVD RLLTESNERL 480
QLHLKERMAA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKRLSELD QLMRTGSLI 540
EPTIPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRPRR GRMGVRRDEP KVKSLGDHWE 600
NRTQIQIGVL SHEFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTLA MMLQEQDLAI 660
NKEIRLIQEE KESTLRQME IENRVASVSL EGLNLARVHP GTSITASVTA SSLASSPPPS 720
GHSTPKLTPR SPAREMDRMG VMILPDLRK HRRKIIVVEE DGREDKATIK CETSPPPTPR 780
ALRMHTLPLS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKGI KSSIGRLFGK 840
KEKARLQQLR CFMTEAQAQ ESLGLGLGT QAEKDRRLKK KHELLEEAR KGLPFAQWDG 900
PTTVANLELM LGMPAWYVAA CRANVKSgai MSALSDTEIQ REIGISNPLH RLKRLAIQE 960
MVSILTSPSAP PSTRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCPVF LQTLAYGDMN 1020
HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMVDSFH RTSLYGIMC 1080
LKRLNYDRKE LERRREASQH EIKDVLVWSN DRIIRWIQAI GLREYANNIL ESGVHGLIA 1140
LDENFDYSSL TLLLIQIPTN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200
FPPREVHGIS MMPGSSETLP AGFRLTTTSG QSRKMITDVA SSRLQLRLNS TVRTYSCLE

```

**A223 DNA SEQUENCE**

Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75  
80

```

1 11 21 31 41 51
| | | | |
ATGAGGCGAC TGAATCGGAA AAAAAGTTTA AGTTTGGTAA AAGAGTTGGA TGCTTTTCG 60
AAGGTTCTCG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
TTTACAACCTA TGGCTTTATT AACCATAAAT GAATTCTCAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
ACTGTTGCCA TGAAGTGTC AATATGTTGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
GTTGCATCTG CATAGTGGTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACIT 420
CAAGATGTGA TATTTAAAG TCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480

```

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATAAAA 540
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
CATTTGGCAG CACTGTCTCA CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTG 660
TCTTTGGAG AGCTTGTTCC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAATTGCT 720
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTCTCTT 900
ATGGTGACAG TTAGTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAACT ACTCTGTGGT 960
ATTGTTGGAG GAATCTTTTC AACAAACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020
GAAATAATTT GCTGTCGTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080
GAGGATGGCC ACACAGACAA CCACCTACCT CTTTATGAAA ATAATACACA TGA

```

A224 Protein sequence:

Gene name: CDA14  
Unigene number: Hs.26813  
Probeset Accession #: N32912  
Protein Accession #: NP\_057654  
Signal sequence: none found  
Transmembrane domains: none found  
Cellular Localization: nuclear

1 11 21 31 41 51  
MRLNRKIKTL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60  
KYEYEVNDKF SSKLRINIDI TVAMKQYVVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120  
KEMQRMQLI QSRQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGLYVNM 180  
VAGNFHITVG KAIPHPRGHA HLAALVNHEH YNFSHRIDHL SFGELVPAII NPLDGTAKIA 240  
IDHNQMFQYF ITVVFTELKT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300  
MVTVEEHMP FQCFEVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRIG SYKPVNSVPF 360  
EDGHTDNHLP LLENNTN

UterineA225 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Nucleic Acid Accession #: AA487468  
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60  
CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTGCTCAAG TTTCTTCCAA CCTTGCCATT 120  
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG AACTCTCAA GAGGATGGGG AGATGACATC 180  
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
ATGGTTATTC ATCACTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGTC 300  
CAAAATGAAG AATAACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
GAACCACTG ATAAGAATT ATCACTGAT GGGCAATATG TGCTAGAAT CATGTTTGT 420  
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTTCAACAG ATTGTACACA 480  
TATGAGCTC GGGATTAC CTTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540  
CAGTCAAGC TATPAGAGAT GATAGAAAA AGCCTTCACT TCAAGAAGT CAAATTTTCA 600  
GAAGAAACC TCTGGCAGT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660  
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720  
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

A226 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Protein Accession #: none found  
Signal sequence: 1-23  
Transmembrane domains: none found  
Cellular Localization: secreted

1 11 21 31 41 51  
MMLHSALGLC LLLVTSSNL AIAIKKEKRP PQTLSRGWD DITWVQYEE GLFYAQKSEK 60  
PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120  
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A227 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
Unigene number: Hs.285529  
Probeset Accession #: AA460530  
Nucleic Acid Accession #: NM\_003667  
Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)



```

1      11      21      31      41      51
|      |      |      |      |      |
GTGGCGGCAA CCGGCACCTC AGTCCCCGCC GCGCTTCTCC TCGCCGCCCA CGCCGTGGGG 60
TCAGGAACGC GCGGTCTGGC GCTGCAGACG CCGCTGAGT TGCAGAAACC CACGAGCGG 120
CGCCCGCGCG GCCACGCGCC GTAGCAGTCC GGTGCTGCTC TCCGCCCGCG TCCGGCTCGT 180
GGCCCCCTAC TTCCGGCACC ATGGACACCT CCGSGCTCGG TGTGCTCCTG TCCTTGCGCTG 240
TGCTGCTGCA GCTGGCGACC GGGGGCAGCT CTCCAGGTC TGGTGTGTG CTGAGGGGCT 300
GCCCCACACA CTGTCTATGC GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG 360
ACCTGGGCTC CTGGAGCTG CCTTCCAACC TCAGCGTCTT CACCTCTTAC CTAGACCTCA 420
GTATGAACAA CATCAGTCAG CTGCTCCCGA ATCCCTGCC CAGTCTCCGC TTCTGGAGG 480
AGTTACGTCT TCGGGGAAC GCTCTGACAT ACATTCCCAA GGGAGCATT ACTGGCCTTT 540
ACAGTCTTAA AGTTCTTATG CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC 600
TGCAGAAATT GCGAAGCCTT CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC 660
CCCCAAGCTG TTTCAGTGGC CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT 720
TAACAGAAAT CCCCCTCCAG GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG 780
CCCTGAACAA AATACACCAC ATACCAGACT ATGCCCTTGG AAACCTCTCC AGCTTGGTAG 840
TTCTACATCT CCATAACAAT AGAATCCACT CCGTGGGAAA GAAATGCTTT GATGGGCTCC 900
ACAGCCTAGA GACTTTAGAT TTAATATACA ATAACCTTGA TGAATTCGCC ACTGCAATTA 960
GCACACTCTC CACCTTAA GAACTAGGAT TTATAGCAA CAATATCAGG TCGATACCTG 1020
AGAAAGCATT TGTAGGCAAC CCTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC 1080
AATTTGTGTG GAGATCTGCT TTTCAACATT TACCTGAAC TGAACACTG ACTCTGAATG 1140
GTGCTCTACA AATAACTGAA TTTCCTGATT TAACCTGGAAC TGCAAACTCG GAGAGCTCGA 1200
CTTTAACTGG AGCAGAGATC TCATCTCTTC CTCAAACCGT CTGCAATCAG TTACTTAATC 1260
TCCAAGTCTC AGATCTGTCT TACAACCTAT TAGAAGATT ACCCAGTTTT TCAGTCTGCC 1320
AAAAGCTTCA GAAATTTGAC CTAAGACATA ATGAAATCTA CGAAATTTAA GTTGACACTT 1380
TCCAGCAGTT GCTTAGCCTC CGATCGCTGA ATTTGGCTTG GAACAAATTT GCTATTATTC 1440
ACCCCAATGC ATTTTCCACT TTGCCATCCC TAATAAGCT GGACCTATCG TCCAACCTCC 1500
TGTCGTCTTT TCCTATAACT GGGTTACATG GTTTAACTCA CTTAAATTA ACAGGAAATC 1560
ATGCCATTACA GAGCTTGATA TCATCTGAAA ACTTTCAGAA ACTCAAGGTT ATAGAAATGC 1620
CTTATGCTTA CCACTGCTGT GCATTGGAG TGTGTGAGAA TGCCTATAAG ATTTCTAATC 1680
AATGGAATAA AGGTGACAC AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT 1740
TTCAGGCTCA AGATGAACGT GACCTTGAAG ATTTCTGCT TGACTTTGAG GAAGACCTGA 1800
AAGCCCTTCA TTCAGTGCAG TGTTCACCTT CCCCAGGCC CTTCAAACCC TGTGAACACC 1860
TGCTTGATGG CTGGCTGATC AGAATTGGAG TGTGGACCAT AGCAGTTCTG GCACTTACTT 1920
GTAATGCTTT GGTGACTTCA ACAGTTTTC GATCCCTCT GTACATTTC OCCATTAAAC 1980
TGTTAATTGG GGTCACTCGA GCAGTGAACA TGCTCACGGG AGTCTCCAGT GCGGTGCTGG 2040
CTGGTGTGGA TGGTTCACT TTTGGCAGCT TTGCACGACA TGGTGCTCG TGGGAGAATG 2100
GGGTGTGGTG CCATGTCAAT GGTTTTTTGT CCATTTTTCG TTCAGAATCA TCTGTTTTCC 2160
TGCTTACTCT GAGCCCTCG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTGAAA 2220
CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCATTTTGTCT CTGTGCCCTG CTGGCCTTGA 2280
CCATGGCCGC AGTTCCCTCG CTGGGTGGCA GCAAGTATGG CGCCTCCCTT CTCTGCTGC 2340
CTTTGCCCTT TGGGAGGCC AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT 2400
CCCTTGTCTT CCTCATGAT ACCATTGCCCT ACACCAAGCT CTACTGCAAT TTGGACAAGG 2460
GAGACCTGGA GAAATTTTGG GACTGCTCTA TGGTAAACCA CATTGCCCTG TTGCTCTTCA 2520
CCAAGTGCAT CCTAACTGC CCTGTGGCTT TCTTGTCTT CTCTCTTTA ATAAACCTTA 2580
CATTATCAG TCCTGAAGTA ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTCTGCTCAT 2640
GTCTCAATCC CCTTCTCTAC ATCTTGTTC ATCTCACTT TAAGGAGGAT CTGGTGAGCC 2700
TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAACACCC AAGCTTGATG TCAATTAATC 2760
CTGATGATGT CGAAAAACAG TCCTGTGACT CAATCAAGC CTGTGTAACC TTTACCAGCT 2820
CCAGCATCAC TTATGACCTG CCTCCAGTT CGTGCCATC ACCAGCTTAT CCAAGTACTG 2880
AGAGTGCCA TCCTTCTCT GTGGCATTG TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940
AATGTTTTCA AAGGTTGAGA ACCTGAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000
ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

```

**A228 Protein sequence**

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
PSNLSVFYSY LDLSMNNISQ LLPNPPLPSLR FLEELRLAGN ALTYIPKGF TGLYSLKVLN 120
LQNNQLRHVP TEALQNLRLS QSLRLDANH SYVPPSCPSG LHSRLRLWLD DNALTEIPVQ 180
AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240
LNNYNNLDEFP TAIRTLNLK ELGFHSNNIR SIPEKAFVGN PSLLTIHFYD NPIQFVGRSA 300
FQHLPELRTL TIANGAQITE FPDLTGTANL ESLTLTGAQI SSLPQTVQNO LPNLQVLDLS 360
YNLLEDLPSP SVQQLKIKID LRHNEIYEIK VDTTQQLLSL RSLNLAWNKI AIIHPNAFST 420
LPSLIKLKDL SNNLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480
AFGVCEYAYK ISNQWNGKDN SSMDDLHKKD AGMFOAQDER DLEDFLDPE EDLKALHSVQ 540
CSPSPGFFPK CEHLLDGWL I RIGVWTIAVL ALTCLNALVTS TVFRSPLYIS PIKLLIGVIA 600
AVNMLTGVS AVLAGVDAFT PGSFARHGA WENGVGCHVI GFLSIFASE SVFLTLAAL 660
ERGFVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGCKYKASP LCLPLPFGE 720
STMGYMLVAL LLNSLCFLMM TIAYTKLYCN LDKGDLNIN DCSMVKHIAL LLFTNCILNC 780
PVAFLSFSLL INLTFFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKEO LVSLRKQTYV 840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
VAFVPCIL

```

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigeneID; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

5

10

Seq ID No:	Sequence ID No for sequences in table
Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
Pred Subcell Loc:	Predicted sub-cellular localization

	Seq ID No	Pkey	ExAccn	UnigenelD	Unigene Title	Pred Subcell Loc
15	Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	plasma membrane
	Seq ID 3 & 4	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	plasma membrane
	Seq ID 5 & 6	429423	AJ016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	plasma membrane
	Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
20	Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
	Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
	Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
	Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
	Seq ID 17 & 18	414577	AJ056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
25	Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
	Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
	Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
	Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
	Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	plasma membrane
	Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
30	Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
	Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
	Seq ID 35 & 36	423961	D13666	Hs.136348	perlestin (OSF-2os)	secreted
	Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
35	Seq ID 39 & 40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
	Seq ID 41 & 42	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
	Seq ID 43 & 44	424399	AJ905687		AJ905687:IL-BT095-190199-019 BT095 Homo	secreted
	Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
	Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
40	Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
	Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
	Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
	Seq ID 57 & 58	411789	AF245505	Hs.72157	Adlican	secreted
	Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
45	Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
	Seq ID 63 & 64	421552	AF026892	Hs.105700	secreted frizzled-related protein 4	secreted
	Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
	Seq ID 67 & 68	415539	AJ733881	Hs.72472	BMP-R1B	plasma membrane
50	Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
	Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
	Seq ID 73 & 74	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	plasma membrane
	Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
	Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
	Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
55	Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
	Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
	Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
	Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
	Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
60	Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
	Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
	Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
	Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
65	Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
	Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
	Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
	Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
	Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
70	Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
	Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
	Seq ID 115 & 116	428179	AI127772	Hs.279695	serum/glucocorticoid regulated kinase-II	intracell
	Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
	Seq ID 119 & 120	447033	AJ357412	Hs.157601	ESTs	secreted
75	Seq ID 121 & 122	447033	AJ357412	Hs.157601	ESTs	secreted
	Seq ID 123 & 124	447033	AJ357412	Hs.157601	ESTs	secreted
	Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
	Seq ID 127 & 128	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	plasma membrane
	Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
80	Seq ID 131 & 132	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	secreted
	Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
	Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
	Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
5	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	A1572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
10	Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	secreted
	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
15	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uroplakin 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uroplakin 2	plasma membrane
	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to DJ365012.1 [H.s.a	plasma membrane
20	Seq ID 176 & 177	402075			ENSP00000251056*:Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
25	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
	Seq ID 194 & 195	404875			NM_022819*:Homo sapiens phospholipase A2	intracell
30	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (I	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
35	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
40	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0	intracell
	Seq ID 221 & 222	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0	intracell
45	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
	Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
50	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
55	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	della (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
	Seq ID 252	429466	M85835	Hs.12827	ESTs	
60	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glut high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
65	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
	Seq ID 265 & 266	444471	AB020584	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrevin, alpha	secreted
	Seq ID 269 & 270	413053	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
	Seq ID 271 & 272	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
70	Seq ID 273	458435	AJ418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 274	458435	AJ418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	plasma membrane
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	secreted
	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	plasma membrane
75	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-like	plasma membrane
	Seq ID 283 & 284	404049			NM_018937*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018936*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
80	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gbhd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
10	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
20	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
	Seq ID 337 & 338	431958	X63529	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progesterone-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
45	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
50	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
60	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188*gil12738842[ref NP_073725.1] p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter)	plasma membrane
70	Seq ID 435 & 436	407242	M18728		gb:human nonspecific crossreacting antig	plasma membrane
	Seq ID 437 & 438	407242	M18728		gb:human nonspecific crossreacting antig	plasma membrane
	Seq ID 439 & 440	407242	M18728		gb:human nonspecific crossreacting antig	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
80	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT107???	plasma membrane
	Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT107???	plasma membrane
5	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW369771	Hs.52620	integrin, beta 8	plasma membrane
	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
10	Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
15	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	secreted
	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neurosin/ovasin) (KLK8)	secreted
	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
20	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076543	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	secreted
	Seq ID 511 & 512	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	intracell
25	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
30	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (	secreted
	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
35	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (tastisin)	secreted
40	Seq ID 541 & 542	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	secreted
	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	plasma membrane
	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
45	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
50	Seq ID 561 & 562	418396	AF765805	Hs.26691	ESTs	plasma membrane
	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
	Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
55	Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
60	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	plasma membrane
	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656*Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656*Homo sapiens transmembrane pr	plasma membrane
	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
65	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
70	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
75	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI166431	Hs.296638	prostate differentiation factor	secreted
	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
80	Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

## 5 Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

10 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

## 15 Table 76C:

20 Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

25 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

5	Seq ID No:	Sequence ID No for sequences in table		
	Pkey:	Unique Eos probeset identifier number		
	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung.	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
15	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
20	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
25	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
30	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
35	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
40	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
45	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
50	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
	Seq ID 69 & 70	416836	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 71 & 72	416836	breast, pancreas, uterine	Ab, sm, CTL, imaging
55	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 79 & 80	451398	breast, ovarian	CTL
60	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
65	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
70	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
75	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
80	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
75	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
80	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
80	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
80	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 423330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	sm
	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, diagnostic
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428296	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging



	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 429610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
15	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	Ab,sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL, diagnostic
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	Ab, sm, imaging
	Seq ID 391 & 392 332180	lung	Ab,sm, CTL, imaging
	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
45	Seq ID 395 & 396 408790	lung	Ab, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, diagnostic
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, diagnostic
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
70	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
	Seq ID 447 & 448 428392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
75	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, CTL, diagnostic
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, sm, imaging
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, CTL, diagnostic
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436992	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	Ab, CTL, diagnostic
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, imaging
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, sm, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, diagnostic
	Seq ID 527 & 528 452097	ovarian	Ab, CTL, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	CTL
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	Ab, sm, CTL, diagnostic
35	Seq ID 539 & 540 411773	ovarian	Ab, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, sm, CTL, imaging
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, sm, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, CTL, diagnostic
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, sm, CTL, imaging
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, CTL, diagnostic
	Seq ID 567 & 568 433466	prostate	Ab, sm, CTL, imaging
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, diagnostic
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, CTL, imaging
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, sm, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, CTL, diagnostic
	Seq ID 583 & 584 412628	prostate	Ab, sm, CTL, imaging
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
70	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, CTL, diagnostic
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, sm, imaging
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, CTL, diagnostic
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, imaging
	Seq ID 623 & 624 439018	uterine, stomach, prostate	CTL
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	Ab, CTL, diagnostic
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	CTL
80	Seq ID 629 & 630 456662	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 631 & 632 418281	uterine, ovarian	sm
	Seq ID 633 & 634 429903	lung	

Table 78

Seq ID NO: 1 DNA sequence  
Nucleic Acid Accession #: NM\_001400  
Coding sequence: 251..1399

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55

1	11	21	31	41	51	
TCTAAAGGTC	GGGGGCAGCA	GCAAGATGCG	AAGCGAGCCG	TACAGATCCC	GGGCTCTCCG	60
AACGCAACTT	CGCCCTGCTT	GAGCGAGGCT	GCGGTTTCCG	AGGCCCTCTC	CAGCCAAGGA	120
AAAGGTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	180
CTCGCTCGC	CCTCTAGOGT	TGCTCTGGAG	TAGCGCCACC	COGGCTTCTT	GGGGACACAG	240
GGTTGGCACC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCCACCGCA	GCTCGGTCTC	300
TGACTACGTC	AACATGATA	TCATCGTCCG	GCATTACAAC	TACAOGGGAA	AGCTGAATAT	360
CAGCGCGGAC	AAGGAGAACA	GCATTAAACT	GACCTCGGTG	GTGTTCAATC	TCATCTGCTG	420
CTTTATCATC	CTGGAGAACA	TCTTTGTCTT	GCTGACCATT	TGGAAAACCA	AGAAATTCCA	480
COGACCCATG	TACTATTTTA	TGGCAATCT	GGCCCTCTCA	GACCTGTGTG	CAGGAGTAGC	540
CTACACAGCT	AACCTGCTCT	TGCTGGGGG	CACCACCTAC	AACTCTACTC	CCGCCCAGTG	600
GTTTCTGCGG	GAAGGAGTA	TGTTTGTGGC	CCTGTCAGCC	TCCGTGTTCA	GTCTCTCGC	660
CATCGCCATT	GAGCGCTATA	TCACAATGCT	GAAATGAAA	CTCCACAACG	GGAGCAATAA	720
CTTCGGCTCT	TTCCTGCTAA	TCAGCGCCTG	CTGGGTCTATC	TCCCTCATCC	TGGGTGGCCT	780
GCCTATCATG	GGCTGGAATC	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	840
CTACCACAAG	CACATATATC	TCTTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	900
CGTCACTCTG	TACTGAGAA	TCTACTCCTT	GGTCAGGACT	CGGAGCCGCG	CGCTGAOGTT	960
CCGCAAGAAC	ATTTCCAAAG	CCAGCGCGAG	CTCTGAGAAG	TGCTGGGCGC	TGCTCAAGAC	1020
CGTAATTATC	GTCTGAGGCG	TCTTCATCGC	CTGCTGGGCA	COGCTCTTCA	TCCTGCTCCT	1080
GCTGGATGTG	GGCTGCAAGG	TGAAGACCTG	TGACATCCTC	TTCAAGAGCGG	AGTACTTCTT	1140
GGTGTAGCT	GTGCTCAACT	CCGGCACCAA	CCCCATCATT	TACACTCTGA	CCAACAAGGA	1200
GATGGTGGG	GGCTTCAATC	GGATCATGTC	CTGCTGCAAG	TGCCCGAGCG	GAGACTCTGC	1260
TGGCAAAATC	AAGCGACCCA	TCATCGCCGG	CATGGAATTC	AGCCGACGCA	AATCGGACAA	1320
TTCTCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1380
CGTCAACTCT	TCTTCTAGA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTTACTTGG	1440
TGCTGGCCCA	CCCCAGTGT	TGGAAGAAA	TCTCTGGGCT	TGCACTGCTG	CCAGGGAGGA	1500
GCTGCTGCAA	GCCAGAGGGA	GGAAGGGGGA	GAATACGAAC	AGCCTGGTGG	TGTCGGGTGT	1560
TGGTGGGTAG	AGTTAGTTCC	TGTGAACAT	GCACTGGGAA	GGGTGGAGAT	CAGGTCCCGG	1620
CCTGGAATAT	ATATTCTACC	CCCCTGAGC	TTTGATTTTG	CATGAGCCA	AAGGTCTAGC	1680
ATTGTCAAGC	TCTTAAAGGG	TTCAATTTGG	CCCTCTCTCA	AGACTAATGT	CCCCATGTGA	1740
AAGCGTCTCT	TTGTCTGAG	CTTTGAGGAG	ATGTTTTCCT	TCATTTTAGT	TTCAAAACCA	1800
AGTGAAGTGT	TGCATCTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCCA	CCCCACCTC	1860
CCTTCCCTTC	ATACCCTCTC	TCAACGTTCT	TTTACTTTAT	ACTTTAACTA	CCTGAGAGTT	1920
ATCAGAGCTG	GGGTGTGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTTGAGTACG	1980
TAGGCTGTGG	GAAGATGAAG	ATGGTTTGGG	GGTGTAAAC	AATGTCTTTC	GCTGAGGCCA	2040
AAGTTTCCAT	GTAAGCGGGA	TCCGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTTCTT	2100
TAAAAACAT	CTTTTCAATG	AAATGTGTTA	CCATTTCATA	TCCATTGAAG	CCGAAATCTG	2160
CATAAGGAAG	CCCACTTTAT	CTAAATGATA	TTAGCCAGGA	TCCTTGGTGT	CCTAGGAGAA	2220
ACAGACAAGC	AAAACAAAGT	GAAGACCGAA	TGSAATTAAT	TTTGCAAAAC	AAGGGAGATT	2280
TCTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTCTTC	CCACTTTTGT	TGATGTTTAT	2340
TTCAGAATCT	TGTTGATTC	ATTTCAAGCA	ACAACATGTT	GTATTTTGT	GTGTTAAAG	2400
TACTTTTCTT	GATTTTGA	TGTATTTGTT	TCAGGAAGAA	GTCATTTTAT	GGATTTTCTT	2460
AACCGGTGTT	AACTTTCTA	GAATCCACCC	TCTTGTGCC	TTAAGCATT	CTTTAACTGG	2520
TAGGGAACGC	CAGAACTTTT	AAGTCCAGCT	ATTCATTAGA	TAGTAATTGA	AGATATGTAT	2580
AAATATTACA	AGAATAAATA	ATATATTACT	GTCTCTTTAG	TATGTTTTC	AGTGAATTA	2640
AACCGAGAGA	TGCTTGTGTT	TTTAAAAAG	AATAGTATTT	AATAGGTTTC	TGACTTTTGT	2700
GGATCATTTT	GCACATAGCT	TTATCAACTT	TTAAACATTA	ATAAACTGAT	TTTTTTAAAG	

Seq ID NO: 2 Protein sequence  
Protein Accession #: NP\_001391

60  
65  
70

1	11	21	31	41	51	
MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHYN	YTGKLNISAD	KENSILKTSV	VFILICCFII	60
LENIFVLLTI	WTKKFKHRPM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
EGSMFVALSA	SVFSLLAIAI	ERYITMLQMK	LENGSNNPRL	FLILSACWVI	SLILGGLPIM	180
GNICISALSS	CSVLPLPYHK	HYILFCTTVF	TLILLSIVIL	YCRIYSLVRT	RSRRLTFRKN	240
ISKASRSSEK	SLALLKTVII	VLSVFIACWA	PLFILLLLDV	GCKVRTCDIL	FRAEYFLVLA	300
VLNSGTNPPI	YTLTNKEMRR	APIRIMSCKK	CPSGDSAGRF	KRPIIAGMEF	SRSKSDNSSH	360
PQKDEGDNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence  
Nucleic Acid Accession #: NM\_002205.1  
Coding sequence: 1..3149

75  
80

1	11	21	31	41	51	
ATGGGGAGCC	GGACGCCAGA	GTCCCTCTC	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
CGCGACCCCC	CGCTSSGTCC	GCTGCTGTG	CTGCTSSGTG	CGCGCCACCC	CAGGGTCGGG	120
GGCTTCAACT	TAGACGCCGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
GGATTCTCAG	TGGAGTTTTA	CCGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
CCCAAGGCTA	ATACCAAGCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTC	300
TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAAG	CTCTCGGCTC	360
CTGGAGTCTT	CAGTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
TGGTTGGGGG	CAACAGTTGG	AGCCCATGGC	TCTTCCATCT	TGGCATGCGC	TCCACTGTAC	480
AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
GATAACTTCA	CCCGAATTTT	GGAGTATGCA	CCCTGCCGCT	CAGATTTTCA	CTGGGCAGCA	600

5  
10  
15  
20  
25  
30  
35  
40  
45

```

GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT 660
TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGCTGCCAC TCAGGAGCAG 720
ATTGCAGAAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 840
TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC 900
GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGATGCC TCTACAATT CTCAGGGGAA 960
CAGATGGCCT CTAATCTTGG CTATGCAGTG GCGCCACAG ACGTCAATGG GGACGGGCTG 1020
GATGACTTGC TGGTGGGGGC ACCCTTGCTC ATGGATCGGA CCCCTGACGG GCGGCTCAG 1080
GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACC 1140
CTTACCCCTA CTGGCCATGA TGAGTTTGGC GATTTTGGCA GCTCCTTGAC CCCCTGGGG 1200
GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCTTTGG TGGGGAGACC 1260
CAGCAGGGAG TAGTGTGTGT ATTTCTGGG GCGCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
CAGTTTCTGC AGCCCTGTGG GGCAGCCAG CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
CGAGGAGGCG GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTTGGT 1440
GTGGCAAGG CTGTGTGATA CAGGGGCGGC CCATCGTGT CCGCTAGTGC CTCCTCACC 1500
ATCTTCCCGC CCATGTTCAA CCGAGAGGAG CGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
GCCTGCATCA ACCTTAGCTT CTGCTCAAT GCTTCTGGA AACACGTTGC TGACTCCATT 1620
GGTTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGCGGGGCA 1680
CTGTTCTGGC CCTCCAGGCA GGCAACCTCG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAA 1800
CTCTCGCCG TATTCACGCT TCTCAACTTC TCCTTGGACC CCAAGCCCC AGTGGACAGC 1860
CAGGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCGTG ACCTGCAGCT GGAAGTGT 1980
GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCC TGAACCTCAC TTTCCATGCC 2040
CAGAATGTGG GTAGGGTGG GCGCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG 2100
GCTGAGTACT CAGGACTCTG CAGACACCA GGAACCTTCT CCAGCCTGAG CTGTGACTAC 2160
TTTGCGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220
GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280
ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGAGCTGGTT 2340
TCCTTTCGCG TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCTAAGCT 2400
GAGGCACTGC TATTCACGCT AAGCGACTGG CATCCCGAG ACCAGCCTCA GAAGGAGGAG 2460
GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
AGCCAGGGTG TGCTGGAAGT CAGCTGTCCC CAGGCTCTGG AAGGTACGCA GCTCTATAT 2580
GTGACCAAG TTAGGGGACT CAATGCACCC ACCAATCACC CCATTAACCC AAAGGGGCTG 2640
GAGTTGGATC CCGAGGGTTC CCTGCACAC CAGCAAAAC GGAAGCTCC AAGCCGACG 2700
TCTGCTTCTC CGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760
TGTGAGCTCG GGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAATTGCA TTTCCGAGTC 2820
TGGGCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880
TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCA AAAAGAGCGT 2940
CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAAGCA GCTATGGCGT CCCACTGTGG 3000
ATCATCTCC TAGCCATCTT GTTGGCCTC CTGCTCTAG GTCTACTCAT CTACATCTCT 3060
TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CGCCATGGA AAAAGCTCAG 3120
CTCAAGCTC CAGCCACCTC TGATGCCTGA

```

Seq ID NO: 4 Protein sequence  
Protein Accession #: NP\_002196.1

50  
55  
60  
65  
70

```

1 11 21 31 41 51
MGSRTPEPL HAVQLRWGR RRPPLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DFCVCTCYLST 180
DNFRILEYA PCRSDFSNAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ QQLSATQEQ 240
IAESYYPEYL INLVQQLQRT QRASSIIDDS YLGSYVAVGE FSGDDTDETV AGVPKGNLTY 300
GVVTLNGSD IRLSYNFSGE QMASYFGYAV AATDVNGDGL DLLLVGAPLL MDRTPDGRPY 360
EVGRVYVYLQ HPASIEPTPT LTLTHGDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGRDLDGNG YPDLYVGSFG 480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLBGNPV ACINLSFCLN ASGKHVADSI 540
GPTVELQLDW QKQKGSVRRR LPLASRQATL TQTLILQNGA REDCREMKIY LRNBSEPRDK 600
LSPHIALNF SLDPQAPVDS HGLRPAHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLED KNALNLTFFA QNVGEGGAYE AELRVTAPE AEYSGLVHRP GNFSSLSCDY 720
FAVNQSRLLV CDLGNPMKAG ASLWGGRLFT VPHLRDTKKT IQDFDQILSK NLNNSQSDVV 780
SFRLSVEAQA QVTINGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLLHR QKREAPSR 900
SASSGQILK CPEAECFLR CELGPLHQE SQSLQLHFRV WAKTFLQREH QPFLQCEAV 960
YKALKMPYRI LPRQLPKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
YKLGPFKRSL PYGTAMEKAQ LKPPATSDA

```

Seq ID NO: 5 DNA sequence  
Nucleic Acid Accession #: NM\_002211.1  
Coding sequence: 1..2397

75  
80

```

1 11 21 31 41 51
ATGAATTAC AACCAATTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTGCT 60
CAAACAGATG AAAATAGATG TTTAAAGCA AATGCCAAT CATGTGGAGA ATGTATACAA 120
GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180
TCTGCACGAT GTGATGATT AGAAGCCTTA AAAAGAAGG GTTGCCCTCC AGATGACATA 240
GAAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CCGTAGCAAA 300
GAAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA GCAGTTGGTT 360
TTGCGATTAA GATCAGGGGA GCCACAGACA TTACATTAA AATTCAAGAG AGCTGAAGAC 420
TATCCCATTT ACCTCTACTA CCTTATGATC CTGTCTTACT CAATGAAGA CGATTTGAG 480
AATGTAAAAA GTCTTGAAC AGATCTGATG AATGAATGA GGAGGATTAC TTCGACTTC 540

```

5  
10  
15  
20  
25  
30

```

AGAATTGGAT TTGGCTCATT TGTGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600
GCTAAGCTCA GGAACCCCTG CACAAGTGAA CAGAAGTCA CAGCCCATTT TAGCTACAAA 660
AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGGG AAAACAGCGC 720
ATATCTGGAA ATTTGGATTG TCCAGAAGGT GGTTTCGATG CCATCATGCA AGTTGCAGTT 780
TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTTTC CACAGATGCC 840
GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAA TGATGGACAA 900
TGTCACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
CACCTTGTCC AGAACTGAG TGAATAATAT ATTACAGCAA TTTTTCAGT TACTGAAGAA 1020
TTTCAGCCTG TTTCAAGGA GCTGAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
TCTGCAATTT CTAGCAATGT AATTCAGTTG ATCATGTATG CATACAATTC CCTTTCCTCA 1140
GAAGTCATTT TGGAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
TGCAAGAACG GGGTGAATGG AACAGCGGAA AATGGAAGAA AATGTTCCAA TATTTCCATT 1260
GGAGATGAGG TTCAATTTGA AATTAGCATA ACTTCAATA AGTGTCCAAA AAAGGATTCT 1320
GACAGCTTTA AATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
AATGGGACAT TTGAGTGGG CGCTGCAGG TGCAATGAAG GGGTGTGTGG TAGACATTGT 1500
GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
AGTTGAGAAA TCTGCAGTAA CAATGGAGAG TGGCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
AGGGATAATA CAAATGAAT TTTTCTGGC AAATCTGCG AGTGTGATAA TTTCAACTGT 1680
GATAGATCCA ATGGCTTAA TTGTGGAGGA AATGGTGTGT GCAAGTGTG TGTTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTT TGGATACTAG TACTTGTGAA 1800
GCCAGCAACG GACAGATCTG CAATGGCCCG GGCATCTGCG AGTGTGGTGT CTGTAAAGTGT 1860
ACAGATCCGA AGTTTCAAGG GCAAAAGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
GCTGAGCATA AAGAAATGTGT TCAAGTGCAG GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
TGCAACAGG AATGTTCTTA TTTTAACATT ACCAAGGTAG AAAGTCGGA CAAATTACCC 2040
CAGCCGTTCC AACCTGATCC TGTGTCCCAT TGTAAGGAGA AGGATGTGTA CGACTGTGG 2100
TTCTATTTTA CGTATTTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAA 2160
CCAGATGTTC CCATGGTCC AGACATCAT CCAATTGTAG CTGGTGTGGT TGCTGGAAAT 2220
GTTCTTATTG GCCTTGCATT ACTGCTGATA TGGAAAGCTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAATAAT 2340
CCTATTTATA AGAGTGCCGT AACACTGTG GTCATCCGA AGTATGAGG AAAATGA

```

Seq ID NO: 6 Protein sequence  
Protein Accession #: NP\_002202.1

35  
40  
45  
50

```

1 11 21 31 41 51
| | | | |
MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
SARCDLEAL KKKGCPDDI ENPRGSKDIK KKNVITNRSK GTAELKLPED ITQIQPQLV 120
RLRLSGEPQT PTLKFKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
RIGGSGPVER TVMEYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKG VFNELVKGQR 240
ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFSTDA GFHPAGDGKL GGIVLPNDQ 300
CHLENNMYT SHYDYDPSIA HLVOQLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGT 360
SANSNNVIOL IIDAYNSLSS EVILENGKLS EGVITISYKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFISL TSNKCPKIDS DSKIRPLGF TEEVEVILQY ICECEQSEB IPESPKCHEG 480
NGTFECACAR CNEGRVGRHC ECSTDENVSE DMDAYCRKEN SSEICSNNGE CVCGQCVCRK 540
RDNTNEIYSG KFCECDNFNC DRNGLICGG NGVCKRCVCE QNPNYTGSA CDSLDTSTCE 600
ASNGQICNGR GICECGVKC TDPKFQGTG EMCQTCLGVC AEHKECVQCR APNKGKKDT 660
CTQECSEAFNI TKVESRDLKP QPVQPDVSH CKEKDVEDCW FYPTYSVNGN NEVMVHVVEN 720
PECPGTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIHHR REFAKFEREK MNAKWDGTEN 780
PIYKSAVTTV VNPKYEGK

```

55  
Seq ID NO: 7 DNA sequence  
Nucleic Acid Accession #: NM\_002425  
Coding sequence: 26..1453

60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
AAAGAAGSTA AGGCGAGTGA GAATGATGCA TCTTGCACTT CTTGTGCTGT TGTGTCTGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCCGACAA TACCTAGAAA AGTACTACAA CCGGAAAGG GATGTGAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTG TTAATAAAT CCAAGGAATG CAGAAGTCC TTGGGTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGGAT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCT 660
CGTGTCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA AACTGGAAG 720
TTTGATGTAC CCACTCTACA ACTCATTAC AGAGCTCGCC CAGTTCGACC TTTGCAAGA 780
TGATGTGAAT GGCATTTCAGT CTCTCTACGG ACCTCCCTCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCA CAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTTCTTAAAG ACAGATATT 960
TTGGGAGTGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAG AGCAGGGACA CCGTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCTCTCAAC CATAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTGG AGCGGACAAA TACTGGAGAT TTGATGAAA 1260
TAGCCAGTCC ATGAGCAAGG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCAAGGTTT GTGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAA TGGTTAATTT TTCTGTCATG TTTGTGACT 1560

```

GAAGAAGATG AGCCTTCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATCTTTC 1620  
 ACTTGCTTTT GAATGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680  
 ATGTATTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGCCTGTTC 1740  
 CTT

Seq ID NO: 8 Protein sequence  
 Protein Accession #: NP\_002416

1 11 21 31 41 51  
 MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQOYLEKY YNLEKDVQKF RRKDSNLIVK 60  
 KIQQMQKFLG LEVTKGLDLD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120  
 PDLPRDAVDS AIEKALKVNE EVTPLTFSRL YEGEADIMIS FAVKEHGDYF SFDGPGHSLA 180  
 HAYPPGGLY GDIHFDDEK WTEDASGTLN FLVAHELGH SLGLFHSANT EALMYPLYS 240  
 FTSLAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDF ALSFDAISTL 300  
 RGEYLFFKDR YFWRSHWNP EPEFHLISAF WPSLPSYLD AYEVSNRDTV FIFKGNEFWA 360  
 IRGNEVQAGY PRGIHTLGFP PTIRKIDAAV SDKEKKKCTYF PAADKYWRPD ENSQSMEQGF 420  
 PRLIADDPFG VEPKVDVLIQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

Seq ID NO: 9 DNA sequence  
 Nucleic Acid Accession #: XM\_058189.2  
 Coding sequence: 169..774

1 11 21 31 41 51  
 GAAGACCAGC TCAGCTCTTC AGTTGTGAT CATGTCTAT TGTCTCCAA ACAGTAAACC 60  
 AGTATTTTAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCCGGTC TCCTCATGAA 120  
 TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTCTTAAGC AGGCCAAAT GGGGTCTCGG 180  
 AAGTGTGGAG GCTGCTAAG TTGTTTGTCT ATTCGCTTG CACTTTGGAG TATAATCGTG 240  
 AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC 300  
 AACTAGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360  
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAACTGTC 420  
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCTT 480  
 GGATACTGCC TGGTCATCTC TGCCTTGGGT CTTGTCCAAG GGCCATATTG CGCACCCCTT 540  
 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGAGCTT TCCTTACAGA TTCTAGCATA 600  
 TGGATTCACT GCCTGGAACC TGCACATGTT GTGGAGTGGA ACATCATTTT ATTTTCCATT 660  
 CTCATAACCC TCACTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720  
 TCCAGATAC TGTGTGGAAG CTATTCAGTG ATCTTCCAGC CTGGAATCAT TTGAATAAGG 780  
 ACAAAATGTT TTCAATTATC AAGACATGGC CATCTATCTA AATATTATAT CAACGTGTGA 840  
 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTATTAT TTGTAAAAAA 900  
 TTTGCACTGC TCACATGCACA TGCAAGTATA CCACCTTCC ATTTAGTATG TTTTAAAGT 960  
 AATATGCATC AGAAACTTCA GAAATCTTC TGCCCTTTGA TCAACAAAT CCATTTCCAA 1020  
 GAATCTGTAC TAGGGAAGTA AATAAGATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080  
 TGCAACATTA TTTAATATTC TGGAAAATTG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140  
 AGGATTAAGT AAAGAGTGGT ACATACTGTA AATGTTTCTT GATATTAAAA AAAAAATTAA 1200  
 ATAAAAATA AAGAGTACTA CATGTTTGA AAA

Seq ID NO: 10 Protein sequence  
 Protein Accession #: XP\_058189.1

1 11 21 31 41 51  
 MGSRKCGGCL SCLLIPLALW SIIVNILLYF PNGQTSYASS NKLTINVWYF EGICFSGIMM 60  
 LIVTTVLVLV ENNNNYKCCQ SENCCKKYVT LLSIIFSSLG IAFSGYCLVI SALGLVQGPY 120  
 CRTLDGWEYA FBTAGRFLT DSSIWIQCLE PAHVVEWNII LPSILITLSG LQVIICLIRV 180  
 VMQLSKILCG SYSVIFQPGI I

Seq ID NO: 11 DNA sequence  
 Nucleic Acid Accession #: NM\_002421.2  
 Coding sequence: 1..1409

1 11 21 31 41 51  
 ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60  
 CCAGCGACTC TAGAAACACA AGAGCAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120  
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180  
 GTTGAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACAGAT 240  
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCGTGATG GCCTCAGTTT 300  
 GTCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360  
 TACAGCCAG ATTTCGCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420  
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480  
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540  
 CTTGCTCATG CTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600  
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTGCGGC TCATGAATC 660  
 GGCCATTCTC TTGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720  
 ACCCTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780  
 GGAGTTCCT AAAATCTCTG CCAGCCCATC GGGCCACAAA CCCCAGAGC ATGTGACAGT 840  
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGAGAGAG TGATGTTCTT TAAAGACAGA 900  
 TTCTACATGC GCACAAATCC CTTCTACCGG GAAGTTGAGC TCAATTCAT TTCTGTTTTC 960  
 TGGCCCACTC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020  
 CGGTTTTCAC AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080  
 CCCAGGACA TCTACAGCTC CTTTGGCTTC CTAGAAGCTG TGAAGCATAT CGATGCTGCT 1140  
 CTTTCTGAGG AAAACACTGG AAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200  
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260

GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTTCCTTCAT 1320  
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380  
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

5

Seq ID NO: 12 Protein sequence  
 Protein Accession #: NP\_002412.1

1 11 21 31 41 51  
 10 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60  
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120  
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDHRD NSPFDGPGGN 180  
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSLGLSHST DIGALMYPST 240  
 15 TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300  
 FYMRINPFYP EVELNFISVF WPQLPNGLA AYEFADRDEV RPFKGNKYNA VQGQNVLHGY 360  
 PKDIYSSFGF PRTVGHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDPG YPKMIAHDFP 420  
 GIGHKVDVAV MKDGFYFFPH GTRQYKDFPK TKRILTLQKA NSWFNCRKN

20

Seq ID NO: 13 DNA sequence  
 Nucleic Acid Accession #: NM\_002421.2  
 Coding sequence: 1..1409

1 11 21 31 41 51  
 25 ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTCTCTGG GTGTGGTGTG ACACAGCTTC 60  
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120  
 TACTACAACC TGAGAAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180  
 GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCGAT 240  
 30 GCTGAAACCC TGAAGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300  
 GTCTCAGCTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360  
 TACACGCCAG ATTTGCCAAG AGCAGATGT GACCATGCCA TTGAGAAAGC CTTCCAACTC 420  
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGTCTCTG AGGGTCAAGC AGACATCATG 480  
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540  
 CTTGCTCATG CTTTCAAC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600  
 35 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660  
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCTAGCTAC 720  
 ACCTTCAGTG GTGATGTTC GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780  
 GGACGTTCCT AAAATCCTGT CCAGCCCATC GGCCCAAAA CCCCAGGAGC ATGTGACAGT 840  
 40 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGGAG TGATGTTCTT TAAAGACAGA 900  
 TTCTACATGC GCACAAATCC CTTCTACCGG GAAGTTGAGC TCAATTTTCT TTCTGTTTTC 960  
 TGGCCCAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCGGACAG AGATGAAGTC 1020  
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGAC AGAATGTGCT ACACGGATAC 1080  
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140  
 45 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200  
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTC 1260  
 GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTTCCTTCAT 1320  
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380  
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

50

Seq ID NO: 14 Protein sequence  
 Protein Accession #: NP\_002412.1

1 11 21 31 41 51  
 55 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60  
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120  
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDHRD NSPFDGPGGN 180  
 60 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSLGLSHST DIGALMYPST 240  
 TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300  
 FYMRINPFYP EVELNFISVF WPQLPNGLA AYEFADRDEV RPFKGNKYNA VQGQNVLHGY 360  
 PKDIYSSFGF PRTVGHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDPG YPKMIAHDFP 420  
 GIGHKVDVAV MKDGFYFFPH GTRQYKDFPK TKRILTLQKA NSWFNCRKN

65

Seq ID NO: 15 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 141..1580

1 11 21 31 41 51  
 70 TCTGCGTGTG CCGGGGCTAG GGGCTGGAAG TCCTGGCTCT AGTTGCACCT CGGAAGGAAA 60  
 AGGCAACAG AGGAGGGGAG GCGTCTTAGG ACTGCTTGA TCCAGAGCAC TTTCCTCGGC 120  
 75 CTTACAGGCG CTGTGTGCT ATGGGTTTCC CCGCGGCCCC GGAGGGAGCG CTGGGCTAAG 180  
 TCGCGAGATT CACTCGCCAC TCCTCCGACG TGCTGGGCAA CCTCAACGAG CTGCGCTGCG 240  
 GCGGATCCT CACTGACGTC ACGCTGCTGG TTGGCGGGCA ACCCTCAGA GCACACAAGG 300  
 CAGTTCTCAT CGCTCGAGT GGCTCTTCT ATTCAATTT CCGGGGCCGT GCGGGAGTGG 360  
 GGGTGGACGT GCTCTCTCTG CCCGGGGGTC CCGAAGGAG AGGCTTCGCC CCTCTATTGG 420  
 80 ACTTCATGTA CACTTCGCGC CTGCGCCTCT CTCAGGCCAC TGCAACGACA GTCTAGCGG 480  
 CCGCCACCTA TTTCAGATG GAGCAGCTGG TCCAGGCATG CCACCGCTTC ATCCAGGCCA 540  
 GCTATGAACC TTTGGGCATC TCCCTGCGCC CCTTGAAGC AGAACCCCA ACACCCCAAG 600  
 CGGCCCCCTC ACCAGGTAGT CCCAGGCGCT CCGAAGGACA CCCAGACCA CCTACTGAAT 660  
 CTCGAAGCTG CAGTCAAGGC CCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTGCAACT 720  
 GGAAAAAGTA CAAGTACATC GTGCTAAACT CTCAGGCTCT CCAAGCAGG AGCCTGGTGG 780

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

GGGAGAGAAG TTCTGTCCT CTTGCCCCC AAGCCAGGCT CCCCAGTGGG GACGAGGCCT 840  
CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCTT GGTCCCCAGA 900  
GCAGGCTCTC TCCAACCTGT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960  
CCTACCTCCT CACATCCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020  
CACTACCCGG AAGTGAATTT TTCAGCTGCC AGAACTGTGA GGCTGTGGCA GGGTGCTCAT 1080  
CGGGCTGGA CTCCTTGGTT CCTGGGGAGC AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140  
GGTCTCTGTT CCGCTACAAG GSCAACCTTG CCAGTCAATG TACAGTGCAC ACAGGGGAAA 1200  
AGCCTTACCA CTGCTCAATC TGCGGAGCCC GTTTTAACCG GCCAGCAAAC CTGAAAACGC 1260  
ACAGCCGCAT CCATTGCGGA GAGAAGCCGT ATAAGTGTGA GACGTGCGCG TOGCGCTTTG 1320  
TACAGGTGGC ACATCTGCGG GCGCACGTGC TGATCCACAC CGGGGAGAAG CCTACCCCTT 1380  
GCCCTACCTG CGGAACCCGC TTCCGCCACC TGCAGACCCCT CAAGAGCCAC GTTCGCATCC 1440  
ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGGCCT GCATTTCCGG CACAAGAGTC 1500  
AACTGCGGCT GCATCTGCGC CAGAAACACG GAGCTGTCTAC CAACACCAA GTGCACTACC 1560  
ACATTCTCGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCC CACTTGCTTC CTGCGGGTGG 1620  
GAAAGCTGCA GGGCCAGGCC TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGGC 1680  
CAATTTGGT GCGAAATTTT CCACCTCTT AATTTCTCAC TGGGGAGAGC AGGGGTGGCA 1740  
GATCCTGGCT AGATCTGCTT CTGTTTGTCT GGTCAAAACC TCTTCCCCAC AAGCCAGATT 1800  
GTTTCTGAGG AGAGAGCTAG CTAGGGGCTG GGAAGGGGGA GAGATTGGAG TCCTGGTCTC 1860  
CCTAAGGGA TAGCCCTCCA CCTGTGGCCC CCAATTGCATT CAGTTTATCT GTAAATATAA 1920  
TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTCATTGCA TTGCATTCCC CACTCCCCCTC 1980  
TTCCACAAGT GTGATTAAAA GTGACCAGAA ACACAGAAGG TGAGATCACA GCTCTGCTGG 2040  
CAGAGATTAC TAGCCCTTGG CTCTCTCGTT TGGCTTGGGT ATTTTATATT ATTTCTGTCA 2100  
TAACTTTAT CTTTAGAATT GTTCTTCTC CTGTTTGTCT GCTTGTAGT TGTTTAAAA 2160  
TGAAGAAAGG GGTCTCTGT GTTCTGCCCC TGTAACTCTA GGTCTGGAAC CTTTATTTGT 2220  
TCTAGGGCAG CTCTGGGAAC ATGCGGGATT GTGGAATTGG GTCAGGAACC CTCTCTGGTA 2280  
TTCTGGATGT TGTAGTTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTCTCT 2340  
CAAGGGTGAT AGGAACCAT ATGTTGAGCC CAAAATGGAA GTAATAATA ATGCTCTCTG 2400  
GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCGGTA TCACTCCAAC TGGAGGCTGT 2460  
GGGTGTGGG GATTCTGTAT CTGGATTCCG TATCACTCCA AGTGGAGGCT GGCAGGTTTT 2520  
TCTGCAAGT GTTCAGAAAT CTAAATATGC CCATTAACTT GGTCACTTGG GTTGTGCTCT 2580  
GCTGTATGAT CCTATTAGTG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCTCTC 2640  
CACGGGGGCC TGTCTTACG ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTC 2700  
TTATCAGAGA TGATGTGACC TTTTCTGACT CTGCCCAGTC TCTATGAATG TTATGGCCTA 2760  
GGGAAGAATC ATGAACCTCT TTAGCTTGAT TAGATGGTAA ACAGTGTAA CCCATCCTTT 2820  
ACTACAGAGG CATATGGGTT TGAATGTTAC CTGGGGTTCT CTCTATTGAG TTGAGCCCTT 2880  
TCTTCCCTTA TGTGGTTTGG GACATCTTCT GGCAAGTGTC CAGATGCCAG AACCTTCTTT 2940  
TCCTCTAGAA GGGATGGTGC TTGGTAACCT TACCTTTTAA AAGCTGGGTC TGTGACCTGG 3000  
TCTTCCCATC CTGCACTTCC TGCTTGAAC CAGTGAATGC ATTAGAACCT TCCATAGGAA 3060  
AAGAAAAGGG GCTGAGTTCC ATTCTGGSTT TGCTGTAGTT TGGTGGGAT TATTGTGGC 3120  
ATTACAGATG TAAAGATTG ACTAGCCCAT AGGCCAAAGG CCTGTTCTAG TTGACCAAGT 3180  
TTCAAGTAGG ATTAAGAGGT TGGTTGAGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA 3240  
GAAAGTGAGG AACAGGGTTG CCTCTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC 3300  
GCTGAAGCCT TGATTGATAG TTTGCCCCCT TGTGCCCCG GGGCTTATCT GATTATGGGA 3360  
CGAGGGTAGA AAGTAAGAAG CACTTTTGAA TTTGTGGGGT AGAATCTCAA CAATAAGTCA 3420  
GTTCTAGTGG CTGTCGCCCT GGGACTAGT AGAAAGCTAC TCTTCTCCCT CTTCCCTCTT 3480  
TCTTCCCTGA GCSSGLDSL PGDEKPYKC QLCRSSFRYK GNLSHRTVH TGEKPYHCIS 3540  
AGAAGGAATC ATGATTTCTA TTTAGCAGAT TGGATGGGCA GGTGGAGAAT GCCTGGGGGT 3600  
AGAAATGTGA GATCTTGCAA CATCAGATCC TTGGAATAAA GAAGCCTCTC TGYGCNRAAA 3660  
AAAAAAAAA AAAAAA

Seq ID NO: 16 Protein sequence  
Protein Accession #: FGENESH predicted

55  
60  
65

1 11 21 31 41 51  
MGSPAPEGA LGVYREFTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS 60  
GFFYSIFRGR AGVGVLDVSL PGPEARGFA PLLDFMYTSR LRLSPATAPA VLAAATYLMQ 120  
EHVVQACHRF IQASYEPLGI SLRPLEARPP TPPTAPPPGS PRRSEGHDPD PTESRSCSQG 180  
PPSPASDPK ACNWKYKYI VLNSQASQAG SLVGERSSGQ PCPQARLPSP DEASSSSSSS 240  
SSSSEEGPIP GPQRLSFTA ATVQPKGAP ASTPYLLTSQ AQDTSGSPSE RARPLPGSEF 300  
PSCQCEAVA GCSSGLDSL PGDEKPYKC QLCRSSFRYK GNLSHRTVH TGEKPYHCIS 360  
CGARFNRPAN LKTHSRHISG EKPYKCETOG SRFVQVAHLR AHVLIETGEK PYPCTCGTR 420  
FRHLQTLKSH VRIHTGKPY HCDPQGLHFR HKSQRLRLHLR QKHGAATNTK VHYHILGGP

65  
70

Seq ID NO: 17 DNA sequence  
Nucleic Acid Accession #: XM\_039209  
Coding sequence: 1..2049

70  
75  
80

1 11 21 31 41 51  
ATGCTGAAGA TGCTCTCCTT TAAGCTGCTG CTGCTGGCCG TGGCTCTGGG CTTCTTTGAA 60  
GGAGATGCTA AGTTTGGGGA AAGAAACGAA GGGAGCGGAG CAAGGAGGAG AAGGTGCCTG 120  
AATGGGAACC CCCCGAAGCG CCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG 180  
CTGCTGAGTG GGGGAGAGAT GCTGTGCGGT GGCCTTCTACC CTCGGCTGTC CTGCTGCCCTG 240  
CGGAGTGACA GCGCGGGGCT AGGGCGCCCTG GAGAATAAGA TATTTTCTGT TACCAACAAC 300  
ACAGATTGTG GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCAA 360  
AGCCTGTTC ACTCACCTGA GAGAGAAGTC TTGGAAGAG ACCTAGTACT TCCTCTGCTC 420  
TGCAAGACT AITGCAAGA ATTCTTTTAC ACTTCCCGAG GGCATATTC AGGTTTCTCT 480  
CAAAACAATG CGGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTCTGCTTT 540  
CCAGATTTTC CAAGAAAAA AGTCAGAGGA CCAGCATCTA ACTACTTGGA CCAGATGGAA 600  
GAATATGACA AAGTGGGAAGA GATCAGCAGA AAGCACAAC ACAACTGCTT CTGTATTCTG 660  
GAGGTTGTGA GTGGGCTGGC GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTCGCAA 720  
CGTCTCTTCA TTTTGAAAAA AGAAGGTTAT GTGAAGATAC TTACCCCTGA AGGAGAAATT 780  
TTCAAGGAGC CTTATTGGGA CATTACAAA CTTGTTCAAA GTGGAATAAA GGGAGGAGAT 840



5  
10  
15  
20

```

GAAAGAGGAC TGCTAAGCCT CGCATTCCAT CCCAATTACA AGAAAAATGG AAAGTTGTAT 900
GTGTCTCTATA CCACCAACCA AGAACGGTGG GCTATCGGGC CTCATGACCA CATTCTTAGG 960
GTTGTGGAAT ACACAGTATC CAGAAAAAAT CCACACCAAG TTGATTGTAG AACAGCCAGA 1020
GTCTTTCTTG AAGTTGCAGA ACTCCACAGA AAGCATCTGG GAGGACAACT GCTCTTTGGC 1080
CCTGACGGCT TTTTGTACAT CATTCTTGGT GATGGGATGA TTACACTGGA TGATATGGAA 1140
GAAATGGATG GGTAAAGTGA TTTCAAGGC TCAGTGTCTAC GGCTGGATGT GGACACAGAC 1200
ATGTGTAACG TGCTTATTTC CATACCAAGG AGCAACCCAC ACTTCAACAG CACCAACCAG 1260
CCCCCGAAG TGTTTGTCTA TGGGCTCCAC GATCCAGGCA GATGTGCTGT GGATAGACAT 1320
CCCACTGATA TAAACATCAA TTAAACGATA CTGTGTTTCAG ACTCCAATGG AAAAAACAGA 1380
TCATCAGCCA GAATTTCTACA GATAATAAAG GGGAAAGATT ATGAAAGTGA GCCATCACTT 1440
TTAGAATTCA AGCCATTACG TAATGGTCTT TTGGTTGGTG GATTGTGATA CCGGGGCTGC 1500
CAGTCAGAAA GATTGTATGG AAGCTACGTG TTTGGAGATC GTAATGGGAA TTCTCTAACT 1560
CTCCAGCAAA GTCTGTGAC AAAGCAGTGG CAAGAAAAAC CACTCTGTCT CGGCACTAGT 1620
GGGTCTGTGA GAGGCTACTT TTCCGGTCAC ATCTTGGGAT TTGGAGAAGA TGAAC TAGGT 1680
GAAGTTTACA TTTTATCAAG CAGTAAAAGT ATGACCCAGA CTCACAATGG AAAACTCTAC 1740
AAAAATTGAT ATCCCAAAG ACCTTTAATG CCTGAGGAAT GCAGAGCCAC GSTACCAACT 1800
GCACAGACAC TGACTTCAGA GTGCTCCAGG CTCTGTGCGA ACGGCTACTG CACCCCAACG 1860
GGAAAGTGCT GCTGCACTCC AGGCTGGGAG GGGGACTTCT GCAGAACTGC AAAATGTGAG 1920
CCAGCATGTC GTCAATGGAG TGTCTGTGTT AGACCGAACA AGTGCTCTGT TAAAAAAGGA 1980
TATCTTGGTC CTCAATGTGA ACAAGTGGAC AGAAACATCC GCAGAGTGAC CAGGGCAGAC 2040
ATCACCTAG

```

25 Seq ID NO: 18 Protein sequence  
Protein Accession #: XP\_039209

30  
35  
40

```

1 11 21 31 41 51
MLKMLSFKLL LLAVALGFPE GDAKFGERNE GSGARRRRCL NGNPPKRLKR RDRRMMSQLE 60
LLSGGEMLCG GFYPRLSCLL RSDSPGLGRL ENKIFSVTNN TECGKLEELI KCALCSPHSQ 120
SLFHSPPEREV LERDLVLP LL CKDYCKEFFFY TCRGHIPGFL QTTADEFCFY YARKDGGLCF 180
PDFPRKQVRG PASNVLDQME EYDKVEEISR KHKHNCFCIQ EVVSGLRQPV GALHSGDGSQ 240
RLFILKEGY VKILTPGEI FKEPYLDIHK LVQSGIKGGD ERLLSLAFH PNYKKNKLY 300
VSYTTNQERW AIGPHDHLR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
PDGFLYIILG DGMITLDDME EMDGLSDFTG SVLRDLVDVTD MCNPYSIPR SNPHFNSTNQ 420
PREVFAHGLH DGRCAVDRH PTDININLTI LCSDSNGKNR SSARILQIIK GKDYSESEPSL 480
LEFKPFSSNGP LVGGFVYRGC QSERLYGSYV FGDRNGNFLT LQSPVTKQW QEKPLCLGTS 540
GSCRGYPSGH ILGFGEDELG EYVILSSSKS MTQTHNGKLY KIVDPKRELM PEECRATVQP 600
AQTLTSECSR LCRNGYCTPT GKCCSPGWE GDFCRTAKCE PACRHGGVCV RPNKCLCKKG 660
YLGPCQEQVD RNIRRVTRAD IT

```

45 Seq ID NO: 19 DNA sequence  
Nucleic Acid Accession #: NM\_014331.2  
Coding sequence: 1..1506

50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
ATGGTCAGAA AGCCTGTTGT GTCCACCATC TCCAAAGGAG GTTACCTGCA GGGAAATGTT 60
AACGGGAGGC TGCTTCCCTT GGGCAACAAG GAGCCACCTG GGCAGGAGAA AGTGCAGCTG 120
AAGAGGAAAG TCACCTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTTGGAGCA 180
GGAACTCTCA TCTCTCTTAA GGGCGTGCTC CAGAACAACG GCAGCGTGGG CATGTCTCTG 240
ACCATCTGGA CGGTGTGTGG GGTCTGTGTA CTATTGGAG-CTTGTCTTA TGCTGAATTG 300
GGAACAATA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGAAGT CTTTGGTCCA 360
TTACCAGCTT TTGTACAGAG CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420
GTGATATCCC TGSCATTGGG ACCTACATCT CTGGAACCAT TTTTATTACA ATGTGAAATC 480
CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCTCTAAT 540
AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA 600
GCAATCTGTA TAATATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCA AACGCAGAAC 660
TTTAAAGACG CGTTTTCAGG AAGAGATTCA AGTATTACGC GGTTCGCACT GGCTTTTAT 720
TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTACTGTA AGAAGTAGAA 780
AACCCCTGAA AAACCATTC CTTGCAATA TGTATATCCA TGGCCATTGT CACCATTGGC 840
TATGTGCTGA CAAATGTGGC CTACTTTAGC ACCATTAAAT CTGAGGAGCT GCTGCTTTCA 900
AATGCAGTGG CAGTGACCTT TTTGAGCGG CTACTGGGAA ATTCTCAIT AGCAGTTCCG 960
ATCTTTGTTG CCGTCTCTCG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG 1020
TTATTTCTATG TTGCTCTCG AGAGGGTCAC CTTCCAGAAA TCCTCTCCAT GATTCAATGTC 1080
CGCAAGCACA CTCCTCTACC AGCTGTATT GTTTTGACCC CTTTGACAT GATAATGCTC 1140
TTCTCTGGAG ACCTGACAG TCTTTGAAT TTCTCAGTT TTGCGAGGTG GCTTTTATT 1200
GGGCTGGCAG TTGCTGGGCT GATTATCTT CGATACAAAT GCCAGATAT GCATCGTCT 1260
TTCAAGGTGC CACTGTTTCA CCGAGCTTTG TTTTCTTCA CATGCCCTT CATGGTTGCC 1320
CTTTCCTCT ATTCCGACCC ATTTAGTACA GGGATTGGCT TGTCTATCAC TCTGACTGGA 1380
GTCCCTGCGT ATTATCTCT TATTATATGG GACAGAAGAC CCAGGTGGTT TAGAATAATG 1440
TCAGAGAAAA TAACCAAGAA ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500
TTATGAACATA ATGGACTTGA GATCTTGGCA ATCTGCCCAA GGGGAGACAC AAAATAGGGA 1560
TTTTTACTTC ATTTCTGAA AGTCTAGAGA ATTACAACTT TGGTGATAAA CAAAAGGAGT 1620
CAGTTATTTT TATTATATA TTTTAGCATA TTCGAACATA TTTCTAGAAA ATTTAGTTAT 1680
AACTCATGTG ATTTATAGAA AGTGAATATG CAGTTATCT ATGAGTGCAG CAATCTCTGA 1740
GTCTCTGATA CCTACCTATT GGGGTTAGGA GAAAAGACTA GACAATTAAT ATGTGGTCAT 1800
TCTCTACAAC ATATGTTAGC ACGGCAAGAA ACCTTCAAAT TGAAGACTGA GATTTTTCTG 1860
TATATATGGG TTTGTAAAG ATGGTTTAC AACTACAGA TGTCTACTAT GTGAAAAGTG 1920
TTTTCAATT TGAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980
ATTTTCAATT GAAATGATG TGCTTCCOCT TAGATACCAA TTTAGATAAC AAACACTCAT 2040
GCTTTAATGG ATTATACCCA GAGCACTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA 2100
TTAAAGAAGA GTTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAAGT 2160
AAAAATCCTT GAGAATTTAT TATGTCAGAT GTTTTTTCAT TCATTATCAG GAAGTTTATG 2220

```

5 TTATCTGTCA TTTTITTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG 2280  
 AGCAAGAGTT AGTTTGGTAT TAAATCCTCA TTAGAACAAC CACCTGTTTC ACTAATAACT 2340  
 TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAAGCC TTCAAATTAC ATTATCAACA 2400  
 TGAGAGAAAT AACCAACAAA GAAGATGTTT AAAATAATAG TCCCATATCT GTAATCATAT 2460  
 10 CTACATGCAA TGTITAGTAAT TCTGAAGTTT TTTAAATTTA TGGCTATTTT TACACGATGA 2520  
 TGAATTTTGA CAGTTTGTGC ATTTTCITTA TACATTTTAT ATTCTTCTGT TAAAATATCT 2580  
 CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA 2640  
 AAGAAATGTC GCTGTAATAA AGATTACAA CTGATGTTTC TAGAAAATTT CCACCTCTAT 2700  
 ATCTAGGCTT TGTCAATAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA 2760  
 CTGATAAGAA GAAAATTGAA ATGAGAATCT GTGGATAAGT GTTTGTGTTT AGAAGATGTT 2820  
 GTTTTGCAGG TATTAGAAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAATCCCA 2880  
 GCACCTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCCTGAC 2940  
 CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGGCACAT 3000  
 15 GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG 3060  
 GAGGTTGCAG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120  
 CCATCTCCAA AAAAAAAAAA AAAA

Seq ID NO: 20 Protein sequence  
 Protein Accession #: NP\_055146.1

20 1 11 21 31 41 51  
 MVRKPVVSTI SKGGYLQGNV NGRLPSELGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA 60  
 GIFISPKGVL QNTGSVGMSL TIWTVCGVLS LFGALSAYEL GTTIKKSNGH YTYILEVFGP 120  
 25 LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEFFFIQCEI PELAIKLITA VGITVVMVLN 180  
 SMSVSWARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240  
 YGMYAYAGWF YLNFVTEEVE NPEKTIPLAI CISMATITGV YVLTNVAYFT TINAEELLS 300  
 NAVAVTFPSR LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360  
 30 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSPARWLF I GLAVAGLIYL RYKCPDMHRP 420  
 FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLGT VPAYYLFIIW DKKPRNFRIM 480  
 SEKIRTRLQI ILEVPEEDK L

35 Seq ID NO: 21 DNA sequence  
 Nucleic Acid Accession #: NM\_002422.2  
 Coding sequence: 64..1497

40 1 11 21 31 41 51  
 ACAAGGAGGC AGGCAAGACA GCAAGGCATA GAGACAACAT AGAGCTAAGT AAAGCCAGTG 60  
 GAAATGAAGA GTCTTCCAAAT CCTACTGTTG CTGTGGGTGG CAGTTTGCTC AGCCTATCCA 120  
 TTGGATGGAG TCGCRAGGGG TGAGGACACC AGCATGAACC TTGTTCAAGT ATATCTAGAA 180  
 AACTACTACG ACCTCAAAAA AGATGTGAAA CAGTTTGTTA GGAGAAAGGA CAGTGGTCTC 240  
 45 GTTGTAAAAA AAATCGGAGA AATGCGAAG TTCTTGGAT TGGAGGTGAC GGGGAAGCTG 300  
 GACTCGGACA CTCTGGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCTCGA TGTGGTCTAC 360  
 TTCAGAACCT TTCTGGCAT CCGGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG 420  
 AATTATACAC CAGATTGGCC AAAAGATGCT GTTGATTCTG CTGTTGAGAA AGCTCTGAAA 480  
 GTCGCGGAAG AGGTGACTCC ACTCACATTC TCCAGGCTGT ATGAAGGAGA GGCTGATATA 540  
 50 ATGATCTCTT TTGCAGTTAG AGAACATGGA GACTTTTACC CTTTGTATGG ACCTGGAAT 600  
 GTTTTGGCCC ATGCTATATG CCCTGGGCCA GGGATTATAT GAGATGCCCA CTTTGTATG 660  
 GATGAACAAT GGAACAAGGA TACAACAGGG ACCAATTAT TTCTCGTTGC TGCTCATGAA 720  
 ATTGGCCACT CCTGGGTCT CTTTCACTCA GCCAACACTG AAGCTTGTAT GTACCCACTC 780  
 TATCACTCAC TCACAGACCT GACTCGGTTC CGCTGTCTC AAGATGATAT AAATGGCATT 840  
 55 CAGTCCCTCT ATGGACCTCC CCTGAGCTCC CCTGAGACCC CCTGGTACC CACGGAACCT 900  
 GTCCTCTCAG AACCTGGGAC GCCAGCCAAC TGTGATCTGT CTTTGTCTCT TGATGCTGTC 960  
 AGCACTCTGA GGGGAGAAAT CCTGATCTT AAAGACAGGC ACTTTGGCG CAAATCCCTC 1020  
 AGGAAGCTTG AACCTGAATT GCATTGTATC TCTTCATTTT GGCCATCTCT TCCTTCAGGC 1080  
 GTGGATCCG CATATGAAGT TACTAGCAAG GACCTCGTTT TCATTTTAA AGGAAATCAA 1140  
 60 TTCTGGGCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACCCCTA 1200  
 GGTTCCTCT CAACCGTGAG GAAAATCGAT GCAGCCATT CTGATAAGGA AAAGAACAAA 1260  
 ACATATTCTT TTGTAGAGGA CAAATACTGG AGATTGTATG AGAAGAGAAA TTCCATGGAG 1320  
 CCAGGCTTTC CCAAGCAAAT AGCTGAAGAC TTTCAGGGA TTGACTCAA GATTGATGCT 1380  
 GTTTTGAAG AATTGGGTT CTTTATTTT TTTACTGGAT CTTACAGTT GGAGTTTGAC 1440  
 65 CCAATGCAA AGAAAGTGAC ACACACTTGG AAGAGTAACA GCTGGCTTAA TTGTGAAAG 1500  
 AGATATGTAG AAGGCACAA ATGGGCACCT TAAATGAAGC TAATAATTCT TCACCTAAGT 1560  
 CTCTGTGAAT TGAAATGTTT GTTTTCTCCT GCCTGTGCTG TGACTGAGT CACACTCAAG 1620  
 GGAACCTCAG CTTGAATCTG TATCTGCGG GTCATTTTAA TGTATTACA GGGCAITCAA 1680  
 ATGGGCTGCT GCTTAGCTTG CACCTTGTC CATAGAGTGA TCTTTCCTCA GAGAAGGGGA 1740  
 70 AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTGCT TATTTAATAA 1800  
 AGACGATTG TCAGTTGTTT T

Seq ID NO: 22 Protein sequence  
 Protein Accession #: NP\_002413

75 1 11 21 31 41 51  
 MKSLPILLLL CVAVCASAPL DGAARGEDTS MNLVQKYLEN YYDLEKDVQ FVRRKDSGPV 60  
 VKKIREMQKF LGLLEVTKLD SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTIVRIN 120  
 YTTDLFPKAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYPFDGPGNV 180  
 80 LAHAYAPGPG INGDAHFDDQ EQWTKDTTGT NLPLVAABEI GHSLGLEFSA NTEALMYPLY 240  
 HSLTDLTRFR LSQDDINGIQ SLYGPPFDSF ETPLVPTFV PPEPGTPANC DPALSFDAVS 300  
 TLRGEILIFK DRHFWRKSLR KLEPELHLIS SFWPSLPSGV DAAYEVTSKD LVFIFKGNQF 360  
 WAIRGNEVRA GYPRGHTILG FPPTVRKIDA AISDKENKNT YFFVEDKYWR FDEKRNEMEP 420  
 GFPKQIAEDF PGIDSXIDAV PEEFGFFYFF TGSSQLEFDP NAKKVTHTLK SNSWLNC

Seq ID NO: 23 DNA sequence  
Nucleic Acid Accession #: NM\_006528  
Coding sequence: 57..764

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
10    GCGGCCAGCG GCTTCTCTCGG ACGCCTTGCC CAGCGGGCCG CCGGACCCCC TGCACCATGG 60
      ACCCCGCTCG CCCCTGCGGG CTGTCGATTG TGCTGCTTTT CTTGACGAG GCTGCACTGG 120
      GCGATGCTGC TCAGGAGCCA ACAGGAAATA ACGCGGAGAT CTGTCTCTCG CCCCTAGACT 180
      ACGGACCCCTG CCGGGCCCTA CTTCTCCGTT ACTACTACGA CAGGTACACG CAGAGCTGCC 240
      GCCAGTTCTCT GTACGGGGGC TCGAGGGGCA ACGCCAACAA TTTCTACACC TGGGAGGCTT 300
      GCGACGATGC TTGCTGGAGG ATAGAAAAAG TTCCCAAAGT TTGCGGCTG CAAGTGAGTG 360
      TGGACGACCA GTGTGAGGGG TCCACAGAAA AGTATTCTTT TAATCTAAGT TCCATGACAT 420
      GTGAAAAATT CTTTTCGGGT GGGTGTCAAC GGAAACGGAT TGAGAACAGG TTTCCAGATG 480
      AAGCTACTTG TATGGGCTTC TGCGCACCAA AGAAAATTCC ATCATTTTGC TACAGTCCAA 540
      AAGATGAGGG ACTGTGCTCT GCCAATGTGA CTCGCTATTA TTTAATCCA AGATACAGAA 600
      CCTGTGATGC TTTCACCTAT ACTGGCTGTG GAGGGAATGA CAATAACTTT GTTAGCAGGG 660
      AGGATTGCAA ACGTGCAATG GCAAAAGCTT TGA AAAAGAA AAAGAAGATG CCAAAGCTTC 720
      GCTTTGCCAG TACAATCCGG AAAATTCCGA AGAAGCAATT TTAACATTC TTAATATGTC 780
      ATCTTGTTTG TATTATGGG TATTGTGCTT TTATGGTGT ATCTGAAGAA TAATATGACA 840
      GCATGAGGAA ACAATCATT GGTGATTTAT TCACCAAGTT TTAATAATAC AAGTCACTTT 900
      TCAAAATATG CCGATTTTAT TATATATAAC TAGCTGCTAT TCAAAATGTA GCTCACTATT 960
      TTTAATTTAT GGTTCACACT TTTGTGAGAC GAATCTTTCG AATGCATAAG ATATAAAGC 1020
25    AAATATGACT CACTCATTTT TTGGGGTCGT ATTCTGTATT TCAGAAGAGG ATCATAACTG 1080
      AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG 1140
      CC

```

Seq ID NO: 24 Protein sequence  
Protein Accession #: NP\_006519

```

35    1      11      21      31      41      51
      |      |      |      |      |      |
      MDPARPLGLS ILLFLTEAA LGDAAQEPTG NNAEICLLPL DYGPICALLL RYYVDRTQSS 60
      CRQFLYGCEE GNANFYTWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
      TCEKFFSGGC HNRNFIENRFP DEATCMGFCA PKKIPSFCSY PKDEGLCSAN VTRYFFNPRT 180
      RTCAFTYTG CGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASRIRKI RKKQF

```

Seq ID NO: 25 DNA sequence  
Nucleic Acid Accession #: NM\_005458.1  
Coding sequence: 1..2825

```

45    1      11      21      31      41      51
      |      |      |      |      |      |
      ATGGCTTCCC CGCGGAGGTC CGGCGAGCCA GGGCGGCCGC CGCGCGCGCC ACCGCGCGCC 60
      GCGCGCTCTG TACTGCTACT GCTGCTGCGC CTGCTGCTGC CTCTGGCGCC CGGGGCTTGG 120
      GGCTGGGGCG GGGCGCGCCC CCGCGCGCGC CCCAGCAGCC CGCGCTCTCT CATCATGGGC 180
      CTCAATCGCG TCACCAAGGA GGTGGCCAAG GGCAGCATCG GCGCGGTGTG GCTCCCGGCC 240
      GTGGAAGTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGGCGCCCTA CTTCTCGAC 300
      CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAAGGGT TGAAGCCCTT CTACATGACA 360
      ATAAATACAG GGGCGAACCA CTGTGATGGT TTTGGAGGCG TCTGTCCATC CGTCACATCC 420
      ATCATTCAG AGTCCCTCCA AGGCTGGAAT CTGGTGCAAC TTTCTTTTGC TGCAACCAAG 480
      CCTGTTCTAG CCGATAAGAA AAAATACCTT TATTTCTTTC GGACCGTCCC ATCAGACAAT 540
      GCGGTGAATC CAGCCATTCT GAAGTTGCTC AAGCACTACC AGTGAAGCG CGTGGGCACG 600
      CTGACGCAAG ACCTTCAGAG GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCTGTAT 660
      GGGGAGGACA TTGAGATTTC AGACACGAG AGCTTCTCCA ACGATCCCTG TACCAGTGTC 720
      AAAAAGCTGA AGGGGAATGA TGTGCGGATC ATCCTTGCCC AGTTTGACCA GAATATGGCA 780
      GCAAAAGTGT TCTGTTGTGC ATACGAGGAG AACATGTATG TAGTAAATA TCAGTGGATC 840
      ATTCCGGGCT GGTACGAGCC TTCTTGTTGG GAGCAGGTGC ACACGGAAGC CAATCATCC 900
      CGCTGCTTCC GGAAGAATCT GCTTGCTGCC ATGAGGGGCT ACATTGGCGT GGATTCGAG 960
      CCCCTGAGCT CCAAGCAGAT CAAGACCATC TCAGGAAGA CTCACAGCA GTATGAGAGA 1020
      GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGGTA CGCCTACGAT 1080
      GGCATCTGGG TCATGCGCCA GACACTGCAG AGGGCCATGG AGACACTGCA TGCCAGCAGC 1140
      CGGCACGAGC GGATCCAGGA CTTCACTAC ACGGACCAAC CGCTGGGCGA GATCATCTCT 1200
65    AATGCCATGA ACGAGACCAA CTTCTTGGGG GTACCGGGTC AAGTTGTATT CCGGAATGGG 1260
      GAGAGAAATG GGACCATTA ATTTACTCAA TTTCAAGACA GCAGGGAGGT GAAGGTGGGA 1320
      GAGTACAACG CTGTGGCCGA CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA 1380
      TCCGAACACC CAAAAGACAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCTACCTT 1440
      CTCTACAGCA TCCTCTCTGC CCTCACTATC CTGGGATGA TCATGGCCAG TGCTTTCTCT 1500
70    TTCTTCAACA TCAAGAACC GAACTCAGAG CTCATAAAGA TGTCTGATCC ATACATGAAC 1560
      AACCTTATCA TCCTTGAGAG GATGCTCTCC TATGCTTCCA TATTTCTCTT TGGCCTTGAT 1620
      GGATCCTTTG TCTCTGAAAA GACCTTTGAA ACACCTTGCA CGGTGAGGAC CTGGATTCTC 1680
      ACGGTGGGCT ACAGGCGGCT TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCAAGCC 1740
      ATCTTCAAAA ATGTGAAAT GAAGAAGAAG ATCATCAAGG ACCAGAAACT GCTTGTGATC 1800
75    GTGGGGGGCA TGCTGCTGAT CGACCTGTGT ATCTGTATCT GCTGGCAGGC TGTGGACCCC 1860
      CTGGAAGGA CAGTTGAGAA GTACAGCATG GAGCGGAGCC CAGCAGAGCC GGATATCTCC 1920
      ATCGCGCCTC TCCTGGAGCA CTGTGAGAAC ACCATATGA CCATCTGGCT TGGCATCGTC 1980
      TATGCTGGCT ACAGGACTTC CATGTTGTTT GGTGTTTCT TAGCTTGGGA GACCCGCAAC 2040
      GTCAGCATCC CCGCACTCAA CGACAGCAAG TACATCGGGA TGAGTGTCTA CAACGTGGGG 2100
80    ATCATGTGCA TCATCGGGGC CGCTGTCTCC TTCCTGACCC GGGACCAAGC CAATGTGCAG 2160
      TCTGCGATCG TGGCTCTGGT CATCATCTTC TGACGACCA TCACCTCTGT CTTGGTATTTC 2220
      GTGCCGAAGC TCATCACCCT GAGAACAAC CCAGATGCAG CAACGCAGAA CAGGCGATTTC 2280
      CAGTTCACTC AGAATCAAGT GAAAGAAGAT TCTAAAACGT CCACCTCGGT CACCAAGTGTG 2340
      AACAAGCCA GCATATCCCG CTGGAGGGC CTACAGTCAG AAAACCATCG CTTGCGAATG 2400

```

5 AAGATCACAG AGCTGGATAA AGACTTGGAA GAGGTCACCA TGCAGCTGCA GGACACACCA 2460  
 GAAAAGACCA CCTACATTAA ACAGAACCAC TACCAAGAGC TCAATGACAT CCTCAACCTG 2520  
 GGAATCTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATT TAAAAATCA CCTCGATCAA 2580  
 AATCCCCAGC TACAGTGGAA CACAACAGAG CCCTCTCGAA CATGCAAGA TCCTATAGAA 2640  
 GATATAAAT CTCCAGAAC CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCCTCCAC 2700  
 CACGCTTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTGAGCCC CTGCGTCAGC 2760  
 CCCACCGCCA GCCCCGCCA CAGACATGTG CCACCTCTCT TCCGAGTCAT GGTCTCGGGC 2820  
 CTGTAA

10 Seq ID NO: 26 Protein sequence  
 Protein Accession #: NP\_005449.1

15 1 11 21 31 41 51  
 MASPRRSQGP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP PSSPPLSIMG 60  
 LMPLTKEVAK GSGIRGVLPV VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAFYDA 120  
 IKYGNHLMV FGVCPSPVTS IIAESLQGNV LVQLSFAATT FVLADKKKYP YFRTVPSPDN 180  
 AVNPAILKLL KHYQWKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SPSNDPCTSV 240  
 KKLKGNVRI ILGQFDQDMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS 300  
 RCLRKLLAA MEGYIGVDFE PLSSKQIKTI SGKTPOQYER EYNNKRSVG PSKFHGYAYD 360  
 GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRILL NAMNETNFFG VTGQVVRNG 420  
 ERMGTIKFTQ PQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP 480  
 LYSILSALT I LGMTMASAPL FFIKNRNQK LKIMSSPYMN NLILGGMLS YASIFLFGLD 540  
 GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IPKNVMMKKK IIDQKLLVI 600  
 VGGMLLIDL ILICQWAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660  
 YAYKGLMLF GCFLAWETR N VSIPALNDSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ 720  
 FCIVALVII CSTITLCLVF VPKLITLRTN PDAATQNRER QFTONQKRED SKTSTSVTSV 780  
 NQASTSRLEG LQSENHRLRM KITELDKDLE EVMQLQDTP EKTYYIKQNH YQELNDILNL 840  
 GNFTSTDDG KAILKHLDD NPQLQWNTTE PSRTCKDPIE DINSEPHIQ RLSLQLPLIH 900  
 30 HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L

35 Seq ID NO: 27 DNA sequence  
 Nucleic Acid Accession #: NM\_000450.1  
 Coding sequence: 117..1949

35 1 11 21 31 41 51  
 CCTGAGACAG AGGCAGCAGT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC 60  
 CCAAAACGGA AAGTATTTC AAGCTAAACC TTTGGGTGAA AAGAAGCTTT GAAGTCATGA 120  
 40 TTGCTTCACA GTTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAGAG AGTGGAGCCT 180  
 GGTCTTACAA CACCTCCAGC GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTGAGC 240  
 AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAGAAGA GATTGAGTAC CTAAATCCA 300  
 TATTGAGTCA TTCAACCAAT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG 360  
 TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAAGCTGGCT CCAGGTGAAC 420  
 45 CCAACATAG GCAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAGATG 480  
 TGGCATGTG GAATGATGAG AGGTGACGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG 540  
 CTTGTACCAA TGACCTCTGC AGTGGCCAGC GTGAATGTGT AGAGACCATC AATAATTACA 600  
 CTTGCAAGTG TGACCTCTGC TTAGTGAGC TCAAGTGTGA GCAAAATGTG AACTGTACAG 660  
 CCTGGAATC CCTGAGCAT GGAAGCCTGG TTTGCACTCA CCCACTGGGA AACTTCAGCT 720  
 50 ACAATCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGAGAGCCA 780  
 TGCAGTGTAT GTCTCTGGA GAATGAGTG CTCTATTCC AGCCTGCAAT GTGGTTGAGT 840  
 TGATGCTGT GACAAATCCA GCCAATGGGT TCGTGAATG TTTCCAAAC CCTGGAAGCT 900  
 TCCCATGGAA CACAACCTGT ACATTGACT GTGAAGAAGG ATTTGAACTA ATGGGAGCCT 960  
 AGAGCTCTCA GTGTACTTCA TCTGGGAAT GGGACAACGA GAAGCCAAAG TGTAAAGCTG 1020  
 55 TGACATGCA GGCCTGCGC CAGCCTCAGA ATGGCTCTGT GAGGTGAGC CATTCCCTG 1080  
 CTGGAGAGT CACCTTCAA TCATCTGCA ACTTCACCT TGAGGAAGGC TTTATGTTGC 1140  
 AGGACCCAGC CAGGTTGAA TGCACCACTC AAGGCGAGTG GACACAGCAA ATCCAGTTT 1200  
 GTGAAGCTTT CCAGTGCACA GCCTTGTTCA ACCCGAGAG AGGCTACATG AATTGTCTTC 1260  
 60 CTAGTGCTTC TGGCAGTTT CGTTATGGGT CCAGCTGTGA GTTCTCTGT GAGCAGGTT 1320  
 TTGTGTGAA GGGATCCAAA AGGCTCCAAT GTGGCCCCAC AGGGAGTGG GACACAGAGA 1380  
 AGCCCCATG TGAAGCTGTG AGATGCGATG CTGTCCACCA GCCCCGAAAG GGTTTGGTGA 1440  
 GGTGTGCTCA TTCCCTATT GGAGAATTCA CCTACAAGTC CTCTGTGCCC TTCAGCTGTG 1500  
 AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA 1560  
 65 CAGAAGAGGT TCCTTCTGTC CAAGTGGTAA AATGTTCAAG CCTGGCAGTT CCGGAAAGA 1620  
 TCAACATGAG CTGCAAGTGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC GCCTGTCTG 1680  
 AAGGATGAA GCTCAATGTC TCTGAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG 1740  
 GCCTGCTACC TACCTGTGAA GCTCCCACTG AGTCCAACAT TCCTTGTTGA GCTGGACTTT 1800  
 CTGCTGTGTC ACTCTCCCTC CTGACATTAG CACCAATTCT CTCTGCTT CGGAAATGCT 1860  
 70 TACGGAAGC AAAGAAATTT GTTCTGCTCA GCAGCTGCCA AAGCCTTGAA TCAGACGGAA 1920  
 GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAGAA TCAGAAACAG GTGCATCTG 1980  
 GGAATGAGG GAATACACTG AAGTTAACAG AGACAGATAA CTCTCCTGG GTCTCTGGCC 2040  
 CTCTCTGCT ACTATGCCAG ATGCTTTAT GGCTGAAACC GCAACACCCA TCACCACTTC 2100  
 AATAGATCAA AGTCCAGCAG GCAAGGAGCG CCTTCAACTG AAAAGACTCA GTGTTCCCTT 2160  
 75 TCTACTCTC AGGATCAAGA AAGTGTGGC TAATGAAGGG AAAGATATT TTCTTCCAG 2220  
 CAAAGGTGAA GAGACCAAGA CTCTGAAATC TCAGAATTCC TTTTCTAAT CTCCCTGTCT 2280  
 CGCTGATAA TCTTGGCACA GAAACACAAT ATTTGTGGC TTTCTTCTT TTGCCCTTCA 2340  
 CAGTGTGTC ACAGCTGATT ACACAGTTGC TGTCAATAA ATGAATAATA ATTATCCAGA 2400  
 GTTTAGAGGA AAAAATGAC TAAATATATT ATAACTTAAA AAAATGACAG ATGTTGAATG 2460  
 80 CCCACAGGCA AATGCATGGA GGGTTGTTAA TGGTGCAAA CTACTGAAAT GCTCTGTGGC 2520  
 AGGGTTAAG TGCACAAATT AATCACTTTC ATCCCTATGG GATTCACTGC TTCTTAAAGA 2580  
 GTCTTAAAG ATTGTGATAT TTTACTTGC ATTGAATATA TTATACTCT CCATACTTCT 2640  
 TCATTCAATA CAAGTGTGGT AGGACTTAA AAAACTTGTA AATGCTGTCA ACTATGATAT 2700  
 GGTAAAGTT ACTTATTTCTA GATTACCCCT TCATTGTTTA TTAACAAAT ATGTTACATC 2760  
 TGTTTTAAAT TTATTTCAAA AAGGAAACT ATTGTCCCT AGCAAGGCAT GATGTTAACC 2820

5  
10  
15

```

AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTG AAAACATGGT AGAATTGGAG 2880
AGTAAAAAAT GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTGT 2940
CCACGATGAA AAACCTCCAT GAGGCCAAAC GTTTTGAAC TATAAAGCA TAAATGCAAA 3000
CACACAAGG TATAATTTTA TGAATGTCTT TGTGGAAAA GAATACAGAA AGATGGATGT 3060
GCTTTGCATT CCTACAAAGA TGTGTGTCAG ATGTGATATG TAAACATAAT TCTTGTATAT 3120
TATGGAAGAT TTTAAATTCA CAATAGAAAC TCACCATGTA AAAGAGTCAT CTGGTAGATT 3180
TTTAACGAAT GAAGATGTCT AATAGTTATT CCCTATTGTG TTTCTTCTGT ATGTTAGGGT 3240
GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTTAT GTTTATTTAT AAGCAGATT 3300
AACAAATCCA AAGGAATCTC CAGTTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC 3360
AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAATC TCCTACACTT 3420
CCATTAACCT AGCATGTGTT GAAAAAAGAA GTTTCAGAGA AGTTCTGGCT GAACACTGGC 3480
AACGACAAAG CCAACAGTCA AAACAGAGAT GTGATAAGGA TCAGAACAGC AGAGGTTCTT 3540
TTAAAGGGGC AGAAAAACTC TGGGAAATAA GAGAGAACAA CTACTGTGAT CAGGCTATGT 3600
ATGGAATACA GTGTTATTTT CTTTGAAATT GTTTAAGTGT TGTAAATATT TATGTAAACT 3660
GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGTTTGT GTTTGAGTTT TATTGAGAA 3720
TTTAAATTAT AACTTAAAT ATTTTATAAT TTTTAAAGTA TATATTATT TAAGCTTATG 3780
TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT

```

20 Seq ID NO: 28 Protein sequence  
Protein Accession #: NP\_000441.1

25  
30  
35

```

1 11 21 31 41 51
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKKEIEYLN 60
SILSYSPSY WIGIRKVMNV WVVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
DVGMMNDERC SKKLLALCYT AACTNTSCSG HGEVETINN YTKCDPQFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240
ECDAVINPAN GFVECFQNPQ SPFWNTTCTF DCEBGFELMG AQSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPQVQECT TQGWTTQIIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWEN 420
EKPTCEAVRC DAVHQPQKGL VRCASHPICE FTKSSCAFS CEEGFELYGS TQLECTSQGQ 480
WTEEVPSQV VKCSLAVPG KINMCSGSEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKAKKFVP ASSQSLES 600
GSYQKPSYIL

```

40 Seq ID NO: 29 DNA sequence  
Nucleic Acid Accession #: NM\_007036  
Coding sequence: 56..610

45  
50  
55  
60  
65  
70  
75

```

1 11 21 31 41 51
CTTCCCACCA GCAAAGACCA CGACTGGAGA GCCGAGCCGG AGGCAGCTCG GAAACATGAA 60
GAGCGTCTTG CTGCTGACCA CGCTCTCTGT GCGTGCACAC CTGGTGGCCG CCTGGAGCAA 120
TAATTATGCG GTGGACTGCC CTCAACACTG TGACAGCAGT GAGTGCAAAA GCAGCCCGCG 180
CTGCAAGAGG ACAGTGTCTG ACGACTGTGG CTGCTGCCGA GTGTGCGCTG CAGGGCGGGG 240
AGAACTTGC TACCGCACAG TCTCAGGCAT GGATGCCATG AAGTGTGGCC CGGGGCTGAG 300
GTGTGAGCCT TCTAATGGGG AGGATCCTTT TGGTGAAGAG TTTGTATCT GCAAAGACTG 360
TCCTACCGGC ACCTTCGGGA TGGATTGCAG AGAGACCTGC AACTGCCAGT CAGGCATCTG 420
TGACAGGGGG ACGGGAATAA GCCTGAAATT CCCCTTCTTC CAATATTCTG TAACCAAGTC 480
TTCCAAACAG TTTGTTTCTC TCACGGAGCA TGACATGGCA TCTGGAGATG GCAATATTGT 540
GAGAGAAGAA GTTGTGAAGG AGAATGCTGC CGGGTCTCCC GTAATGAGGA AATGTTAA 600
TCCAGGCTGA TCCCGGCTGT GATTCTGAG AGAAGGCTCT ATTTCTGTGA TTGTTCAACA 660
CAGACCAAC ATTTTAGGAA CTCTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT 720
CCAAATTGTG ATGCATGGTG GATCCAGAAA ACAAAAAGTA GGATACTTAC AATCCATAAC 780
ATCCATATGA CTGAACACTT GTATGTGTTT GTTAAATATT CGAATGCATG TAGATTGTGT 840
AAATGTGTGT GTATAGTAAC ACTGAAGAAC TAAAAATGCA ATTTAGGTAA TCTTACATGG 900
AGACAGGTCA ACCAAAGAGG GAGCTAGGCA AAGCTGAAGA CCGCAGTGAG TCAAATTAGT 960
TCTTTGACTT TGAATGACAT TAATGTTGGG ATATGGAATG AAGACTTAAG AGCAGGAGAA 1020
GATGGGGAGG GTGTTGGAGT GGGAAATAAA ATATTAGCC CTTCCTTGGT AGGTAGCTTC 1080
TCTAGAAATT AATTGTGCTT TTTTTTTTTT TTGGCTTTG GGAAGAGTCA AAATAAAACA 1140
ACCAGAAAC CCCTGAAGGA AGTAAGATGT TTGAAGCTTA TGGAAATTG AGTAACAAAC 1200
AGCTTTGAAC TGAGAGCAAT TTCAAAAGGC TGCTGATGTA GTTCCCGGGT TACCTGTATC 1260
TGAAGGACGG TTCTGGGGCA TAGGAAACAC ATACACTTCC ATAAATAGCT TTAACGTATG 1320
CCACCTCAGA GATAAATCTA AGAAGTATTT TACCCACTGG TGGTTGTGT GTGTATGAAG 1380
GTAAATATTT ATATATTTT ATAAATAAAT GTGTTAGTGC AAGTCATCTT CCTACCCAT 1440
ATTATCATC CTCTTGAGGA AAGAAATCTA GTATTATTG TTGAAATGG TTAGAATAAA 1500
AACCTATGAC TCTATAAGGT TTTCAAACAT CTGAGGCATG ATAAATTTAT TATCCATAAT 1560
TATAGGAGTC ACTCTGGATT TCAAAAAATG TCAAAAAATG AGCAACAGAG GGACCTTATT 1620
TAAACATAAG TGCTGTGACT TCGGTGAATT TTCAATTTAA GGTATGAAAA TAAGTTTTTA 1680
GGAGGTTTGT AAAAGAAGAA TCAATTTTCA GCAGAAACA TGTCACATT AAAATATAGG 1740
TGGAATTAGG AGTATATTG AAAGAATCTT AGCACAACA GGACTGTGT ACTAGATGTT 1800
CTTAGGAAAT ATCTCAGAAG TATTTTATTT GAAGTGAAGA ACTTATTTAA GAATTATTTC 1860
AGTATTTACC TGTATTTTAT TCTTGAAGTT GGCCAACAGA GTTGTGAATG TGTGTGGAAG 1920
GCCITTTGAAT GTAAAGCTGC ATAAGCTGTT AGGTTTGTGT TAAAGGAC ATGTTTATTA 1980
TTGTTCAATA AAAAGAACA AGATAC

```

80 Seq ID NO: 30 Protein sequence  
Protein Accession #: NP\_008967.1

85

```

1 11 21 31 41 51
MKSVLLLTLL LVPAPLVAAM SNNYAVDCPQ HCDSECKSS PRCKRTVLDD CGCCRVCAAG 60
RGCTCYRTVS GMDGKMGCPG LRCQPSNGED PFGEFEGICK DCPYGTFGMD CRETCNCQSG 120
ICDRGTGRKL KPFFQYSVT KSSNRFVSLT EHDMAAGDGN IVREEVVKEN AAGSPVMRKW 180

```

LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM\_000963

Coding sequence: 135..1949

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
CAATTGTCAT ACGACTTGCA GTGAGCGTCA GGAGCAGTCC CAGGAAGTCC TCAGCAGCGC 60
CTCCTTCAGC TCACAGAGCA GACGCCCTCA GACAGCAAAG CCTACCCCGG CGCCGCGCCC 120
TGCCCCCGCG TCGGATGCTC GCCCGCGCCC TGCTGCTGTG CGCGGTCTCT GCGCTCAGCC 180
ATACAGCAAA TCCTTGCTGT TCCCACCCAT GTCAAAACCG AGGTGTATGT ATGAGTGTGG 240
GATTTGACCA GTATAAGTGC GATTGTACCC GGACAGGATT CTATGGAGAA AACTGCTCAA 300
CACCGGAATT TTTGACAAGA ATAAATTTAT TTCTGAAACC CACTCCAAAC ACAGTGCAC 360
ACATACTTAC CCACCTTCAAG GGATTTTGA ACGTTGTGAA TAACATTTCC TTCTTCGAA 420
ATGCAATTAT GAGTTATGTC TTGACATCCA GATCACATTT GATTGACAGT CCACCAACTT 480
ACAATGCTAT CTATGGCTAC AAAAGCTGGG AAGCCTTCTC TAACCTCTCC TATTATACTA 540
GAGCCCTTCC TCCTGTGCCT GATGATTGCC CGACTCCCTT GGGTGTCAA GGTAAAAAGC 600
AGCTTCTCTA TTCAATAGAG ATTGTGGAAA AATTGCTTCT AAGAAGAAAG TTCATCCCTG 660
ATCCCCAGGG CTCAAACATG ATGTTTGCA TCTTTGCCCA GCACCTTCAG CATCAGTTT 720
TCAAGACAGA TCATAAGCGA GGGCCAGCTT TCACCAACGG GCTGGGCCAT GGGGTGGATG 780
TAAATCATAT TATCGGTGAA ACTCTGGCTA GACAGCGTAA ACTGCGCTT TTCAAGGATG 840
GAAAAATGAA ATATCAGATA ATTGATGGAG AGATGTATCC TCCCACAGTC AAAGATACTC 900
AGGCAGAGAT GATCTACCTT CCTCAAGTCC CTGAGCATCT ACGTTTGCT GTGGGCGAG 960
AGGTCTTTGG TCTGGTGCCT GGTCTGATGA TGTATGCCAC AATCTGGCTG CGGGAACACA 1020
ACAGAGTATG CGATGTGCTT AAACAGGAGC ATCCTGAATG GGGTGTATG CAGTTGTTCC 1080
AGACAAGCAG GCTAATACTG ATAGGAGAGA CTATTAAGAT TGTGATTGAA GATTATGTGC 1140
AACACTTGAG TGGCTATCAC TTCAAACCTGA AATTGACCC AGAATCTACT TTCAACAAAC 1200
AATTCCAGTA CCAAAATCGT ATTGCTGCTG AATTTAACAC CCTCTATCAC TGGCATCCCC 1260
TTCTGCGCTG CACCTTTTCA ATTCTAGACC AGAAATACAA CTATCAACAG TTTATCTACA 1320
ACAACCTCTAT ATTGCTGAAA CATGGAATTA CCCAGTTTGT TGAATCATTC ACCAGGCAAA 1380
TTGCTGGCAG GGTGCTGCTT GGTAGGAATG TTCCACCCGC AGTACAGAAA GTATCACAGG 1440
CTTCCATTGA CCAGAGCAGG CAGATGAAT ACCAGTCTTT TAATGAGTAC CGCAACGCT 1500
TTATGCTGAA GCCCTATGAA TCATTGGAAG AACTTACAGG AGAAAAGGAA ATGCTGCGAG 1560
AGTTGGAAGC ACTCTATGGT GACATCGATG CTGTGGAGCT GTATCCTGCC CTCTGGTAG 1620
AAAAGCCCTG GCCAGATGCC ATCTTTGGTG AAACCATGGT AGAAGTTGGA GCACCATTTCT 1680
CCTTGAAGAG ACTTATGGGT AATGTTATAT GTTCTCCTGC CTACTGGAAG CCAAGCACTT 1740
TTGGTGGAGA AGTGGGTTT CAAATCATCA AACTGCCTC AATTCAGTCT CTCATCTGCA 1800
ATAAGCTGAA GGGCTGTCCC TTTACTTCAT TCAGTGTTC AGATCCAGAG CTCATTAAAA 1860
CAGTCACCAT CAATGCAAGT TCTTCCCGCT COGGAAGTGA TGATATCAAT CCCACAGTAC 1920
TACTAAAAGA ACGTTCGACT GAACGTGAGA AGTCTAATGA TCATATTAT TATTATTAT 1980
GAACATTATG TATTAAATTA ATTATTAAAT AATATTATA TAAACTCTCT TATGTTACTT 2040
AACATCTTCT GTAACAGAAG TCAGTACTCC TGTGCGGAG AAAGGAGTCA TACTTGTGAA 2100
GACTTTTATG TCACTACTCT AAAGATTTTG CTGTGCTGT TAAGTTTGGG AAACAGTTT 2160
TATTCTGTTT TATAAACCGA AGAGAAATGA GTTTTGACGT CTTTACTCT GAATTTCAAC 2220
TTATATTATA AGAACGAAAG TAAAGATGTT TGAATACTTA AACACTATCA CAAGATGGCA 2280
AAATGCTGAG AGTTTCTTCA CTGTGATGT TTCCAATGCA TCTTCCATGA TGCATTAGAA 2340
GTAACATAAG TTTGAAATTT TAAAGTACTT TTGTTATTT TTCTGTCTAT AAACAAAAAC 2400
AGGTATCAGT GCATTATTAA ATGAATATTT AAATTAGACA TTACAGTAA TTTCTATGCT 2460
ACTTTTAAA ATCAGCAATG AAACAATAAT TTGAAATTT TAAATTCATA GGGTAGAATC 2520
ACCTGTAAA GCTTGTGTTA TTTCTTAAAG TTATTAAACT TGTACATATA CCAAAAAGAA 2580
GCTGTCTGG TATTAAATCT GTAAAATCAG ATGAAATTTT ACTACAATTG CTTGTTAAAA 2640
TATTTTATA GTGATGTCTC TTTTTCACCA AGAGTATAAA CCTTTTAGT GTGACTGTTA 2700
AACTTCTCT TTAATCAAAA ATGCCAAAT TATTAAGTG GTGGAGCCAC TGCAGTGTTA 2760
TTCAAAAATA AGAATATTTT GTTGAGATAT TCCAGAAATT GTTTATATG CTGGTAACAT 2820
GTAAAATCTA TATCAGCAAA AGGGTCTACC TTTAAAATAA GCAATAACAA AGAAGAAAA 2880
CAATATTATG TTTCAATTTA GGTTTAAACT TTTGAAGCAA ACTTTTTTT ATCCTTGTGC 2940
ACTGCAGGCC TGTACTCAG ATTTTGCTAT GAGGTTAATG AAGTACCAAG CTGTGCTTGA 3000
ATAACGATAT GTTTTCTCAG ATTTTCTGTT GTACAGTTTA ATTTAGCAGT CCATATCACA 3060
TTGCAAAAGT AGCAATGACC TCATAAAATA CCTCTTCAAA ATGCTTAAAT TCATTTTACA 3120
CATTAATTTT ATCTCAGTCT TGAAGCCAA TCAGTAGGTG CATTGGAATC AAGCCTGGCT 3180
ACCTGCATGC TGTCTCTTTT CTTTCTTCT TTAGCCATT TTGCTAAGAG ACACAGTCTT 3240
CTCATCACTT CGTTTCTCCT ATTTGTTTT ACTAGTTTA AGATCAGAGT TCACTTCTT 3300
TGGACTCTGC CTATATTTT TTACCTGAAC TTTTGCAGT TTTTCAAGT ACCTCAGCTC 3360
AGGACTGCTA TTTAGCTCCT CTTAAGAAGA TTAAGAAGA AAAAAAAGG CCTTTTAAA 3420
AATAGTATAC ACTTATTTA AGTGAAAGC AGAGAATTTT ATTTATAGCT AATTTTAGCT 3480
ATCTGTAAAC AAGATGGATG CAAAGAGGCT AGTGCTCAG AGAGAACTGT ACGGGGTTG 3540
TGACTGGAAA AAGTACGTT CCATTTCAA TTAATGCCCT TTCTATTATA AAACAAAAAC 3600
CAATATGAT CTAGTAGTT CTCAGCAATA ATAATAATGA CGATAATACT TCTTTTCCAC 3660
ATCTCATTGT CACTGACATT TAATGGTACT GTATATTACT TAATTTATG AAGATTATTA 3720
TTTATGCTCT ATTAGGACAC TATGGTTATA AACTGTGTTT AAGCCTACAA TCATTGATT 3780
TTTTTTGTTA TGTCACAAT AGTATATTTT CTTTGGGGTT ACCTCTCTGA ATATTATGTA 3840
AACATCCAA AGAATGATT GTATTAAGAT TTGTGAATAA ATTTTATGAA ATCTGATTG 3900
CATATTGAGA TATTTAAGGT TGAATGTTG TCCTTAGSAT AGGCCTATGT GCTAGCCAC 3960
AAAGAATATT GTCTCATTAG CCTGAATGTG CCATAAGACT GACCTTTTAA AATGTTTGA 4020
GGGATCTGTG GATGCTTCGT TAATTTGTTT AGCCCAATT TATTGAGAAA ATATTCTGTG 4080
TCAAGACTGT TGGGTTTAA TATTTTAAA TCAACGCTG ATTACAGATA ATAGTATTTA 4140
TATAAATAAT TGAATAAAT TTTCTTTTGG GAAGAGGAG AAAATGAAT AAATATCAT 4200
AAAGATAACT CAGGAGAATC TTCTTTACAA TTTTACGTTT AGAATGTTTA AGGTTAAGAA 4260
AGAAATAGTC AATATGCTTG TATAAAACAC TGTTCAGTGT TTTTATTA AAAAACAAT 4320
GATTTGTTAT TAACATTGAT CTGCTGACAA AACCTGGGAA TTTGGGTTGT GTATGOGAAT 4380
GTTTCAGTGC CTCAGACAAA TGTGTATTTA ACTATGTAA AAGATAAGTC TGGAAATAAA 4440
TGTCTGTTTA TTTTGTACT ATTTA

```

Seq ID NO: 32 Protein sequence  
Protein Accession #: NP\_000954

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MLARALLLCA VLALSHLTANP CSHPCQNRG VCMVGFQDY KDCCTRITGY GENCSTPEFL 60
TRIKLFLKPT PNTVHYILTH FKGFNVVNN IPFLRNAIMS YVLTSSRHLI DSPPTYNADY 120
GYKSWEAFSN LSYTTRALPP VPDDCPTPLG VKGKKQLPDS NEIVEKLLLR RKFIIPDPQS 180
NMMFAFFAQH FTHQFFKTDH KRGPFTNGL GHGVDLNHIY GETLARQRKL RLFKDGKMKY 240
10 QIIDGEMYPF TVKDTQAEI YPPQVPEHLR FAVGQEVFGL VPGLMMYATI WLRHNRVCD 300
VLKQEHPEWG DEQLFQTSRL ILIGETIKIV IEDYVQHLG YHFKLKFDPE LLFNKQFYQ 360
NRIAAEFNTL YHWHPLLPDT FQIHDQKYNV QQFIYNNIL LEHGITQFVE SFTRQIAGRV 420
AGGRNVPPAV QKVSQASIDQ SRQMKYQSFN EYRKRFLMKP YESFEELTGE KEMSAELEAL 480
YGDI DAVELY PALIVEKPRP DAIFGETMVE VGAPPSLKL MGNVICSPAY WKPSTFGSEV 540
15 GFQINTASI QSLICNNVKG CPFTSFSVPD PELIKTVIIN ASSSRSLDD INPTVLLKER 600
STEL

```

Seq ID NO: 33 DNA sequence  
Nucleic Acid Accession #: NM\_001508.1  
Coding sequence: 1..1361

```

20      1      11      21      31      41      51
|      |      |      |      |      |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
CCCAGATTG AGGTGGCCAC CTGGATCAAA ATCACCCCTTA TTCTGGTGA CCTGATCATC 120
25 TTCTGTATGG GCCTTCTGGG GAACAGCGTC ACCATTGCGG TCACCCAGGT GCTGCAGAAG 180
AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGCGACATC 240
TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
ACGTCCAGCT ACACCCGTGC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGTAC 360
30 GCTACGCTGC TGCAGTGTCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCAACCC 420
TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
GTCACTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGTACTGA GTACCCCTG 540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCAACGAG 600
CAGCCCGAGA CTCTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
35 CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGGCGGGGG 780
ACGCGGCCTC CGCAGCTGAG GAAGTCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACAG 900
ATTGCGAGGA TCATGGCTGC GGCCTAACCC AAGCAGACT GAGCAGGCTC CTACTTCGG 960
40 GGTACATGTA TCTCTCTCCC CTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCACTAAC 1020
CGCTCTCTGT ACACGGTGTCT CTGCGAGCAG TTTGCGCGGG TGTCTGTGCA GGTGCTGTGC 1080
TGCCGCTGT CTGTCAGCA CGCCAACCC GAGAAGCGCC TGCGCTGACA TGCGCACTCC 1140
ACCACGACA GCGCCGCTT TGTGAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
45 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACAGCC 1320
AATTCTGCTG CAGAGATGG TTTTCAGGAG CATGAAGTTT GA

```

Seq ID NO: 34 Protein sequence  
Protein Accession #: NP\_001499.1

```

50      1      11      21      31      41      51
|      |      |      |      |      |
MASPSLPGSD CSQIHDHSHV PEFEVATWIK ITLILVLI I FVMGLLGNV TIRVTQVIQK 60
KYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLCKL HTFLFEACSY 120
55 ATLLHVLTL FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTETPL 180
VNVPSHRHGA CTRSSLRHHE QPETSNSIC TNLSSRWTF QSSIFGAFV YLVLLSVAF 240
MCNMMQVLM KSKQKSLAGG TRPQLRKSE SEESRTARRQ TIIFLRILV TLAVCMWPNQ 300
IRIRMAAAKP KHDWTRSYR AYMLLPFSE TFFYLSSVIN PLLTVSSSQ FRRVFVQVLC 360
60 CRLSLQHANH EKRLRVHAHS TTDSARFVQ PLLPASRRQS SARRTEKIFL STFQSEAEQ 420
SKSQSLLES LEPNSGAKPA NSAAENGQFQ HEV

```

Seq ID NO: 35 DNA sequence  
Nucleic Acid Accession #: NM\_006475.1  
Coding sequence: 28..2538

```

65      1      11      21      31      41      51
|      |      |      |      |      |
AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTCTCTACTA 60
TTGCTGCTTA TTGTTAACCC TATAAACGCC AACATCATT ATGACAAGAT CTGGCTCAT 120
70 AGTCGTATCA GGGGTGCGGA CCAAGGCCCA AATGTCTGTG CCTTCAACA GATTTTGGGC 180
ACCAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
TGCCCGCAGC TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATGCT GGGAGCCACC 360
75 ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGAGG AGATCGAGGG AAAGGATCC 420
TTCACTTACT TTGACCGAG TAATGAGGCT TGGGCAACT TGGATTCTGA TATCGTAGA 480
GGTTTGAGGA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
AAGAGATGT TGACCAAGGA CTTAAAAAT GGCATGATTA TTCTTCAAT GTATAACAAT 600
TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGTTGTCA CTGTTAATTG TGCTGAATC 660
80 ATCCATGGGA ACCGATTGTC AACAAATGTT GTTGCCATG TCATTGACCG TGTGCTTACA 720
CAATTTGGTA CCTCAATTC AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTGA 780
GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGA GAGAGCGTCA CTTCACACTC 840
TTTGCTCCCA CCAATGAGGC TTTTGAAGAA CTTCACGAG GTGCTCTAGA AAGGTTTCATG 900
GGAGACAAAG TGGCTTCOGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCAGTGT 960
TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGAGCGCTG AAGGAAATAC AATTGAGATA 1020

```

5  
10  
15  
20  
25  
30  
35  
40

GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080  
 GTGACAAATA ATGGTGTGAT CCATTGTGAT GATCAGGTCC TAATTCTCTGA TTCTGCCAAA 1140  
 CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA 1200  
 GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260  
 GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCTCC TTAATAATAT TCTGCAGAA 1320  
 CACATATTGA AAGTAAAGT TGGCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAAACC 1380  
 ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGCTGCAAT TGAAATTTCA 1440  
 TGCAATGGAG AAGGGAGTAA GCAAGGGAGA AACGGTGCGA TTCACATATT CCGGAGATC 1500  
 ATCAAGCCAG CAGAGAATAT CCTCCATGAA AAGTTAAAC AAGATAAGCG CTTTAGCACC 1560  
 TTCTTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG 1620  
 ACATTATTGG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680  
 CTGATACGGG ACAAATATGC TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT 1740  
 TTCATTGGAA AAGGATTTGA ACCTGGTGT ACTAACATT TAAAGACCAC ACAAGGAAGC 1800  
 AAAATCTTTC TGAAGAAGT AAATGATACA CTTCTGGTGA ATGAATTGAA ATCAAAAGAA 1860  
 TCTGACATCA TGACAACAAA TGGTGTAAAT CATGTTGTAG ATAACTCTCT CTATCCAGCA 1920  
 GACACACCTG TTGGAATAGA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC 1980  
 CAAATTAAGT TTGTTGCTGG TAGCACCTTC AAAGAAATCC CCGTGAAGT CTATACAACT 2040  
 AAAATATATA CCAAGTTTGT GGAACCAAAA ATTAAGTGA TTGAAGGCAG TCTTCAGCCT 2100  
 ATTATCAAAA CTGAAGGACC CACACTAACA AAGTCAAAA TTGAAGGTGA ACCTGAATTC 2160  
 AGACTGATTA AAGAAGGTGA AACATAACT GAAGTGAATC ATGGAGAGCC AATTATTAAA 2220  
 AAATACACCA AAATCATTTA TGGAGTGCTT GTGAAATAA CTGAAAAGA GACACGAGAA 2280  
 GAACGAATCA TTACAGGTCC TGAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340  
 ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTGAC CAAATTCATT 2400  
 GAAGGTGGTG ATGGTCAATT ATTTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC 2460  
 ACACCCGTGA GGAAGTTGCA AGCCCAACAA AAGTTCAAG GTTCTAGAAG ACGATTAAAG 2520  
 GAAGGTGCTT CTCAGTGAAT ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC 2580  
 AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAAGCT AAACATCAGC 2640  
 ACAAGGAAGC AATCATCAAA TAATTTCTGAA CACAAATTTA ATATTTTTTT TTCTGAATGA 2700  
 GAAACATGAG GGAATTTGCT GAGTTAGCCT CCGTGGTAA AGGAATTGAA GAAATATATA 2760  
 CACCTTACAC CCTTTTTCAT CTGACATTA AAGTTCTGG CTAACCTTGG AATCCATTAG 2820  
 AGAAAAATCC TTGTCAACAG ATTCAATACA ATTCAAATCG AAGAGTTGTG AACTGTTATC 2880  
 CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940  
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000  
 TCAAAAGGCT TTGACATTTT CTATATGAGT GGGTTTACTG GTAAATTTATG TTATTTTTTA 3060  
 CAACTAATT TTGACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA 3120  
 TCTCAACGTT TTCAATAAAA CCAATTTTCA GATATAAAGA GAATTACTTC AAATTGAGTA 3180  
 ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA

Seq ID NO: 36 Protein sequence  
 Protein Accession #: NP\_006466.1

45  
50  
55  
60

1 11 21 31 41 51  
 MIPFLPMFSL LLLLVNPN ANNHDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC 60  
 KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTGLGIVGA TTTQRYSDAS 120  
 KLREIEEGKG SPTYFAPSNE AWDNLDSDIR RGLSNVNVLE LLNALHSHMI NKRMLTKDLK 180  
 NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IHHGNQIATN GVHVHIDRVL TQIGTSIQDF 240  
 IEAEDDLSSP RAAATSDIIL EALGRDGHFT LFAPTNEAPE KLPRGVLERF MGDKVASEAL 300  
 MKYHILNTLQ CSESIMGGAV FETLENTIE IGCODGSITV NGIKMVNKID IVTNNGVIHL 360  
 IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLMS 420  
 VORLLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKSKQSG 480  
 RKGAIHFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTPQGD WTLFVPNTDA 540  
 FKGMTSEKE ILIRDKNALQ NIILYHLTPG VPIGKGFEFG VTNILKTTQG SKIPLKEVND 600  
 TLLVNELESK ESDIMTTNGV IHVVDKLLYP ADTPVGNLQ LELNLKLIKY IQIKFVRGST 660  
 FKEIPVPTYY TKIIFKVVEP KIKVIBGSLQ PIKTEGPTL TKVKIEGEPE FRLLIKEGETI 720  
 TEVIHGEPII KVIYKIIDGV PVEITEKETR EERIITGPBI KYTRISTGGG ETEETLKKLL 780  
 QEEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ

Seq ID NO: 37 DNA sequence  
 Nucleic Acid Accession #: NM\_002416  
 Coding sequence: 40..417

65  
70  
75  
80

1 11 21 31 41 51  
 ATCCAATACA GGAGTGACTT GGAACCTCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTT 60  
 TTCTCTCTGG GCATCATCTT GCTGGTTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120  
 AAGGGTGGCT GTTCTGTCAT CAGCACCAAC CAAGGACTA TCCACTACA ATCCTTGAAA 180  
 GACCTTAAAC AATTGCCCCC AAGCCCTTCC TGCAGAAAA TTGAATCAT TGCTACACTG 240  
 AAGAATGGAG TTCAACATG TCTAAACCCA GATTGACGAG ATGTGAAGGA ACTGATTAAA 300  
 AAGTGGGAGA AACAGGTGAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360  
 AAGAAGTTC TGAAGATTG AAAATCTCAA CGTCTCGTC AAAAGAAGAC TACATAAGAG 420  
 ACCACTTCAC CAATAAGTAT TCTGTGTAA AAATGTTCTA TTTTAATTAT ACGCTATCA 480  
 TTCCAAGGA GGATGGCATA TAATACAAG GCTTATTAAT TTGACTAGAA AATTAAAAAC 540  
 ATTACTCGA AATTGTAACT AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA 600  
 TTGTTAAAGG CTATGATTGT CTTGTGTTCT CTACACCCA CCAAGTTGAA TTCTATCATG 660  
 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCAACCAA CCACATCOCA 720  
 CTCACAACAG CTGCTGGAAG GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCCAGAGAG 780  
 TATCTGAGGC ACATGTGAGC AAGTCTTAAG CCGTTAGCA TGCTGGTGAG CCAAGCAGTT 840  
 TGAATTTGAG CTGACCTTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900  
 CTACAGGCCCT CACACAATAT GTGTCTGAGA GATTGATGCT GATTGTTATT GGTATCACC 960  
 ACTGGAGATC ACGAGTGTGT GGCTTTTCTA GCCTCCTTTC TGGCTTTGGA AGCCATGTGA 1020  
 TTCCATCTTG CCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCTCTT TGCTTCACTC 1080  
 AAGTCAGCTC TTCTCATATC TACCACAATG CAGTGCCTTT CTCTCTCTCA GTGCACCTGT 1140  
 CATATGCTCT GATTTCATG AGTCAACTCC TTTCTCATCT TGTCCTCAAC ACCCCACAGA 1200



5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

AGTGCTTTCT TCTCCCAATT CATCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT 1260  
AAATAAACCT TTTTGGACAC ACAAAATTATC TTAATACTCC TGTTTCACTT GGTTTCAGTAC 1320  
CACATGGGTG AACACTCAAT GGTAACTAA TTCTTGGGTG TTTATCCTAT CTCTCCAACC 1380  
AGATTGTGAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCTGTGTTCT TCCACAGTGC 1440  
CTAATAATAC TGTGGAACATA GGTTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500  
TGGCAACCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560  
CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620  
GATGCAACAT CCTGTCTTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680  
GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740  
AAAATCATAT AATCTTACAA TGAAGAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800  
CCAACCATAC AAAAATTCCT TTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860  
TCTAAGATCT AACAAAGTAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATATG 1920  
AGTTTTATTG TCCGTTTACT TGTTCAGAG TTGTATTGTT GATTATCAAT TACCACACCA 1980  
TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040  
TAGTGGAAAG ATGATTGGTG CCCAGTTAGC CTCGACAGGA TGTGGAACCC TCCTTCCAGG 2100  
GGAGGTTTCAG TGAATTGTTG AGGAGAGGTT GTCTGTGGCC AGAATTAACT CCTATACTCA 2160  
CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATT AGAGTGCTGT CCGGTGGAGA 2220  
TCCACCCGGA ACCTGTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280  
AAAAATCTAA GTGTTTCTAA AATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340  
GTAGACAGTA TATACTAAC AACCAAGAC TACATATTGT CACTGACACA CACGTTATAA 2400  
TCATTATCA TATATATACA TACATGCATA CACTCTCAA GCAATAATT TTCACTTCA 2460  
AAACAGTATT GACTTGATA CCTTGAATT TGAATATTT TCTTGTGTA AATAGAATGG 2520  
TATCAATAAA TAGACATTA ATCAG

Seq ID NO: 38 Protein sequence  
Protein Accession #: NP\_002407

1 11 21 31 41 51  
MKKSGVLELL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPPSCEK 60  
IEIIATLKNQ VQTCNLNDSA DVKELIKKWE KQVSQKKKQK NGKHQKQKKV LKVRKSQRSR 120  
QKKT

Seq ID NO: 39 DNA sequence  
Nucleic Acid Accession #: NM\_006670  
Coding sequence: 85..1347

40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
CCGGCTCGGG CCTCCGGGCG CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC 60  
AGCTCCGGGG AAAAGCGAGC CGCGATGCCT GGGGGGTGCT CCGGGGGCCC CGCGCGGGGG 120  
GACGGGGCGTC TGGCGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCTCGTCT 180  
TCTCCCACTT CCTCGGCATC CTCTTCTTCC TCTCTGGGCG CGTTCTCTGGC TTCCGCCGCTG 240  
TCGCGCCGAG ACCTCGTGGC GGACCACTGC CCGCGCTGCT GCGAGTGTCT CGAGGCAGCG 300  
CGCACAGTCA AGTGCCTTAA CGCAATCTG ACCGAGGTGC CCAAGGACCT GCCCGCTAC 360  
GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCGGTGC TCCTTGGCGG CGCTTCTGCG 420  
CGCGGGCGCG CGCTGGCGGA GCTGGCGCGG CTCACCTCA GCGGCAGCGG CTTGGACGAG 480  
GTGCGCGCGG GCGCCTTGA GCATCTGCC AGCCTGGCGC AGCTCGACCT CAGCCACAAC 540  
CCACTGGCGG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCT CTGCGCCCC 600  
AGTCCCTCTG TGAAGTGAAT CCTGAACCA ATCGTCCCC CTGAAGTGA CCGGCAGAAC 660  
CGAGCTCTCG AGGCGATGTT GTGGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720  
CGCGCTTGG AGCTGGCCAG CAACCACTTC CTTCACCTGC CGCGGATGT GCTGGCCCAA 780  
TCGCCCAGCC TCAGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840  
TCCTTCGCGA ACCTGACACA TCTAGAAAGC CTCCACCTGG AGGACATGCT CCTCAAGGTC 900  
CTTCACAATG GCACCTCGGC TGAGTTGCAA GGTCTACCCC ACATTAGGCT TTTCTGGAC 960  
AACAACTCCT GGGCTCTGCA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020  
GAGGTAGTGC AGGCGAAGA CCGGCTCACC TGTGCATATC CGGAAAAAT GAGGAATCGG 1080  
GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC GATTTCTTCC CCCATCCCTG 1140  
CAAACTCTTT ATGTCTTCT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200  
GTTTTGTATT TGAACGCGAA GGGGATAAAA AAGTGGATGC ATAAACATCAG AGATGCGCTG 1260  
AGGGATCACA TGAAGGGTGA TCATTACAGA TATGAATCA ATGCGGACCC CAGATTAACA 1320  
AACTCAGTT CTAACCTGGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380  
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440  
TAGATACAAC GGACTTTGAC TAAAGCAGT GAAGGGGATT TGCTTCTCTG TTATGTAAAG 1500  
TTTCTCGGTG TGTCTGTGTA ATGTAAGAGC ATGAACAGTT GTGTATAGTG TTTTACCTTC 1560  
TTCTTTTCTT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620  
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680  
ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTCGAG AAAAATACTT TATTCATAAA 1740  
TATCAGTTTT ATTCTCATGT ACCTAAGTGT TGGAGAAAAT AATTGCATCC TATAAAGTGC 1800  
CTGCAGAGCT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CTGTCATCCA 1860  
AGAGCATGCT TACATTGTTT TGTCTGCTAT ATTACAAAAA ATAACCTTGA ACTTCATAAC 1920  
TTCTTTGACA AAGTAAATTA CTTTCTTGAT TGCAGTTTAT ATGAAATGT ACTGATTTT 1980  
TTTTAATAAA CTGATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040  
ATTCTTAAAA GAA

Seq ID NO: 40 Protein sequence  
Protein Accession #: NP\_006661

80  
1 11 21 31 41 51  
MPGGCSRGPA AGDGLRLRL LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60  
QCPALCESE AARTVKCVNR NLTEVPTDLP AYVRNLFITG NQLAVLPAGA FARRPPLAEL 120  
AALNLSGSRL DEVRAFAFEH LPSLRQLDLS HNPLADLSPP AFSGSNASVS APSPLVELIL 180  
NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRLRLASLN HFLYLPDVL AQLPSLRHL 240

LSNNSLVSLT YVSRNLTSL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPNVDCD 300  
HMADMVTLWK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDGDPILPP SLQTSYVFLG 360  
IVLALIGAIF LVLVLYLNRKG IKWMHNRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

5 Seq ID NO: 41 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..927

10 1 11 21 31 41 51  
ATGCGCTGGG GGTGCTCCG GGGCCCCGCC GCGGGGACG GCGCTCTGCG GCTGGCGCGA 60  
CTAGCGCTGG TACTCCTGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC 120  
TTCTCCTCCT CGGCGCCGTT CTTGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCGGAC 180  
15 CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240  
AATCTGACCG AGGTGCCACG GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGCG 300  
AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360  
AGCCTCAGCG ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCTGACCTA CGTGTCTTTC 420  
CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTTTCAC 480  
AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACATTA GGGTTTTCCT GGACAACAAT 540  
20 CCTGGGTCTT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600  
GTGACAGGGA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGTCCTCT 660  
TTGGAACCTA ACAGTGTGTA CCTGGACTGT GACCCGATTC TTCCCCCATC CCTGCAAAAC 720  
TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCTT CTGTGTTTGT 780  
TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGACGGGAT 840  
25 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900  
AGITCTAACT CGGATGTCTT CGAGTGA

30 Seq ID NO: 42 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
MPGGCSRGA AGDGRRLRLR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPLPFD 60  
35 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFITG NQLASNHFLY LPRDVLALQLP 120  
SLRHLDSNN SLVSLTYVSF RNLTHLES LH LEDNALKVLH NGTLAELOGL PHIRVFLDNN 180  
PWVCDCHMAD MVTLKETE VQGDRLTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240  
SYVFLGIVLA LIGAIFLLVL YLNRKGIKW MHNRDACRD HMEGYHYRYE INADPRLTNL 300  
SSNSDVLE

40 Seq ID NO: 43 DNA sequence  
Nucleic Acid Accession #: NM\_058173  
Coding sequence: 68..340

45 1 11 21 31 41 51  
AGCGCCTTGC CTTCTCTTAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT 60  
CACCACCATG AAGTCTCTAG CAGTCTGSGT ACTCTTGGGA GTTTCATCTT TCTGCTCTC 120  
TGCCAGAAAT CCGACACAGC CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGA 180  
50 TGATGAAGCC CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240  
TACCACTGCA ACCACCGCTG CTTCTACCAC TGCTCGTAAA GACATTCAG TTTTACCCAA 300  
ATGGGTGGG GATCTCCCGA ATGGTAGAGT GTGTCCTGTA GATGGAATCA GCTTGAGTCT 360  
TCTGCAATTG GGTCACAACT ATTCATGCTT CCGTGATT CATCCAACTA CTACCTTGC 420  
CTACGATATC CCTTTATCT CTAATCAGTT TATTTCTTT CAAATAAAAA ATAACATGA 480  
GCGAGCTAAC AT

55 Seq ID NO: 44 Protein sequence  
Protein Accession #: NP\_477521

60 1 11 21 31 41 51  
MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETTAAT TTATTAAPTT 60  
ATTAASTTAR KDIPVLPKWV GDLNPRVCP

65 Seq ID NO: 45 DNA sequence  
Nucleic Acid Accession #: NM\_000095.1  
Coding sequence: 26..2299

70 1 11 21 31 41 51  
CAGCACCCAG CTCCCGGCCA CCGCCATGGT CCGGACACC GCCTGCGTTC TTCTGCTCAC 60  
CTGGCTGCC CTGGGCGCT CTGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCC 120  
GCAGATGCTT CGGAACTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180  
GCGGCAGCAG GTCAGGGAGA TCACGTTCTT GAAAAACAG GTGATGGAGT GTGACGCGTG 240  
CGGGATGCAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CCGCCCTGTC TCCACTGCGC 300  
75 GCGGATGCAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CCGCCCTGTC TCCACTGCGC 360  
GCCCGGCTTC TGCTTCCCGG CGGTGGCGTG CATCCAGAGC GAGAGCGCGG GCCGCTGCGG 420  
CCCTGCCCC GCGGGCTTCA GGGGCAACGG CTGCACTGC ACCGACGTCA ACGAGTGCAA 480  
CGCCACCCCG TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCGCTGCGA 540  
GGCTTGGCCG CCGGGGTACA GCGGCCAC CCACGAGGGG GTGGGCTGCT CTTTGGCCAA 600  
80 GGCCAAACAG CAGGTTTGCA CGGACATCAA CAGTGTGAG ACCGGGCAAC ATAACGTGCT 660  
CCCAACTCC GTGTGCATCA ACACCGGGG CTCTTCCAG TGCGGCCCTG GCCAGCCCGG 720  
CTTGTGGGCG CAGCAGGCGT CCGGCTGCCA GCGGCGCGCA CAGCGCTTCT GCCCGAGCG 780  
CTGCGCCAGC GAGTGCCAGC AGCATGCAGA CTGCTGCTTA GAGCGCGATG GCTGCGGCTC 840  
GTGCGGTGTG CGCGTTGGCT GCGCGGCAA CGGATGCTC TGTGCTGCGC ACACGTGACT 900  
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCGGAGCGG CAGTCCCGTA AGGACAACTG

5  
10  
15  
20  
25

CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCTCG 960  
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAG GACAACTGCC CGCTGGTGGC 1020  
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCGG 1080  
GTCCCAAGAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA 1140  
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGTACCCCAA 1200  
CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260  
GAAGAGCAAC CGGGATCAGG CGGATGTGGA CCAAGACTTT GTGGGAGATG CTGTGACAG 1320  
CGATCAAGAC CAGGATGGAG ACGGACATCA GGAATCTCGG GACAACTGTC CCACGGTGCC 1380  
TAACAGTGCC CAGGAGGACT CAGACCAAGA TGCCAGGGT GATGCTGCG ACGACGACGA 1440  
CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCCG CTGGTGCTTA ACCCGGGCCA 1500  
GGAGGACCGG GACAGGGACG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGACAGCAA 1560  
GGTGGTAGAC AAGATCGAGC TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620  
GGCCTTCCAG ACAGTCTGTC TGGACCCGGA GGGTGACCGG CAGATTGACC CCAACTGGGT 1680  
GGTGTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGGACCCAG GCCTGGCTGT 1740  
GGGTACACT GCCTTCAATG GCGTGGACTT CGAGGGCAGC TTCCATGTGA ACACGGTCAC 1800  
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860  
CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920  
GGCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980  
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGGCG CTGCTGTGGA AGGACCGCG 2040  
AAACGTTGGT TGAAGGACA AGAAGTCTTA TCGTTGGTTC CTGCAGCACC GGGCCCAAGT 2100  
GGGTACTATC AGGGTGGGAT TCTATGAGGG CCGTGAGCTG GTGGCCGACA GCAACGTGGT 2160  
CTTGACACA ACCATGCGGG GTGGCCGCTT GGGGCTCTTC TGCTTCTCCC AGGAGAACAT 2220  
CATCTGGGCC AACCTCGCTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280  
TCAGTGGCG CAAGCCTAGG GACCAGGGTG AGGACCGCGG GGATGACAGC CACCCTCACC 2340  
GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAAGTGAG 2400  
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGG

Seq ID NO: 46 Protein sequence  
Protein Accession #: NP\_000086.1

30  
35  
40  
45

1 11 21 31 41 51  
MVPDTACVLL LTLAALGASG GQSQPLGSDL GPQMLRELQE TNAALQDVVD WLRQVREIT 60  
FLKNTYMECD ACGMQQSVRT GLPSVRPLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120  
NGSHCTDVNE CNAHPCFPVR RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180  
INECBTQHN CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQRGAQRFCP DGSPSECEHE 240  
ADCVLERDGS RSCVRCVWNA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPSNGQ 300  
EDVDRDGGD ACDPDADGG VPNEKDNCPV VRNPQDRNTD EDKWDACDN CRSQRNDQK 360  
DTDQDGRGDA CDDIIDGRI RNQADNCPRV PNSDQKSDG DGIGDADCN PQRSNPDQAD 420  
VDHDFVGDAC DSDQDQDGG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480  
RDNCRLVPNF QGEDADRDG GDVQDDEDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD 540  
PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600  
PGYQDSSSFY VVMWQKMEQT YWQANPFRAV ABEPQILKAV KSSTGPGEQL RNALNHTGDT 660  
ESQVRLWKID PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720  
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 47 DNA sequence  
Nucleic Acid Accession #: NM\_001565.1  
Coding sequence: 67..363

50  
55  
60  
65  
70

1 11 21 31 41 51  
GAGACATTC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60  
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC 120  
ATTCAGAGAG TACCTCTCTC TAGAAACGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180  
CCTGTTAATC CAAAGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTGTGCCA 240  
CGTGTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAAG AGAGATGTCT GAATCCAGAA 300  
TGAAGGCCA TCAAGAATT TCTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360  
TAAACCCAGA GGGGAGCAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420  
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480  
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCGTAGGAA 540  
GGTTAATGTT CATCATCTTA AGCTATTGAG TAATACTCT ACCCTGGCAC TATAATGTAA 600  
GCTCTACTGA GGTGCTATGT TCTTAGTGA TGTTCTGACC CTGCTTCAA TATTTCCTC 660  
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTGGGGTTT ATCAGAAATC 720  
TCAGAACTC AAATAACTAA AAGGTATGCA ATCAAACTCT CTTTAAAG AATGCTCTT 780  
ACTTCAAGCA CTTCCTCTGC CATCCTCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840  
CATACAATTC CAAACACATA CAGGAAGSTA GAAATATCTG AAAATGTATG TGAATGATT 900  
CTTATTATAT GAAAGACTGT ACAGAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960  
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020  
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080  
TTTTCAAATA AAAATGAGGT ACTCTCTCTG AAATATTAAG

Seq ID NO: 48 Protein sequence  
Protein Accession #: NP\_001556.1

75  
80

1 11 21 31 41 51  
MNQTALICC LIFLTLGSIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60  
EIIATMKKKG EKRCNLNPEK AIKNLLKAVS KEMSKRSP

Seq ID NO: 49 DNA sequence  
Nucleic Acid Accession #: XM\_057014  
Coding sequence: 143..874

1 11 21 31 41 51  
 5 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCTCGGAG 60  
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG 120  
 CGCTGCCCGG CAGCCGCGGAG CCATGCGACC CCAGGGCCCC GCGGCTCCCG CGCAGCGGCT 180  
 CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240  
 CCCCAGGGGG AAGCAAAAGG CGCAGCTCCG CGCAGGGGAG GTGGTGGACC TGTATAATGG 300  
 AATGTGCTTA CAGGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360  
 CATTCGCGGT ACACCTGGGA TCCCAGGTCC GGATGGATTG AAAGGAGAAA AGGGGGAATG 420  
 10 TCTGAGGGAA AGCTTTGAGG AGTCCCTGGAC ACCCACTAC AAGCAGTGT CATGGAGTTC 480  
 ATTGAATTAT GGCATAGATC TTGGGAAAT TGCGGAGTGT ACATTACAA AGATGCGTTC 540  
 AAATAGTGCT CTAAGAGTTT TGTTCACTGG CTCACCTCGG CTAAATGCA GAAATGCATG 600  
 CTGTACGCTG TGGTATTTC AATTCAATGG AGCTGAATGT TCAGGACCTC TTCCTATTGA 660  
 AGCTATAATT TATTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTATCG 720  
 15 CACTTCTTCT GTGGAAGSAC TTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780  
 CTGGGTTGCT ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCACT 840  
 TTCTCGCATC ATTATTGAAG AACTACCAA ATAAATGCTT TAATTTTCAT TTGTACCTC 900  
 TTTTCTTATT ATGCTTGGGA ATGGTTCAT TAAATGACAT TTTAAATAAG TTTATGTATA 960  
 CATCTGAATG AAAGCAAGG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020  
 20 TTTAAATCTA GCATTATTC TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTCTTAGT 1080  
 TGGTTAGATC ACTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTGT 1140  
 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200  
 TGTACAAATT GTAAATGTGA AGAATTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260  
 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 50 Protein sequence  
 Protein Accession #: XP\_057014

1 11 21 31 41 51  
 30 MRPGPAASP QRLRLGLLLL LLQLPAPSSA SEIPKKGKKA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSFG ANGIPGTPIG PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120  
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCORWYFT FNGAECSSPL PIEAIIYLDQ 180  
 35 GSPMNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240  
 LFK

Seq ID NO: 51 DNA sequence  
 Nucleic Acid Accession #: NM\_020974  
 Coding sequence: 81..3080

1 11 21 31 41 51  
 40 GGCGTCCGCG CACACCTCCC CGCGCGCGCG CGGCCACCGC CCGCACTCCG CGGCTCTGCT 60  
 CGCAACCGC TGAGCCATCC ATGGGGGTCC CGGCGCGCAA CCGTCCCGGG CGGCTCTGGG 120  
 45 CGGTGCTGCT GCTGTGCTG CTGTGCGCGC CACTGCTGCT GCTGGCGGGG GCGCTCCCGC 180  
 CGGTGCGGGG CGGTGCGCGG GGGCGCGAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240  
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATGAGC 360  
 50 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420  
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGGCTGG 480  
 AGAACAAATG CGGCTGCCAG CATACTGTG TCAACGTCAT GGGGAGCTAT GAGTGTGCT 540  
 GCAAGGAGGG GTTTTCTCTG AGTGACAATC AGCACACCTG CATTCACGCG TCGGAAGAGG 600  
 GCCTGAGCTG CATGAATAAG GATCAGGCTG GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660  
 55 CGAGCTGCGC CTGTGAGTGC AGGCTGTGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCCTG 840  
 AGCGAGAGGA CACTGTCTGT GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900  
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG 960  
 60 ACCGACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACCT 1020  
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCCG AATGGAGGTT 1080  
 GTGATCAATT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA 1140  
 AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTGG GATAGGACCT 1200  
 GTGACCACAG CTGCATCAAC CACCCTGGCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA 1260  
 65 CCCTGTATGG CTTACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320  
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CTGGGTGACA 1380  
 AGCTCAATG GAATAAAAA GACTGTGTGG AAGTGAAGGG GCTCTGCCCC ACAAGTGTGT 1440  
 CACCCCGTGT GTCCCTGCAC TGGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500  
 GTCACCTCG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAAT GTAACCTTTA 1560  
 70 AGCTAAATGA AGGCAAGTGT AGTTTGAATA ATGCTGAGCT GTTCCCGAG GGTCTGCGAC 1620  
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680  
 GCAGCTCTGG CAGCAAGTGT CCAGGAGCCC CTGGCCGACC AAGCAACCCCT AAGGAAATGT 1740  
 TTATCACTGT TGAGTTTGAG CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC 1800  
 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860  
 75 AGGCGGTCCA CAGGAGGACG TTTACCTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920  
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCCTG TGGAGTGGGC CAGGGTCACTG 1980  
 CAGAAAACCA ATGTGTCAAT TGCAGGCGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040  
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAATGACT TGTGAACCAT 2100  
 GCCCAGACCC AGGAAATCTT GGGGCCCTGA AGACCCAGAG AGCTTGGAAAT ATGTCTGAAT 2160  
 80 GTGGAGGTCT GTGTCAACCT GGTGAATATT GTGCAGATGG CTTTGACCTT TGCCAGCTCT 2220  
 GTGCCCTGGG CAGCTTCCAG CCTGAAGCTG GTGCAACTTC CTGCTTCCCC TGTGGAGGAG 2280  
 GCCTTGCACC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340  
 GTTCACCTGG ACATTTCTAC AACACCACCA CTCACCGATG TATTCGTTGC CCACTGGGAA 2400  
 CATACCGACC TGAATTTGGA AAAATAAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460  
 ACTTTGATGG CTCACAAAC ATAACCCAGT GTAAAACAG AAGATGTGGA GGGGAGCTGG 2520

5  
10  
15  
20

```

GAGATTTTAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
AGTGTAGGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCCTGAGA 2640
TCTTCTCTGC CATAGAGGAG GACTGTGGGG ACTATCTGGT GATGGGAAA ACCTCTTCAT 2700
CCAATTCTGT GACAAATAT GAAACCTGCC AGACCTACGA ACSCCCATC GCCTTCACTT 2760
CCAGGTCAAA GAAGCTGTGG ATTCAGTTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT 2820
TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTTGAA GACATAGTTC 2880
GAGATGGCAG GCTCTATGCA TCTGAGAAC ATCAGGAAAT ACTTAAGGAT AAGAAACTTA 2940
TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTCAAGTAC ACAGCCAGG 3000
AGTCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060
TTTTGAGACC TTACAAATGA CTCAGCCCAAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
GGTTGGTGGG ACAGAGCTGT CTTCCTTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC 3180
CGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGTTAAATT 3240
GAACCTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGCTGGCT GAGCTGGACT 3360
TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGCTC TTAATCTCTC TCAAGGAGTC 3420
TGATGTGAGA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCCTCTAGC 3480
COGCGCTCTC CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540
CAAGAGGGGA GGAAGGAGA CCCCTGCAGG CTCCTTCCAC CCACCTTGAG ACCTGGGAGG 3600
ACTCAGTTTC TCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
AGTTCTAAGC AGTGCTCGTG AAAAAAAGAA GCAGAAAGAA TTAGAAATAA ATAAAAACTA 3720
AGCATTCTG GAGACAT

```

Seq ID NO: 52 Protein sequence  
Protein Accession #: NP\_066025

25  
30  
35  
40  
45

```

1      11      21      31      41      51
MGVAGNRNRP AAWAVILLLL LPLPLLLLAG AVPPGRGRAA GPQEDVDECA QGLDDCHADA 60
LCQNTPTSYK CSCPKPYQGE GRQCEIDIEC GNELNGGCVH DCLNIPGNYR CTCDFGFMLA 120
HDGHNCLDVD ECLENNQQGQ HTCVNVMSY ECCCCKEFPFL SDNQHTCIHR SEELGSCMNK 180
DHGSHICKE APRGSVACB RPFELAKNQ RDCILTCNHG NGGQHSCHDD TADGPECSCH 240
PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LMETCAVNN GGCDRTCKDT 300
STGVHCSPV GFTLQLDQKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360
SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDNECSIN NGGQQQVCVN 420
TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVPFRVSLH CGKSGGGDGC FLRCHSGIHL 480
SSDVTIRTST VTFKLNEGKC SLKNAELFPE GLRPLPEKH SSVKESFRYV NLTCSSGKQV 540
PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYVDGA RERCILCPNG 660
TFQNEEQMT CBPCPRPGNS GALKTPEAWN MSECGLCQFP GEYSADGFAP CQLCALGTFQ 720
PEAGRTSCFP CGGLATKHKQ GATSFQDCET RVQCSPGHFY NITTRCIRC PVGTYPPEFG 780
KXNCVSCPGN TTFDFDGSIN ITQCKNRRCG GELGDFGTGI ESPNYPGNYP ANTECTWTIN 840
PPPKRRLIV VPEIFLPIED DCGDYLVMRK TSSNSNVITY ETCQTYERPI APTSRSKLW 900
IQFKSNEGNS ARGQVVPYVT YDEDYQELIE DIVRDGRLYA SENHQSIKLD KKLKALFDV 960
LAHPQNYFKY TAQESREMPF RSFIRLLRSK VSRFLRPYK

```

Seq ID NO: 53 DNA sequence  
Nucleic Acid Accession #: NM\_014211  
Coding sequence: 157..1479

50  
55  
60  
65  
70  
75  
80

```

1      11      21      31      41      51
GGGACAGGGC TGAGGATGAG GAGAACCCCTG GGGACCCAGA AGACCGTGCC TTGCCCGGAA 60
GTCTTGCTCG TAGGCCTGAA GGACTTGCCC TAACAGAGCC TCAACAACCTA CCTGGTGATT 120
CCTACTTCAG CCCCTTGGTG TGAGCAGCTT CTCAACATGA ACTACAGCCT CCACCTTGGCC 180
TTGTGTGTC TGAGTCTCTT CACTGAGAGG ATGTGTCATCC AGGGGAGTCA GTTCAACGTC 240
GAGGTGGGCA GAGTGTGACA GCTTTCCTTG CCTGGCTTGG AGAACCTCAC AGCAGGATAT 300
AACAAATTC TCAGGCCCAA TTTTGGTGGG GAACCCGTAC AGATAGCGCT GACTCTGGAC 360
ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACCTC 420
CGACAGCGCT GGATGGACCA CGCGCTGGTG TTTGAAGGCA ACAAGAGCTT CACTCTGGAT 480
GCCCGCCTCG TGGAGTCTCT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC 540
TTCTTCCATG AAGTCACTGT GGGAAACAGG CTCATCCGCC TCTTCTCCAA TGGCACGGTC 600
CTGTATGCCC TCAGAAATCAC GACAACCTGT GCATGTAAAC TGGATCTGTC TAAATACCCC 660
ATGGACACAC AGACATGCAA GTTGACGCTG GAAAGCTGGG GCTATGATGG AAATGATGTG 720
GAGTTCACTT GGCTGAGAGG GAACGACTCT GTGCGTGGAC TGGAACACCT CGCGCTTGCT 780
CAGTACACCA TAGAGCGGTA TTTCACCTTA GTCAACAGAT CGCAGCAGGA GACAGGAAAT 840
TACACTAGAT TGGTCTTACA GTTTGAGCTT CGGAGGAATG TTCTGTATTT CATTTTGGAA 900
ACCTACGTTT CTTCACCTTT CCTGGTGGTG TTGTCTGGG TTTCTATTTG GATCTCTCTC 960
GATTCACTCC CTGCAAGAAC CTGCATTGGA GTGACGACCG TGTATCAAT GACCACACTG 1020
ATGATCGGGT CCGCACTTTC TCTTCCCAAC ACCAAGTCTT TCATCAAGGC CATGATGTG 1080
TACCTGGGGA TCTGCTTTAG CTTTGTGTTT GGGGCCCTTG TAGAATATGC AGTTGCTCAC 1140
TACAGTTCCT TTACTAGGAT GGCAGCCAAA GATAGGGGGA CAACAAGGA AGTAGAAGAA 1200
GTCAGTATTA CTAATATCAT CAACAGCTCC ATCTCCAGCT TTAACCGGAA GATCAGCTTT 1260
GCCAGCATTG AAATTTCCAG CGACACGTT GACTACAGTG ACTTGACAA TGAACCCAGC 1320
GACAAGTTCA AGTTGTCTTT CCGAGAAAAG ATGGGCAGGA TTGTTGATTA TTTCACAATT 1380
CAAAACCCCA GTAAATGTGA TCACTATTCC AAACACTGTG TTCTTTGAT TTTTATGCTA 1440
GCCAATGTAT TTTACTGGGC ATACTACATG TATTTTGGG TCAATGTTAA ATTTCTTGCA 1500
TGCCATAGGT CTTCACAGG ACAAGATAAT GATGTAAATG GTATTTTAGG CCAAGTGTGC 1560
ACCCACATCC AATGGTGCTA CAAGTGACTG AAATAATATT TGAGTCTTTC TGCTCAAGA 1620
ATGAAGCTCC AACCATGTTT CTAAGCTGTG TAGAAGTCTT ASCATTATAG GATCTTGTA 1680
TAGAAACATC AGTCCATTCC TCTTTTCACT TAATCAAGGA CATTCCTCATG GAGCCCAAGA 1740
TTACAATGT AGTCAAGGCT GTTTATTGGG TGGCTCCCTG GTTGTCAATT ACCTCATATA 1800
AAGAATGGGA AGGAGACCAT TGGGTAACCC TCAAGTGTCA GAAGTTGTTT CTAAAGTAAC 1860
TATACATGTT TTTTACTAAA TCTCTGCACT GCTTATAAAA TACATTGTG CCTATTAGG 1920
GAGTAACATT TTTTACTGTT TGTCTCTGGT TAAATGAAA TATGGGCTTA TGTCAATTCA 1980

```

5  
 10  
 15  
 20  
 25

TTGGAAGTCA ATGCACTAAC TCAATACCAA GATGAGTTTT TAAATAATGA ATATTATTTA 2040  
 ATACCACAAC AGAATTATCC CCAATTTCCA ATAAGTCTTA TCATTGAAAA TTCAAATATA 2100  
 AGTGAAGAAA AAATTAGTAG ATCAACAATC TAAACMAATC CCTGGTTCTT AAGATACAAT 2160  
 GGATTCCCCA TACTGGAAGG ACTCTGAGGC TTTATTCCCC CACTATGCAT ATCTTATCAT 2220  
 TTTATTATTA TACACATATC CATCTTAAAC TATACTAAAG CCTTTTCCCC ATGCATGGAT 2280  
 GGAAATGGAA GATTTTTTTG TAACCTGTTC TAGAAGTCTT AATATGGGCT GTTGCCATGA 2340  
 AGGCTTGCGA AATTGAGTCC ATTTTCTAGC TGCCTTTATT CACATAGTGA TGGGGTACTA 2400  
 AAAGTACTGG GTTGACTCAG AGAGTCGCTG TCATTCTGTC ATTGCTGCTA CTCTAACACT 2460  
 GAGCAACACT CTCCCACTGG CAGATCCCCT GTATCAITCC AAGAGGAGCA TTCATCCCTT 2520  
 TGCTCTAATG ATCAGGAATG ATGCTTATTA GAAAAACAA TCCTTGACCC AGGAACAAGT 2580  
 GGCTTAGCTT AAGTAACTT GGCTTTGCTC AGATCCCTGA TCCTTCAGC TGGTCTGCTC 2640  
 TGAGTGGCTT ATCCGCGATG AGCAGGAGCG TGCTGGCCCT GAGTACTGAA CTTTCTGAGT 2700  
 AACCAATGAGA CAGTTACAG AACCTATGTT CAGGTGCGG GTGAGCTGCC CTCTCCAAAT 2760  
 CCAGCCAGAG ATGCACATTC CTCGCCAGT CTGAGCCAAC AGTACCAAAA GTGATTTTTG 2820  
 AGTGTGCCAG GGTAAGGCTT TCCAGTTCAG CCTCAGTTAT TTTAGACAA CTGCGCATCT 2880  
 TTAATTTCTT AAGTTCCTGT TCTAATAAAT GCACGGCTTT ACCTTTCCTG TCAGAAATAA 2940  
 ACCAAGGCTC TAAAGATGA TTTCCCTTCT GTAACCTCCT AGAGCCACAG GTTCTCATT 3000  
 CTTTTCCTAT TATACCTCTC ACAATTCAGT TTCTATGAGT TTGATCACCT GATTTTTTTA 3060  
 ACAAAATATT TCTAACGGGA ATGGGTGGGA GTGCTGGTGA AAAGAGATGA AATGTGGTTG 3120  
 TATGAGCCAA TCATATTGTG GATTTTTTAA AAAAAGTTTA AAAGGAAATA TCTGTCTGA 3180  
 AACCCACTT AAGCATGTT TTTATATAAA AACATGATA AAGATGTGAA CTGTGAAATA 3240  
 AATATACCAT, ATTAGCTACC CACC

Seq ID NO: 54 Protein sequence  
 Protein Accession #: NP\_055026

30  
 35

1 11 21 31 41 51  
 MNYSLHLAFV CLSLFTERMC IQGSQFNVEV GRSDKLSLPG FENLTAGYNK FLRPNFGGEP 60  
 VQIALTLIDIA SSISSISESNM DYTATIYLRQ RWMQRLVFE GNKSFTLDAR LVEFLWVPDT 120  
 YIVESKRIFL HEVTVCNRLI RLFSNGTVLY ALRITTTVAC NMDLSKYPMD TQCKLQLES 180  
 WGYDGNDFEF TWLRGNDSVR GLEHLRLAQY TIERYFTLV T RSQETGNYT RLVLQFELRR 240  
 NVLYFILETY VPSTFLVLS WVSFWISLDS VPARTCIGVT TVLSMTLMI GSRTSLPNTN 300  
 CFKAIDVYL GICFSFVFGA LLEYAVAHYS SLQMAAKDR GTTKEVEEVS ITNIINSSIS 360  
 SFKRKISFAS IEISSNDVDY SDLTMKTS DK FKFVFRKMG RIVDYFTIQN PSNVHDYSKL 420  
 LFPLIFMLAN VFYWAYMYF

Seq ID NO: 55 DNA sequence  
 Nucleic Acid Accession #: XM\_084007  
 Coding sequence: 138..2405

40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 CTCGTGCCGA ATTCGGCAGC AGACCGGCTG TTCGGGCTTG GTAGAGATTT CTCGAAGACA 60  
 CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC 120  
 GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCC 180  
 TCTCTGTAC AAATCCCTT CATGAACATA AAGCAGCTGC TTTCCCCAG ACCACTGAGA 240  
 AAATTAGTCC GAATTGGGAA TCTGGCATTAT ATGTTGACTT GGCAATTTCC ACACGGCAAT 300  
 ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAAATA TTCTTTGTCA GTTGAAGGGT 360  
 TCAGAAAAAT ACTTCAAAT ATAGGCGATG ATAAGATTA AAGAATCCAT ATACCCATG 420  
 ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480  
 AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCCAC CATAATCATG 540  
 CTGCTTCTGG TAAATAAAG CGAAAAGCTC TTTGCCGAGA CCATGACTCA GATAGTTCTG 600  
 GTAAAGATCC TGAATAACAG CAGGGGAAAG GAGCTCACCG ACCAGAATAT GCCAGTGGTA 660  
 GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCACTGTG TACAACACTG 720  
 TCTCTGAAGG AACTCATTCT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAATCTTCC 780  
 CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACTC AAAGAGCCGG GTGAGCCGGC 840  
 TGGCTGTGAG GAAACAAAT GAATCTGTGA GTGAGCCCG AAAAGGCTTT ATGTATTCCA 900  
 GAAACACAAA TGAATAATCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960  
 GCATGGGCAAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAT CTATCTCTGT CCAGCCATG 1020  
 TCAACCAAT TGAATCTAGA TCTGTCTGA TTCATACAG TGAAGAGAG GCTGAAATCC 1080  
 CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTGGTGG TTTTATAGCC ATTTCCATCA 1140  
 TCAGTTTCTT GTCTCTGCTG GGGGTATCT TAGTGCCTCT CATGAATCGG GTGTTTTTCA 1200  
 AATTTCTCCT GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260  
 TACACCTTCT TCCATATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320  
 CAATGGAAAT GAAAGAGGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380  
 GTGCCATATT TGATTCACG TGAAGGGTTC TAACAGCTCT AGGAGGCCGT TATTTCATGT 1440  
 TTCTTGTTGA ACATGCTCTC ACATTGATCA AACAAITTA AGATAAGAAG AAAAAGAATC 1500  
 AGAAGAAACC TGAATAATGAT GATGATGTGG AGATTAAAGAA CAGATTGTCC AAGTATGAAT 1560  
 CTCACCTTTC AACCAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTATC 1620  
 GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCACTC TTGGAAGAG 1680  
 AAGAGGTGAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740  
 GGTGCAAGAA TAAATGCCAT TCACATTTC ACGATACACT CGGCCAGTCA GACGATCTCA 1800  
 TTCACCAACA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCA AACCAACATC 1860  
 CTCACAGTCA CAGCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGCG GTGCCACTT 1920  
 TGGCTGGAT GGTGATTAATG GGTGATGGCC TGCACAAIT CAGCGATGGC TAGCAATGT 1980  
 GTGCTGCTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGTCT GTGTCTGTCT 2040  
 ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100  
 AGCAGGCTGT CCTTTATAAT GCATTGTCTG CCATGCTGGC GTATCTTGGG ATGCGAACAG 2160  
 GAATTTTCAT TGCTCATATT GCTGAAAATG TTTCTATGTG GATATTGGA CTACTGCTG 2220  
 GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280  
 GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340  
 GTTTTGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTC GGTATAAAT 2400  
 TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT 2460

5  
10  
15

```

AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATTT 2520
TTGTATTGAA TATTGCTGTC TGTTACAAAG TCAGTTAAAG GTACGTTTAA ATATTTAAGT 2580
TATTCATCTC TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640
TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAATAATGT CTTTAAATGCT 2700
TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG 2760
TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
AGCAAGAGAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAAG 2940
CAGAATTAGT ATAGAGTACA TTCAATTAAAC ATTTTGTGCA GGATTATTTC CCGTAAAAAC 3000
GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120
TTGCTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGGT ACCTGGTTTA 3240
CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAACT ACCTAAGTA 3300
TCATTTGATT CGATTTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTTG 3360
GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

```

20  
Seq ID NO: 56 Protein sequence  
Protein Accession #: XP\_084007

25  
30  
35

```

1 11 21 31 41 51
MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISPWN ESGINVDLAI STRQYHLQQL 60
PYRYGENNSL SVEGFRKLQK NIGIDKIKRI HHHHDHDSHS DHEHSDHER HSDHEHSDH 120
EHSDDHDSHS HHNHAASGKH KRKALCPDHD SDSSGKDPKN SQGKAHRPE HASGRNRVKD 180
SVSASEVTST VYNTVSEGT FLETIETPRP GKLPKDVSS STPPSVTSKS RVSRLAGRKT 240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGGMQIV PLNATEPNYL CPAIINQIDA 300
RSLIHTSEK KAEIPPKTYS LQIAWVGFI AISIISPLSL LGVILVPLMN RVFFKPLLSF 360
LVALAVGTLS GDAFLHLPLH SHASHHSHS HEPEAMEMKR GPLFSHLSQ NIEESAYFDS 420
TWKGLTALG LYFMEFLVEHV LTLIKQFKDK KKKNQKPKEN DDDVEIKQL SKYESQLSTN 480
EEKVDTDRT EGYLRADSQE PSHFDSQQA VLEEEVEMIA HAHPQEVYNE YVPRGCKNKC 540
HSHFHTLQ SDDLHHHHH YHHIHHHHH QNHHPHSHS RYSREELKDA GVATLAWMVI 600
MGDLHNFSD GLAIGAAFE GLSSGLSTSV AVFCHPELPE LGDFAVLLKA GMTVKQAVLY 660
NALSAMLAYL GMATGIFIGH YAENVSMHIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720
RWGYFFLQNA GMLLGFGLML LISIFEKIV PRINF

```

40  
Seq ID NO: 57 DNA sequence  
Nucleic Acid Accession #: NM\_015419.1  
Coding sequence: 1..8487

45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
ATGCCCAAGC GCGCGCACTG GGGGGCCCTC TCCGTGGTGC TGATCCTGCT TGGGGCCCAT 60
CCGCGAGTGG CGCTGGCCTG CCGGCATCCT TGTGCCTGCT ACGTCCCCAG CGAGGTCCAC 120
TGACGTTTCC GATCCCTGGC TCCGTGGCCC GCTGGCATTG CTAGACAGST GGAAGAATC 180
AATTTGGGGT TTAATAGCAT ACAGGCCCTG TCAGAAACCT CATTTGACAG ACTGACCAAG 240
TTGGAGCTAC TTATGATTTA CGGCAATGAG ATCCCAAGCA TCCCGATGG AGCTTTAAGA 300
GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT GATCAGGAA 360
CAGACCCCTC AGGCTCTCTC TAACTTAATG AGGCTGCACA TTGACCAACA CAAGATCGAG 420
TTTATCCACC CTCACGCTTT CAACGCTTCA ACGTCTCTGA GGCTACTCCA TTTGGAAGAA 480
AATCTCCTCC ACCAGCTGCA CCCCAGCACC TTCTCCACGT TCACATTTT GGAATTATTC 540
AGACTCTCCA CCATAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCCTCTGACC 600
AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTTACT TGCAGGGAAT TCCGTGGACC 660
TGCGATTGTG AGATGAGATG GTTTTGGGAA TGGGATGCAA AATCCAGAGG AATCTGAG 720
TGTAAAAAGG ACAAAGCTTA TGAAGGCGGT CAGTTGTGTG CAATGTGCTT CAGTCCAAAG 780
AAGTTGTACA AACATGAGAT ACACAAGCTG AAGGACATGA CTTGTCTGAA GCCTTCAATA 840
GAGTCCCTTC TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAGAA ACAGGAAGAG 900
GATGGTGGCA GCCAGCTCAT CCTGGAGAAA TTCCAACCTG CCGAGTGGAG CATCTCTTTG 960
AATATGACCG ACAGGACCGG GAACATGGTG AACTTGGTCT GTGACATCAA GAAACCAATG 1020
GATGTGTACA AGATTCACTT GAACCAAAAG GATCCTCCAG ATATTGACAT AAATGCAACA 1080
GTTGCCTTGG ACTTTGAGTG TCCAATGACC CGAGAAAACAT ATGAAAAGCT ATGGAAATG 1140
ATAGCATACT ACAGTGAAGT TCCCGTGAAG CTACACAGAG AGCTCATGCT CAGCAAAGAC 1200
CCCAGAGTCA GCTACCACTA CAGGCAGGAT GCTGATGAGG AAGCTCTTTA CTACACAGGT 1260
GTGAGAGCCC AGATTCTTGC AGAACCAAGAA TGGGTCTATG AGCCATCCAT AGATATCCAG 1320
CTGAACCGAC GTCAGAGTAC GGCCAAGAAG GTGCTACTTT CCTACTACAC CCAGTATTCT 1380
CAACAATAT CCACCAAGA TACAAGCAG GCTCGGGSCA GAAGCTGGT AATGATTGAG 1440
CCTAGTGGAG CTGTGCAAGG AGATCAGACT GTCTTGGAG GGGTCCATG CAGTTGAGC 1500
TGCAACGTGA AAGCTTCTGA GAGTCCATCT ATCTTCTGGG TGCTTCCAGA TGGCTCCATC 1560
CTGAAGCGC CCATGAGTGA CCCAGACAGC AAGTTCTCCA TTCTCAGAG TGGCTGGCTG 1620
AGGATCAAGT CCATGGAGCC ATCTGACTCA GGCTTGTACC AGTGCATGCT TCAAGTGGG 1680
GATGAAATGG ACOGCATGCT ATATAGGCTA CTGTGTCAGT CTCCCTCCAC TCAGCCAGCC 1740
GAGAAAGACA CAGTGACAAT TGGCAAGAAC CCAGGGGAGT CGGTGACATT GCCTTGCAAT 1800
GCTTTAGCAA TACCCGAGC CCACCTTAGC TGGATTCTTC CAAACAGAA GATAATTAAT 1860
GATTTGGCTA ACACATCACA TGTATACATG TTGCCAAATG GAACCTTTTC CATCCCAAG 1920
GTCCAAGTCA GTGATAGTGG TTACTACAGA TGTGTGGCTG TCAACAGCA AGGGCAGAG 1980
CATTTTACGG TGGGAATCAC AGTGACCAAG AAAGGGTCTG GCTTGCATC CAAAAGAGGC 2040
AGAGCCCCAG GTGCAAAAGC TCTTTCCAGA GTCAGAGAAG ACATCGTGA GGATGAAGG 2100
GGCTCGGCA TGGGAGATGA AGAGAACACT TCAAGGAGAC TTCTGCATCC AAAGGACCAA 2160
GAGGTGTTCC TCAAAACAAA GGATGATGCC ATCAATGGAG ACAAGAAAGC CAAGAAAGGG 2220
AGAGAAAGC TGAACCTCTG GAAGCATTCC GAAAAGAAC CAGAGACCAA TGTTCAGAA 2280
GGTCGACAG TGTTTGAATC TAGACGAAGG ATAAACATGG CAAACAACA GATTATCCG 2340
GAGCGCTGG CTGATATTTT AGCCAAAGTC CGTGGGAAAA ATCTCCCTAA GGGCAGAGAA 2400
GTACCCCGCT TGATTAAGAC CACAAGTCTT CCATCCTTGA CCCTAGAAGT CACACCACCT 2460

```

	TTTCTGCTG	TTTCTCCCC	CTCAGCATCT	CCTGTGCAGA	CAGTAACCA	TGCTGAAGAA	2520
	TCCTCAGCAG	ATGTACTCT	ACTTGGTGAA	GAAGAGCAGC	TTTTGGGTAC	CAITTCCTCA	2580
	GCCAGCATGG	GGCTAGAACA	CAACCACAAT	GGAGTTATTC	TTGTTGAACC	TGAAGTAACA	2640
5	AGCACACCTC	TGGAGGAAGT	TGTTGATGAC	CTTCTGAGA	AGACTGAGGA	GATAACTTCC	2700
	ACTGAAGGAG	ACCTGAAGGG	GACAGCAGCC	CCTACACTTA	TATCTGAGCC	TTATGAACCA	2760
	TCTCTACTC	TGCACACATT	AGACACAGTC	TATGAAAAGC	CCACCCATGA	AGAGACGGCA	2820
	ACAGAGGGTT	GGTCTGCAGC	AGATGTTGGA	TCGTCAACCAG	AGCCCCATC	CAGTGAGTAT	2880
	GAGCCTCCAT	TGGATGCTGT	CTCCTTGGCT	GAGTCTGAGC	CCATGCAATA	CTTTGACCCA	2940
10	GATTTGGAGA	CTAAGTCAAC	ACCAGATGAG	GATAAGATGA	AAGAAGACAC	CTTTGCACAC	3000
	CTTACTCCAA	CCCCCACCAT	CTGGGTTAAT	GACTCCAGTA	CATCAGATT	ATTTGAGGAT	3060
	TCTACTATAG	GGGAACCAAG	TGTCCAGGC	CAATCACATC	TACAAGSACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAAGTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
	AAAGAGATGT	CTCAGACACT	ACAGGGAGGA	AAATGCTAG	AGGGAGACCC	CACACACTCC	3240
15	AGAAGTTCTG	AGAGTGAGGG	CCAAGAGAGC	AAATCCATCA	CTTTGCCTGA	CTCCACACTG	3300
	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGGGG	AAACCCAGAT	TGGTACCCCTC	3360
	CTAGACAAAG	ACACCAACAA	AGTAACAACA	ACACCAAGGC	AAAAGTTGTC	TCCGTATCC	3420
	ACCATGAGCA	CTCACCCCTC	TGGAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCCAC	3480
	AAATTCOGCC	ACCGGCACAA	GCAAAACCCA	CCCAACACTT	TTGCCCATC	AGAGACTTTT	3540
20	TCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAA	GTCAGGTGGA	GAGTTCTCTG	3600
	GTTCTCTACG	CTTGGGTGGA	TAACACAGTT	AATACCCCCA	AACAGTTGGA	AATGGAGAAG	3660
	AATGCAGAAC	ACACCACTCA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCCTTCTAC	AGTGAGCTCA	AGAGCGTCCG	GATCCAAGCC	CAGCCCTTCT	3780
	CCAGAAAATA	AACATAGAAA	CATTGTTACT	CCCAGTTCAG	AACTATACT	TTTGCCCTAGA	3840
25	ACTGTTTCTC	TGAAAACCTGA	GGGCCCTTAT	GATTCCCTTAG	ATTACATGAC	AACCACCAGA	3900
	AAAATATATT	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCCACA	3960
	TCAGATGGAA	AAGAAATTAA	GGATGATGTT	GCCACAAATG	TTGACAAACA	TAAAGTGAC	4020
	ATTTTAGTCA	CTGTGTAATC	AATTACTAAT	GCCATACCAA	CTTCTCGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AAATTAAAGGA	AGAATCCTCT	CCTGTAGGCT	TTCCAGGAAC	TCCAACCTGG	4140
30	AAATCCCTCA	GGAGTCCGCC	GCCTGGGAGG	CTACAGACAG	ACATACCTGT	TACCACTTCT	4200
	GGGGAATACT	TTACAGACCC	TCCCCTTCTT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
	GAGTTTGTGT	CCTCTTTGAC	AGTCTCCACA	CCATTTCACC	AGGAAGAAGC	TGGTCTTCC	4320
	ACAACCTCTC	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCTTT	4380
	GATCAAGATC	ATCTTGAACAC	CAGTGTGGCT	ATTCTCCTTT	CTGAAACTAG	ACCACAGAAT	4440
35	CACACCCCTA	CTGCTGCCCG	GATGAAGGAG	CCAGCATCCT	CGTCCCCTATC	CACAATTCTC	4500
	ATGTCTTTGG	GACAAACCAAC	CACCACTAAG	CCAGCACTTC	CCAGTCCAAG	AATATCTCAA	4560
	GCATCTAGAG	ATTTCAAAGGA	AAATGTTTTC	TTGAATTATG	TGGGAATCC	AGAAACAGAA	4620
	GCAACCCCA	TCAACAATGA	AGGAACACAG	CATATGTGAG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCGG	ACCGGGATGC	ATTTAACTTG	TCTACAAAGC	TGGAATTGGA	AAAGCAAGTA	4740
40	TTTGGTAGTA	GGAGTCTACC	ACGTGGCCCA	GATAGCCCAAC	GCCAGGATGG	AAGAGTTTAT	4800
	GCTTCTCATC	AACTAACCAAG	AGTCCCTGCC	AAACCCATCC	TACCAACAGC	AACAGTGAGG	4860
	CTACCTGAAA	TGTCACACAA	AAGCGCTTCC	AGATACTTTG	TAACTTCCCA	GTCACTCTGT	4920
	CACTGGACCA	ACAAACCCGA	AATAACTACA	TATCCTTCTG	GGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACAA	CTCCAAGATT	ATCAAGTACA	ACAATTCCTC	TCCCATTGCA	CATGTCCAAA	5040
45	CCAGCATTC	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AATTCAATGG	TTACTCCAAA	5100
	GTGTTTGGAA	ATAACAACAT	CCCTGAGGCA	AGAAACCCAG	TTGGAAGGCC	TCCAGTCCA	5160
	AGAATTCCTC	ATTATTCCAA	TGGAAGACTC	CTTTCTTTA	CCAACAAGAC	TCTTTCTTTT	5220
	CCACAGTTGG	GAGTCAACCG	GAGACCCCA	ATACCCACTT	CTCCTGCCCC	AGTAATGAGA	5280
	GAGAGAAAAG	TATTTCCAGG	TTCTTACAAC	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
50	GACTTTGGCC	CTCGGACACC	TCCGTTGTTG	CACACTCCGC	AGACCAACGG	ATCACCCCTCA	5400
	ACTAACTTAC	AGAAATATCC	TATGTTCTCT	TCCACCCAGA	GTTCTATCTC	CTTTATAACA	5460
	TCTCTGTGAA	AGTCTCTAGG	AAGCTTCCAC	CAGAGCAGCT	CAAAGTTCTT	TGCAGGAGGA	5520
	CCTCTGTCAT	CCAAATTTCTG	GTCTCTTGGG	GAAGAGCCCC	AAATCCTCAC	CAAGTCCCCA	5580
	CAGACTGTGT	CCGTCAACGC	TGAGACAGAC	ACTGTGTTCC	CCTGTGAGGC	AACAGGAAAA	5640
55	CCAAAGGCTC	TGCTTACTTG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAATACC	5700
	AGGATACAA	GGTTTGAGGT	TCTCAAGAAC	GGTACCTTAG	TGATACGGAA	GGTTCAAGTA	5760
	CAAGATCGAG	GCCAGTATAT	GTGCACCGCC	AGCAACCTGC	ACGGCCTGCG	CAGGATGGTG	5820
	GTCTTGCTTT	CGGTCAACCT	GCAGCAACCT	CAAATCCTAG	CCTCCCACTA	CCAGGACGTC	5880
	ACTGTCTACC	TGGGAGACAC	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCCAAGCCCC	5940
60	CAAAATTTCT	GGATCTTCCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	GCATCAACCC	TGCACGAAAA	CCGGAACCTT	TCCATCAAGG	AGGCGTCTCT	CTCAGACAGA	6060
	GGGCTCTATA	AGTGGGTGGC	CAGCAATGCA	GCCGGGGCGG	ACAGCCTGGC	CATCCGCTGT	6120
	CACGTGGCGG	CAGTGCACCC	CGTTATCCAC	CAGGAGAAGC	TGGAGAACAT	CTCGTGGCCC	6180
	CCGGGGCTCA	GCATTCACAT	TCACTGCACT	GCCAAGGCTG	CGCCCCCTGCC	CAGGTGGGCG	6240
65	TGGGTGCTCG	GGGAOGGTAC	CCAGATCCGC	CCCTGCGAGT	TCTTCCACGG	GAACCTGTTT	6300
	GTTTTTCCCC	ACGGGACGCT	CTACATCCGC	AACTTCCGCG	CCAAAGGACAG	CGGGGCTAT	6360
	GAGTGGGTGG	CCGCAACCTT	GGTAGGCTCC	GCGCGCAGGA	CGGTGCAAGT	GAAOGTGCAG	6420
	CGTGACGAG	CCAAACGCGG	CATCACGGGC	ACCTCCCGCG	GGAGGACGGA	CGTCAGGTAC	6480
	GGAGGAACCC	TCAAGCTGGA	CTGCAGCGCC	TCCGGGGACC	CCTGGCCGCG	CATCCTCTGG	6540
70	AGGCTGCGST	CCAAGAGGAT	GATCGACGCG	CTCTTCAGTT	TTGATAGCAG	AATCAAGGTTG	6600
	TTTGCCAATG	GGACCTTGGT	GGTGAATCA	GTGACGGACA	AAGATGCGCG	AGATTACCTG	6660
	TGGGTAGCTC	GAATTAAGGT	TGGTATGAC	TACGTGGTGC	TCAAAGTGGG	TGTGGTGATG	6720
	AAACCGGCCA	AGATTGAACA	CAAGGAGGAG	AAOGAACCA	AAGTCTTCTA	CGGGGGTGAC	6780
	CTGAAAGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCG	AGATCTCCTG	GAGCCTCCCA	6840
75	GACGGGAGTC	TGGTGAACCT	CTTCATGCAG	TGGGATGACA	GCGGTGGAGC	CACCAAGCGC	6900
	TATGTGCTCT	TCAACATGAG	GACACTCTAC	TTTAAACGAG	TGGGGATGAG	GGAGGAAGGA	6960
	GACTCAAGCT	GCITTTGCTGA	AAATCAGGTC	GGGAAGGAGC	AGATGAGAGT	CAGAGTCAAG	7020
	GTGGTGACAG	CGCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGTTTCA	GGTGCCCTAT	7080
	GGAGAGCTGG	TCACTGTAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
80	TTGTCCCAA	CAACAAAGGT	GATCCCCACC	TCTCTGAGA	AGTATCAGAT	ATACCAAGAT	7200
	GGCACTCTCC	TTATTGAGAA	AGCCCAAGCT	TCTGACAGCG	GCAACTACAC	CTGCTTGCTG	7260
	AGGAACAGAG	CGCGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	7320
	AAGATCAACG	GTAACCCCAA	CCCATCACCC	ACCGTGGCGG	AGATAGCAGC	CGGGGGCAGT	7380
	CGGAAACTGA	TTGACTGCAA	AGCTGAAGGC	ATCCCCACCC	CGAGGGGTGT	ATGGGCTTTT	7440
	CCGAGGGTGG	TGGTTCTGCC	AGCTCCATAC	TATGGAAACC	GGATCAGTGT	CCATGGCAAC	7500



5 GGTTCCTCGG ACATCAGGAG TTTGAGGAAG AGCGACTCCG TCCAGCTGGT ATGCATGGCA 7560  
 CGCAACGAGG GAGGGGAGGC GAGGTTGATC GTGCAGCTCA CTGTCTCTGA GCCCATGGAG 7620  
 AAACCCACTT TCCACGACCC GAGGTTGATC GATCAGCGAG AAGATCACGG CCATGGCGGG CCACACCATC 7680  
 AGCCTCAACT GCTCTGCGCG GGGGACCCCG ACACCCAGCC TGSTGTGGST CCTTCCCAAT 7740  
 GGCACCGATC TGCAGAGTGG ACACGAGCTG CAGCGCTTCT ACCACAAGGC TGACGGCATG 7800  
 CTACACATTA GCGGTCTCTC CTCGGTGGAC GCTGGGGCCT ACCGCTGCGT GGCCCGCAAT 7860  
 GCGCTGGCCC ACACGGAGAG GCTGGTCTCC CTGAAGGTGG GACTGAAGCC AGAAGCAAAC 7920  
 AAGCAGTATC ATAACCTGGT CAGCATCATC AATGGTGAGA CCTGAAGCT CCCCTGCACC 7980  
 10 CCTCCCGGGG CTGGGCGGGG ACGTTTCTCC TGGAGCTGCC CCAATGGCAT GCATCTGGAG 8040  
 GGCCCCCAAA CCCTGGGACG CGTTTCTCTT CTGGACAATG GCACCCCTAC GGTTCGTGAG 8100  
 GCCTCGGTGT TTACACGGGG TACCTATGTA TGCAGGATGG AGACGGAGTA CGGCCCTTCG 8160  
 GTCACACGCA TCCCGTGAT TGTGATCGCC TATCTCTCCC GGATCACCAG CGAGCCCAAC 8220  
 CCGGTCTACT ACACCCGGCC CGGGAACACC GTGAACTGA ACTGCATGCC TATGGGGATT 8280  
 15 CCCAAAGCTG ACATCAGTGG GGAGTTACCG GATAAGTGGC ATCTGAAGGC AGGGGTTTCAG 8340  
 GCTCGTCTGT ATGGAACAG ATTTCTTCA CCCCAGGGAT CACTGACCAT CCAGCATGCC 8400  
 ACACAGAGAG TACACAGGGG CTACAAGTGC ATGGCAAAA ACATTCTCGG CAGTGAATCC 8460  
 AAAACAACCT ACATCCAGCT CTTCTGAAAT GTGGATTCCA GAATGATTGC TTAGGAACCTG 8520  
 ACAACAAAGC GGGGTTTGTG AGGGAAGCCA GGTGGGGGAA TAGGAGCTCT TAAATAATGT 8580  
 20 GTCACAGTGC ATGGTGGCCT CTGGTGGGTT TCAAGTTGAG GTTGATCTTG ATCTACAATT 8640  
 GTTGGGAAAA GGAAGCAATG CAGACACGAG AAGGAGGGCT CAGCCTTGCT GAGACACTTT 8700  
 CTTTGTGTGT TTACACGGGG CAGGGGCTTC ATTCAAGGTG TCTGTGCTCT GACTGCAATT 8760  
 TTTCTTCTTT TGCAATGCC ACTCGACTGC CTTCAATAGC GTCCATAGGA TATCTGAGGA 8820  
 ACATTATCA AAAATAAGCC ATAGACATGA ACAACACCTC ACTACCCAT TGAAGAGCA 8880  
 25 TCACCTAGTT AACCTGCTGC AGTTTTTACA TGATAGACTT TGTTCAGAT TGACAAGTCA 8940  
 TCTTTCACTT ATTTCTCTG TCACITCAAA ACTCCAGCTT GCCCAATAAG GATTTAGAAC 9000  
 CAGAGTGACT GATATATATA TATATATTTT AATTCAAGAT TACATACATA CAGTACCAT 9060  
 TTTATATGAA AAAAGAAAAA CATTTCTTCC TGGAACTCAC TTTTATATA ATGTTTATA 9120  
 TATATATTTT TTCTTTTCAA ATCAGACGAT GAGACTAGAA GGAGAAATAC TTTCTGCTT 9180  
 30 ATTAATAATT ATAAATTTAT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA 9240  
 ATATAATTTT AAAAAATTC TCTCCAACCT CCTTCAAAT CAGTCAACAC TGTTATATTA 9300  
 CCTCTCCAG GAACCCCTCA GTGGGGAAGG CTGCGATATT AGATTCTCT GTATGCAAG 9360  
 TTTTGTGTA AAGCTGTGCT CAGAGGAGGT GAGAGGAGAG GAAGGAGAAA ACTGCATCAT 9420  
 AACTTTACAG AATTGAATCT AGAGTCTTCC CCGAAAAGCC CAGAACTTC TCTGCAGTAT 9480  
 35 CTGGCTTGTG CATCTGGTCT AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC 9540  
 CCATGAATAA TACACGACCT GTTATTCCA TGACTGCTT ACTGTATTT TAAGTCAAT 9600  
 ATACTGTACA TTGTATAATA AAATAATATT CTCCCAAAAA AAAAA

Seq ID NO: 58 Protein sequence  
 Protein Accession #: NP\_056234.1

40 1 11 21 31 41 51  
 MPKRAHWGAL SVVLILLWGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60  
 NLGFNSIQAL SETSPAGLTK LELLMIHGNE IPSIPDGALR DLSSLQVFKP SYNKLRLVITG 120  
 45 QTLQGLSNLM RLHIDENKIE FIHPQAFNGL TSLRLHLLEG NLLHLQHPST FSTFTFLDYP 180  
 CLSTIRHLVY AENMVRTLPA SMLRNMPLLE NLYLQGNPWT CCEMRWFLE WDAKSRGILK 240  
 CKKDKAYEGG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRSR SIEEBQEQUE 300  
 DGGSQLILEK FQLPQMSISL NMTDEHGMNV NLVCDIKIPM DVYKIHNLQT DPFDIDINAT 360  
 50 VALDFECPMT RENYEKLWKL IAYYSEVPVK LHRELMLSKD PRVSYQYRQD ADEEALYYTG 420  
 VRAQILAEPE WVMQPSIDIQ LNRQSTAKK VLLSYTYQYS QTISTKDTRO ARGRSWVMIE 480  
 PSGAVORDQT VLEGQPQLS CNVKASESPS IFWVLPDGS I LKAPMDDPDS KFSILSSGWL 540  
 RIKSMESPSD GLYQCIQVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN 600  
 ALAIPEAHL WILPNRRIIN DLANTSHVYM LPNGTSLIPK VQVSDSGYYR CVAVNQQGAD 660  
 55 HFTVGTIVTK KSGGLPSKRG RRPKAKALSR VREDIVEDEG GSGMGDEENT SRLLHPKDQ 720  
 EVFLKTKDDA INGDKAKKKG RRKLKLWKS EKEPETNVAE GRRVFESRRR INMANKQINP 780  
 ERWADILAKV RGNLKPQTE VPFLIKTTSP PSLSLVETPP FPAVSPPSAS PVQTVTSAGE 840  
 SSADVPLIGE EEHVLTGTS ASMGLEHNHN GVILVEPEVT STPLEEVVDD LSEKTEEITS 900  
 TEGDLKGTA PTLISEPYEP SPTLHTLDTV YEKPTHEETA TEGWSAADVG SSPEPTSEY 960  
 60 REPPLDAVSLA ESEPMQYFDP DLETQSPDE DKMKEDTFAH LTPTPTIWNV DSSTSQQLFED 1020  
 STIGEPGVPQ QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQSG NMLEGDPHTS 1080  
 RSSESEGGES KSITLPDSTL GIMSSMSPVK KPAETTVGTL LDKDTTTTVT TPRQKVAPSS 1140  
 TMSTHPSRRR PNGRRRLRPN KFRHRKQTP PTTAPSETF STQPTQAPDI KISSQVESSL 1200  
 VPTAWVDNTV NTPKQLEMEK NAEPSTKGTG RRIKHKRPNK HRYTPSTVSS RASGSKPSPS 1260  
 65 PENKHRNIVT PSSETILLPR TVSLKTEGYP DSLDYMTTTR KIYSSYPKVQ ETLFVTYKPT 1320  
 SDGKEIKDDV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKEESS PVGPPGTPTW 1380  
 NPSRTAQPRR LQTDIPVITS GENLTDPPLL KELEDVDFTS EFLSSLTVST PFHQEEAGSS 1440  
 TTLSSIKVEV ASSQAETTL DQDHLETTVA ILLSETRPON HTPTAARMKE PASSSPSTIL 1500  
 MSLGQTTTTK PALPSPRIQ ASRDSKENVF LNVVGNPETE ATPVNEGTO HMSGPNELST 1560  
 70 PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620  
 LPEMSTQAS RYFVTSQSPR HWTNKPEITT YPSGALPENK QFTTFLRLST TIPLPLHMSK 1680  
 PSIPSKFDRR RTDQFNGYSK VPGNNNIPEA RNPVGKPPSP RIPHYSNGLR PFFNTKTLSP 1740  
 FQLGVTRRPQ IPTSPAPVMR ERKVIPGSYN RIHSHSTFHL DFGPPAPPLL HTPQTGTSPS 1800  
 TNLQNIPIVS STQSSISPI STSQSSGFSH QSSSKFFAGG PPASKFWSLG EKPQILTKSP 1860  
 75 QTVSVTAETD TVFPCEATGK PKPFVTWTKV STGALMTPNT RIQRFELVKN GTLVIRKVVQ 1920  
 QDRGQVMCTA SNLHGLDRMV VLLSVTVQPP QILASHYQDV TVYLGDTIAM ECLAKGTAP 1980  
 QISWIFPDRR VMDVSPVES RITLHENRTL SIKEASFSDR GUYKCVASNA AGADSLAIRL 2040  
 RVALPEFVH QEKLEINISL PGLSIHICT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100  
 VFPNGTLYIR NLAPKDSGRY ECVAANLVGS ARRTVOLNVQ RAAANARITG TSPRRTDVRY 2160  
 80 GGTLLKDCSA SGDPWPRIWL RLPKSRMIDA LPSFDSRIKV FANGTLVVKV VTDKADAGDYL 2220  
 CVARNKVDQD YVVLKVDVVM KPAPIEKKEE NDHKVFGGDD LKVDCAVATG PNPEISWNL 2280  
 DGSLVNSFMQ SLDGSGRTK YVVFNGTLY FNEVGMREEG DYTCEANQV GKDEMVRVRK 2340  
 VVTAPATIRN KTYLAVQVYP GDVVTVACEA KGEPMKVTM LSPNTNKVIPT SSEKYQIYQD 2400  
 GTLLIQKAQR SDSGNYTCLV RNSAGEDRKT VNIHVNQPP KINGNPNFIT TVREIAAGGS 2460  
 RKLIDCKAEG IPTPRVLWAP PEGVVLPAFY YGNRITVHGN GSLDIRSLRK SDSVLVCM 2520

RNEGGEARLI VQLTVLEPME KPIFHDPIS KITAMAGHTI SLNCSAAGTP TPSLVVWLPN 2580  
 GTDLQSGQQL QRFYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVLKPEAN 2640  
 KQYHNLVSII NGETLKLPCP PPGAGQGRFS WTLPNGMHLE GPQTLGRVSL LDNGLTLVRE 2700  
 ASVFDRTYTV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAMGI 2760  
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820  
 KTTYIHVF

Seq ID NO: 59 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..5001

1 11 21 31 41 51  
 15 ATGCCAGGCA CAAAATAAC CGAACAGGC GCCCAGCAG ACTACAGAGT GATATTGAAG 60  
 ACCTCTCAAG AGGACGAATT GGATGTACCT GACGACATCA GCGTCCGGGT TATGTCATCT 120  
 CAGTCTGTGC TTGTGTCTCT GGTGGATCCT GTTCTGGAAA AACAGAAGAA AGTTGTTGCA 180  
 TCAAGACAGT ACACCGTGCG CTATCGAGAG AAGGGGGAAT TGGCCAGGTG GGATTATAAG 240  
 CAGATCGCTA ACAGCGGTGT GCTGATTGAG AACCTGATTG CAGACACTGT GTATGAATTT 300  
 GCAGTCGCTA TTTCACAGGG TGAAGAGAT GGCAATGGA GTACGTGAGT CTTCCAAAGA 360  
 20 ACACCAAGAT CTGCCCTTAC CACAGCTCCT GAAACTTGA ACGTCTGCC AGTCAATGGC 420  
 AAACCTACAG TTGTGCTGTC ATCTTGGGAT GCGCTACCAG AGACTGAGGG GAAAGTGAAA 480  
 GTCTGTCTGC TGGACACAGG ACTGTTTTCA GTTCTCTCCT TCCAACCATT TGCCAAATCA 540  
 TTTCAAGAATA CATTCTTTCA TACGCCCCGG CTCTCAAAACC ATTGGAGACA AAGTCCCTCA 600  
 CCTATCCCTGG AGACACTACT TCTGCCCTGG TGGATGGTCT GCAGCCTGGG GAACGCTATC 660  
 25 TTTTCAAAT CCGGGCCACA AACAGGAGAG GCCTGGGACC TCACTCCAAA GCCTTCATTG 720  
 TCGCTATGCC AACAAAGATG CAGCTGTACC CAGAAGGATT TCAGTTGTCT AGCTTACCTG 780  
 ATCGATATCC AAACCAAACA AGTTAATAAA GATCCACAAC TGGAAAGGAG TGTTTTGGAA 840  
 CCATGTTTTT TTTTCTACTT CCTCACATT ATGCTGGATA TTGCGCGCTT TTCTTCATT 900  
 ATGTGCTATG AGACCTCANN TGTTCCTCT TTGACAGGCA ATTCCTTAAA ATCTGTGCA 960  
 30 GCCAGTAAGG CCGATGTTC A CAGAACACG GAGGACAATG GGAACCCGGA AAACCTGTAG 1020  
 CCTTCTCAC CTCTCCAG AGCTCCAGCT TCCTCCCAAC ACCCTCTGT GCCTGCTCT 1080  
 CCCCAGGGA GAAATGCCAA GGACCTTCTT CTTGACTTGA AGAACAAAT ATTGCTAAT 1140  
 GGTGGGGCGC CCGGAAAACC CCAGCTTCGC GCCAAGAAAG CAGAGGAGCT GGATCTTCAG 1200  
 35 TCGACAGAAA TCATCTGGGA GGAGGAGCTG GGTTCGCGGG AGGACTCGCC CATGTCAACC 1260  
 TCAGACACCC AACACAGAA ACGGACCTCG AGGCCGCGAA GTAGACACGG CCACTCGGTG 1320  
 GTTGCTCCCG GCAGGACTGC AGTGAGGGCC CGGATGCCAG CGCTGCCCGG AAGGGAAGGC 1380  
 GTAGATAAGC CTGGCTTTTC CTTGGCCACG CAGCCCCGCC CAGGGGCGCC CCCCCTCGCT 1440  
 TCGGCTCTCT CTGCCACCA CGCGTCCACC CAGGGCACTT CTCATCGTCC TTCCCTGCCT 1500  
 40 GCCAGCTTGA ATGACAACGA CTTGGTGGAC TCAGACGAAG ATGAGCGCGC TGTGGGCTCC 1560  
 CTCACCCCA AGGGCGCTT CGCCAGCCCG CGGCCAGCCC TGTCCCCAG CCGCCAGTCC 1620  
 CCGTCCAGCG TTCTCGCGCA CAGAAGCTCT GTGCAACCCG GCGCAAGGCC AGCCTCGCG 1680  
 GCGCGGAGGA CCCCCATTTC AGGGCGCGCA GAGGAAGATT CCACTGCTTC AGCCCCACCC 1740  
 TCAAGACTTT CTCACCCCA TGGGGGATCA TCTCGGCTGC TGCCCAACCA GCCACACCTG 1800  
 45 AGCTCTCCAC TTTCTAAGGG CGGGAAGGAT GGTGAGGAGC CCCCAGCCAC CAACTCCAAT 1860  
 GCGCCATCAC GGTCCACCAT GTCTCTCTCC GTCTCTCTCT ATCTCTCGTC CAGGACCGAG 1920  
 GTCTCTGAGG GAGCGGAGGC TTCTGATGCT GAAAGCCACG GTGACGGCGA TAGGGAAGAC 1980  
 GCGCGAAGGC AGGCGGAGGC CACGGGCCAG ACGCTGCGGG CCGCGCTGCG CTCTGGACAC 2040  
 TTCCATTGTC TCAGACACAA ACCCTTTGCT GCCAACCGGA GGTCTCCAAG CAGGTTCAAG 2100  
 50 ATTGGGCGGG GACCTCGCTG CAGGCCCTCC AGCTCCCCAC AGTGGACTGT GCCCTCCCGA 2160  
 GCCCACCCCA GGGTTCCTCT TCACTCTGAT TCCACCCCTA AGCTTAGCTC AGGTATCCAT 2220  
 GGAGACGAGG AGGATGAGAA GCCGCTTCTT GCCACGTTG TCAATGACCA CGTGCCTTCC 2280  
 TCCTCCAGGC AGCCCATCTC CCGGGGCTGG GAGGACTTAA GGAGAAGCCC GCAGAGAGGG 2340  
 GCCAGCTCTG ATCGGAAGGA ACCCATCCCA GAGAACCCCA AATCCACAGG GGCAGATACA 2400  
 55 CATCTCAGG TCAAGTACTC CTCCCTGGCC TCCAAGGCTC AGGATGTTCA ACAGAGCACA 2460  
 GACGCGGACA CCGAGGGTCA TTCTCCCAA GCACAGCCAG GGTCCACAGA CCGCCACGGG 2520  
 TCCCTGCTC GTCTCCCGC AGCACGCTCA CAGCAGCATC CCACTGTTCC CAGAAGGATG 2580  
 ACACCCGGCC GGGCCCCAGA ACAGCAGCCC CCTCTCCCG TCGCCACGTC CCAGCACCAC 2640  
 CCGGAGCCCC AGAGCAGAGA CGCGGTCCGG TCACTTCCC AGCCCAAGGT CTCACGTACC 2700  
 60 CAGGCGGGCG GCGCCGCCCC CACGTGCGAG GCGCGCTCCC ACTCCTCTCT GGACCTTAC 2760  
 ACGGCGAGCT CCAAGAGGAT GCTCCCAAG GGCCTCCAGA ACCAGGACGA GGATGCCAG 2820  
 GGCAGCTAAG ACGACGACAG CACAGAAGTC GAGGCCCAGG ATGTGCGGGC CCGCGGCAC 2880  
 GCGCGCGCG CCAAGGAGGC AGCTGCGTCC CTTCCTCAAG ACCAGCAGGT GGAGTCTCCC 2940  
 ACAGGCGCAG GGGCAGGTGG CGACCAAGG TCCCAGCGCG GACATGCGGC CTCCTCCGCC 3000  
 65 AGGCCACGCC GACCCGCGGG CCCCCAGTCC CGCGCCCGGG TCCCCAGCAG GGCAGCGCG 3060  
 GGGAAAGTGG AGCCTCTCTT CAGCGCGCCC CTGTCTCCA AGTCCACAGA GTCGGTCTCA 3120  
 GCGGAGGAGG AGGAGGAGGA GAGCGCGGGG TTTTTTAAAG GCGGGAAGA AGACCTTCTG 3180  
 TCTTCTCTG TGCCAAAGTG GCCCTTCTCC TCCACTCCCA GGGCGGCA AGACGCGGAT 3240  
 GGGAGCCTCG CCAAGGAAGA GAGGGAGCCT GCCATGCGGC TTGCCCTCTG CGGAGGGAGC 3300  
 70 CTGGCTCTG TGAAGCGACC TCTCCCCCA CCTCCAGGCA GCTCCCCAG GGCCTCCAC 3360  
 GTCCCTTCCC GACCGCCGCC TCGCAGCGCT GCCACCGTGA GCGCGGTGCG GGGACCCAC 3420  
 CCTTGGCGCG GGTACACCA GCGCGCCCV CTTGCCACT TCTCCACCAC CCGATGCTG 3480  
 TCCTTGGCGC AGAGGATGAT GCATGCCAGA TTCGTAACC CTCTCTCCG ACAGCCTGCC 3540  
 AGACCTCTT ACAGACAAGG TTATAATGGC AGACCAATG TAGAAGG3AA AGTCTTCTCT 3600  
 75 GGTAGTAATG TGAAGCGAA TGGACAGAGA ATTATCAATG GCCCTCAAG AACAAAGTGG 3660  
 GTTGTGGACC TTGATCGTGG GTTAGTATTG AATGCAGAAG GAAGGTACCT CCAAGATTCA 3720  
 CATGGAATC CTCTTCGGAT TAAACTAGGA GGAGATGGTC GAACCATGT AGATCTGGAA 3780  
 GGGACCCCCG TGGTGAATCC TGACGCGCTC CCACTCTTTG GGCAGGCGCG ACATGGCACA 3840  
 CCTCTGGCCA ATGCCCAAGA TAAGCCAATT TTGAGTCTTG GAGGAAAGCC GCTGGTGGC 3900  
 80 TTGGAGTGA TCAAAAAC CACCCATCCC CTTACCACTA CCATGCAGCC CACCACTACT 3960  
 ACCAGCGCCC TGCTTACCAC TACAACCCCG AGGCCACCA CTGCCACCA CATGCAGCCC 4020  
 ACCACTACTA CGACGCCCCT GCCTACCACT ACACCGAGGC CCACTACTGC CACCAACCGC 4080  
 CGCAGACCA CCAAGGCTCC AACAAACCA GTCCGAACCA CTACGCGGAC AACCAACACC 4140  
 ACCACCCCA AACCCACCAC TCCATCCCC ACCTGTCCCC CTGGAGCTT GGAACGGCAC 4200  
 GAGATGATG CCAACCTGAT AATGAGTCCC AATGGGATCC CAGAGTACTA CGCTGAAGAA 4260

5  
10  
15  
20  
25  
30

GATGAGTTCT CAGGCTTGGG GACTGACACT GCAGTACCTA CGGAAGAGGC CTACGTTATA 4320  
TATGATGAAG ATTATGAATT TGAGACGTCA AGGCCACCAA CCACCACTGA GCCTTCGACC 4380  
ACTGCTACCA CACCGAGGGT GATCCAGAG GAAGGSCCA TCAGTTCCTT TCCTGAAGAA 4440  
GAATTTGATC TGGCTGGAAG GAAACGATT GTTGCTCCTT ACCTGACGTA CCTAAATAAA 4500  
GACCCATCAG CCCCCGTCTC TCTGACTGAT GCACTGGATC ACTTCCAAGT GGACAGCCTG 4560  
GATGAAATCA TCCCAATGA CCTGAAGAAG AGTGATCTGC CTCCCAGCA TGCTCCCCGC 4620  
AACATCACCG TGGTGGCGGT GGAAGGTTGC CACTCATTTG TCATTGTGGA TTGGGACAAA 4680  
GCCACCCGAG GAGATTGGT CACAGGTTAT TTGGTTTACA GTGCATCCTA TGAAGATTTC 4740  
ATCAGGAACA AGTTTTCCAC TCAAGCTTCA TCAGTAACCT ACTTGCCCAT TGAGAACCTA 4800  
AAGCCCAACA CGAGGTATTA TTTTAAAGTG CAAGCACAAA ATCCTCATGG CTACGGACCT 4860  
ATCAGCCCTT CGGTCTCATT TGTCACGAA TCAGATAATC CTCTGCTTGT TGTGAGGCC 4920  
CCAGGCGGTG AGCTATCTGG ATCCCATTCG CTTTCAAACA TGATCCAGC TACACGGACT 4980  
GCCATGGAGC GCAATATGTG AAGCGCACGT GGTATCGAAA GTTCGTGGGA GTTGTCTTT 5040  
GTAATTCAC T GAGGTATAAA ATCTACCTCA GTGACAACT GAAAGATACA TTCTACAGCA 5100  
TTGGAGACAG CTGGGGAAGA GGTGAAGACC ATTGCCAATT TGTGGATTCA CACCTTGATG 5160  
GAAGAACAGG GCCTCAGTCC TATGTAGAAG CCTCCCTAC TATTCAAGC TACTATCGCC 5220  
AGTATCGTCA GGAGCCTGTC AGGTTTGGGA ACATCGGCTT CGGAACCCCT TACTACTATG 5280  
TGGGCTGGTA CGAGGTGGGG GTCTCCATCC CTGGAAGTG GTAATCACAG GACCGTCATG 5340  
CTGCAAGCTT GCCCTGCCCA GCCCCACCAA CTAAGTGCCT CTAGGGGCTG TGAGCAAGA 5400  
CAGCCAGCAT GCTCAGCCCC GCTGCCCTAG GTGCCAGGAA GGTACAGAT GGACACTGGC 5460  
CATTCTGGTC TCTCAGTCTG GGAACCTCAGT CCACTTCTT GGCTGAGCA ATGACAGGA 5520  
TTCAGTTTGT CTGTTAACTT TGCTTCTCTA CTTTCTTTT TTTGTTTGT ATAGCACATC 5580  
CCAGAGACAT CAGAAACCG CAACGTATTG AGTGTGATT CCCAGACTT TTAGGCATGA 5640  
AATTGCGGAT TCTCAGTATT TCCAGGAATA GCATATGCAC GCTGTTCTTG CTTCATGGA 5700  
TGCTACATCT TTTCTGTTT TCTCATTTG GATTCTCTCA AAATAACTG AATTAAAGCT 5760  
TCAGGTCCTT TTGTATGAG TAGAAAGGAA TTATTAATAA CACCACCAA GAAATAAAT 5820  
ATATCCTACT TGAAATTAC TCTATGACT TACCACATGC TAGAATAAAT GTATCAAATC 5880  
TTATTTGTAA ATTCTCAAT TTGATATATA TATGATATA TGCATATACA TATCCACACT 5940  
TGCTGCAAG AATATTGATT AAAATTGCTA AATTGTACT TGTTCACCA AAAAAA 6000  
AAAAAA

Seq ID NO: 60 Protein sequence  
Protein Accession #: Eos sequence

35  
40  
45  
50  
55  
60  
65

1 11 21 31 41 51  
MFGTKLRTG APADYRVILK TSQDELDVDP DDISVRVMS QSVLVSWVDP VLEKQKKVVA 60  
SRQYTVRYRE KGLARWDYK QLANRRVLIE NLIPDTVYEF AVRISQGERD GKWSTSVFQR 120  
TPESAPTTAP ENLANVWPVNG KPTVVAASWD ALPETEGVKV VCLLDITGLFS VSPFQPSAKS 180  
FQNTFFHTPR LSNHLEQSPS PILETLLLPW MWVCSLGNAI FSKSGPQTGE AWDLTPKPSL 240  
SLCQCECST QHDFSLAYL IDIQTKQVNK DPQLEGSVFG PCFLFYFLTF MLDIGGFSFI 300  
MCYEDPVSSL TGNLSKSVAA SKADVQONTE DNGKPEKPEP SSPSPRAPAS SQHPSVPASP 360  
QGRNAKDLIL DLKNIKILANG GAPRKPQLRA KKAELDLQS TEITGEEELG SREDSPMSPS 420  
DTQDQKRLR PPSRHGSHV APGRTAVRAR MPALPRREGV DKPGFSLATQ PRPGAPPSAS 480  
ASPAHASTQ GTSRHPSLPA SLANDNLVDS DEDERAVGSL HPKGAFAQPR PALSPSRQSP 540  
SSVLDRSSV HPGAKPASPA RRTPHSGAAE EDSSASAPPS RLSPPHGGSS RLLPTPHLS 600  
SPLSKGKGKG EDAPATNSNA PSRSTMSSSV SSSLSSRTQV SEGAEASDGE SHGDGDREDG 660  
GRQAEATAQT LRARPASGHF HLLRHKPFPA NGRSPSRFSI GRGPRLPQSS SPQSTVPSRA 720  
HPRVPSHSDS HPKLSGSHG DEEDEKPLPA TVVNDHVPSS SRQPSRGWE DLRRSPQSGA 780  
SLHRKEPIPE NPKSTGADTH PQGKYSSLAS KAQDVQQSTD ADTEGHSPLA QPGSTDRHAS 840  
PARPPAARSQ PPTSTVPRMT PGRAPEQQPP PPVATSQHHP GPQSRDAGRS PSQPRLSLTQ 900  
AGRPRPTSQ RSHSSSDPYT ASSRGMLEPTA LQNDQEDAQG SYDDSTEVE AQDVRAPAHA 960  
ARAKEAAASL PKHQVESPT GAGAGGDHRS QRGHAAAPAR PSRPGGPQSR ARVPSRAAPG 1020  
KSEPPSKRFL SSKSQSVSA EDEEEDAGF PKGKEDLLS SSVKWPSSS TPRGGKDADG 1080  
SLAKEEREP AIALAPRGSL APVKRPLPPP PGSSPRASHV PSRPPPSRAA TVSPVAGTHP 1140  
WFRYTTTRAP GHFTSTPMLS LRQRMHARF KNLSRQPAR PSYRQYNGR PNVEGKVLPG 1200  
SNGKPNQRI INGPQGTQKV VDLDRGLVLN ABGRYLQDSH GNPLRIKLG DGRTIVDLEG 1260  
TPVSPDGLP LFGQGRHGT LANAQDKPIL SLGGKPLVGL EVIKKTHPP TTTMQPTTTT 1320  
TLPPTTTTPT PTATTMQPT TTTTLPPTT PRPTTATRR TTTTRPTTT RTTTRTTT 1380  
TPKPTTPTPT CPPGTLERHD DGNLIMSSN GIPECYAED EFSGLETDTA VPTEEAIVYI 1440  
DEDEYEFESR PPTTEPSTT ATTPRVIEE GAISFFEEE FDLAGRKRIV APYVTYLNKD 1500  
PSAPCSLTD LDHPQVDSL DIIIPNDLKS DLPPHAPRN ITTVAVEGCH SFVIVDWDKA 1560  
TPGDLVTGYL VYSASYEDFI RNKFTQASS VTHLPFENLK PNTRYVFKVQ AQNPHGVGPI 1620  
SPSVSVFTES DNPLLVVRPP GGELSGSHSL SNMIPATRTA MDGNM

Seq ID NO: 61 DNA sequence  
Nucleic Acid Accession #: NM\_022743  
Coding sequence: 128..1237

70  
75  
80

1 11 21 31 41 51  
GTGGATTTTA GAGATACCTC CCTCTCTCT GCTCAGCTGC CTTCGAGTAA TTAACCTCT 60  
TCTCTGCTGC AACACCCCTA CTGTTCTCCG TGTATTGGCT TTTCTGGGCA GCAGGAAGGA 120  
AAAGCTGATG CGATGCTCTC AGTGCCTCGT CGCCAAATAC TGTATGCTA AGTGTGAGAA 180  
AAAAGCTTGG CCAGACACCA AGCGGGAATG CAAATGCCTT AAAAGCTGCA AACCAGATA 240  
TCTCTCAGAC TCCGTTGAC TTTCTGGCAG AGTTGTCTTC AAACCTATGG ATGGAGCACC 300  
TTCAGATCA GAGAAGCTTT ACTCATTTTA TGATCTGGAG TCAATATTA ACAAACTGAC 360  
TGAAGATAAG AAAGAGGGCC TCAGGCAACT CGTAATGACA TTTCAACATT TCATGAGAGA 420  
AGAAATACAG GATGCTCTC AGCTGCCACC TGCCCTTGAC CTTTGTGAAG CCTTTGCAAA 480  
AGTATCAGT AACTCTTTCA CCATCTGTAA TGCGGAGATG CAGGAAGTTG GTGTTGGCCT 540  
ATATCCCACT ATCTCTTTGC TCAATCACAG CTGTGACCCC AACTGTTOGA TTGTGTTCAA 600  
TGGGCCCCAC CTCTTACTGC GAGCAGTCCG AGACATGAG GTGGGAGAGG AGCTCACCAT 660  
CTGCTACTCG GATATGCTGA TGACCAGTGA GGAGCGCCGG AAGCAGCTGA GGGACAGTA 720  
CTGCTTTGAA TGTGACTGTT TCCGTTGCCA AACCAGGAGC AAGGATGCTG ATATGCTAAC 780

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

TGGTGATGAG CAAGTATGGA AGGAAGTTCA AGAATCCCTG AAAAAAATTG AAGAACTGAA 840  
GGCACACTGG AAGTGGGAGC AGGTTCTGGC CATGTGCCAG GCGATCATAA GCAGCAATTC 900  
TGAACGGCTT CCCGATATCA ACATCTACCA GCTGAAGGTG CTCGACTGCG CCATGGATGC 960  
CTGCATCAAC CTCGGCCTGT TGGAGGAAGC CTGTCTCTAT GGTACTCGGA CCATGGAGCC 1020  
ATACAGGATT TTTTCCAG GAAGCCATCC CGTCAGAGGG GTTCAAGTGA TGAAGTTGG 1080  
CAAACTGCAG CTACATCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140  
TGATATTATG AGAGTGACAC ATGGCAGAGA ACACAGCCTG ATTGAAGATT TGATTCTACT 1200  
TTTAGAAGAA TGGCAGGCCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAATA 1260  
CGCGTGTGT CTTTGTGAA TGCTTATTG AGGTACACA CTCTATGCTT TGTTAGCTGT 1320  
GTGAACCTCT CTTATTGAA ATTCTGTTCC GTGTTTGTGT AGGTAAATAA AGGCAGACAT 1380  
GGTTTGCAA CCACAAGAA CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAC 1440  
ATTTGGTTGA GGATGCCAAA AAAAAAATA AAAAAA

Seq ID NO: 62 Protein sequence  
Protein Accession #: NP\_073580

1 11 21 31 41 51  
MRCQCRVAK YCSAKCKKA WPDHKRECKC LKSKCPYPFP DSVRLLRGVV FKLMGAPSE 60  
SEKLYSFYDL ESNINKLTED KKEGLRQLVM TFQHFMRREEI QDASQLPPAF DLFEAFKVI 120  
CNSFTICNAE MOEVGVGLYP SISLNLHSCD PNCSTVFNPGP HLLLRVRDI EVGEELTICY 180  
LDMLMTSEER RKQLRDQYCF ECDPCRCQTO DKDADMLTGD EQVWKEVQES LKIEELKAH 240  
WKWEQVLAMC QAIISNSER LPDINIYQLK VLDCCAMDACI NLGLLEALP YGTRTMEPYR 300  
IFFPGSHFVR GVQVMKVGL QHQGMFPQA MNLRLAFDI MRVTHGREHS LIEDLILLE 360  
ECCANIRAS

Seq ID NO: 63 DNA sequence  
Nucleic Acid Accession #: NM\_003014.2  
Coding sequence: 238..648

1 11 21 31 41 51  
GGCGGGTTCG CGCCCCGAAG GCTGAGAGCT GGCGCTGCTC GTGCCCTCTG TGCCAGACGG 60  
CGGAGCTCCG CGGCGCGACC CGCGGCCCCC GCTTTGCTGC CGACTGGAGT TTGGGGGAAG 120  
AAACTCTCCT CGCGCCGAGA AGATTCTTTC CTCGCGCAAG GGACAGCGAA AGATGAGGGT 180  
GGCAGGAAGA GAAAGCGGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240  
TTCCTCTCCA TCCTAGTGGC GCTGTGCTG TGGCTGCACC TGGCGCTGGG CGTGCAGGGC 300  
GCGCCCTGCG AGGCGGTGCG CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCACGCGG 360  
ATGCCCAACC ACCTGCACCA CAGCACGCGA GAGAAGCGCA TCCTGGCCAT CGAGCAGTAC 420  
GAGGAGCTGG TGGAGCTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTCTG TGCCATGTAC 480  
GCGCCCATTT GCACCTGGGA GTTCTGTCAC GACCTATCA AGCGGTGCAA GTCCGTGTGC 540  
CAACGCGCGC GCGACGACTG CGAGCCCTTC ATGAAGATGT ACAACCAAG CTGGCCCGAA 600  
AGCCTGGCCT GCGAGGAGCT GCCTGTCTAT GACCGTGCGG TGTGCATTTC GCCTGAAGCC 660  
ATCGTCACGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720  
CAGGAAAGGC CTCCTGATGT TGAAGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGTAAA 780  
AAGGTGAAGT GAACTTTGGC AACGTATCTC AGCAAAAAC ACAGCTATGT TATTATGCC 840  
AAAATAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGTG GGATGTAAA 900  
GAGATCTTCA AGTCTCTATC ACCATCCCTC CGAATCAAG TCCCGCTCAT TACAATTTCT 960  
TCTTGCCAGT GTCCACACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020  
CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080  
AAAAGATATA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140  
AAGAAACAGC CCGGCGCAC CAGTCTAGT AATCCCCCA AACCAAGGG AAGCCCTCT 1200  
GCTCCCAACC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGGCCA GAAGAGAACA 1260  
AACCAGAAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGGA GACTTCCGAC TTCTTACAG 1320  
GATGAGGCTG GGCATGTGCT GGGACAGCCT ATGTAAGGCC ATGTGCCCCT TGCCCTAACA 1380  
ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTTCTTAAGG CTATGCTTCA 1440  
GTTTTTCTTT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT 1500  
GAGTTAAAGC TGGTGGAAAA GGCTTATTGC ATTGCATTCA GAGTAACCTG TGTGCATCT 1560  
CTAGAAGAGT AGGGAATAATA ATGCTTGTTA CAATTGACCC TAATATGTGC ATTGTAAAAT 1620  
AATGGCCATA TTTCAAACAA AACACGTAAT TTTTATACAG TATGTTTTAT TACCTTTTGA 1680  
TATCTGTTGT TGCAATGTTA GTGATGTTTT AAAATGTGAT GAAAAATATA TGTTTTAAAG 1740  
AAGGAACAGT AGTGGAAATG ATGTTAAAG ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800  
TTTTTGTGAT GAAAGGGGAT TTTTGAAGA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860  
TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTATAGT AGAAACTTAA AAACAAAAAT 1920  
AATAATAAAG AAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATTG CTGTTTTTTG 1980  
GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACCAGAA 2040  
ACAGTGAGTT TGTCTGTACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100  
ATTTATACC CACAAGAGAG GTATGTCATC CATCTTACTT CCCAGGACAT CCACCTGAG 2160  
AATAATTGTA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220  
TTAAATATTT TCTTTGCCA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280  
AAGTTGTAGT TCCACTCTG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340  
AAAAAGAACT TATTTGCAGC ATTTATCAAA CAAATTTTCA AATGTGGAGC AATGGAGGCC 2400  
ATTTATTTTA AAAACAATT TTATTGGCCT TTGTCTAACA CAGTAAGCAT GTATTTTATA 2460  
AGGCATTCAA TAAATGCACA ACGCCCAAG GAAATAAAAT CCTATCTAAT CCTACTCTCC 2520  
ACTACACAGA GGTAACTACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580  
GCACCTATAA ATCATTGTA ACAATAAATA CTAGGAACCT GTATACATGT GTTTCATAAC 2640  
CTGCTCTCTT TGCTTGGCCC TTATTGAGA TAAGTTTTC TGTCAGAAA GCAGAAACCA 2700  
TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760  
TATTGGATAC TTAGGTGGTT TCTTCACTGA CRATCTGAA TAAACATCTC ACCGGAATTC

Seq ID NO: 64 Protein sequence  
Protein Accession #: NP\_003005.1

1 11 21 31 41 51

5 MFLSILVALC LMLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60  
YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPKCKV CQRARDDCEP LMKMYNHSWP 120  
ESLACDELFP YDRGVCSISPE AIVTDLPELV KWIDITPDMV VQERPLDVDC KRLSPDRCKC 180  
KKVKPTLATY LSNYSYVIH AKIKAVQSRG CNEVTTVVVD KEIFKSSSPI PRTQVPLITN 240  
SSQCPHILP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300  
KKKTAGRTSR SNPPKPKGKP PPKPASPKK NIKTRSAQKR TNPKRV

10 Seq ID NO: 65 DNA sequence  
Nucleic Acid Accession #: BC010423  
Coding sequence: 248..1780

15 1 11 21 31 41 51  
CACAGCGTGG GAAGCAGCTC TGGGGGAGCT CGGAGCTCCC GATCACGGCT TCTTGGGGGT 60  
AGCTACGGCT GGGTGTGTAG AACGGGGCCG GGGCTGGGGC TGGTCCCTT AGTGGAGACC 120  
CAAGTCCGAG AGGCAAGAAC TCTGCAGCTT CTTGCTTCT GGGTCAGTTC CTTATTCAAG 180  
TCTGCAGCCG CCTCCAGGGG AGATCTCGGT GGAACCTCAG AACCGCTGGG CAGTCTGCCT 240  
TTCAACCATG CCTCTGTCCC TGGGAGCCGA GATGTGGGGG CCTGAGGCTC GGCTGCTGCT 300  
20 GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCGCGG GGTGAGCTGG AGACCTCAGA 360  
CGTGCTAACT GTGTGTCTGT GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC 420  
CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGTGGGAC GCGGCGCAAG GCGCCACAGG 480  
ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC CCGGCTTACG AGGGCCGGGT 540  
GGAGCAGCCG CCGCCCCCAC GCAACCCCTT GGAAGGCTCA GTGCTCCTGC GCAACGCACT 600  
25 GCAGGCGGAT GAGGGCGAGT ACGAGTCCCG GTTCAGCACC TTCCCGCCCG GCAGCTTCCA 660  
GGCGCGGCTG CGGCTCCGAG TGCTGGTGCC TCCCTGCCCC TCACTGAATC CTGTCTCAGC 720  
ACTAGAGAGG GGCCAGGGCC TGACCTGGC AGCTCTCTGC ACAGCTGAGG GCAGCCACGC 780  
CCCCAGCGTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCCAGCGGTT CCTTCAAGCA 840  
CTCCCGCTCT TTCCCGCTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG 900  
30 GCAGCCATG ACTTGTGTGG TGTCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA 960  
CATCTCCAC GTGTCTTTC TTGCTGAGG CTCTGTGAGG GGCCTTGAAG ACCAAAATCT 1020  
GTGGCATT GGCAGAGAAG GAGCTATGCT CAAGTGCTG AGTGAAGGGC AGCCCCCTCC 1080  
CTCATACAAC TGGACACGGC TGGATGGGCC TCTGCCAGT GGGGTACGAG TGGATGGGGA 1140  
CACTTGGGCT TTTCCTCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTCTG 1200  
35 CAATGAGTTC TCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA 1260  
CTCTGGGAAG CAGGTGGACC TAGTGTACG CTCGGTGGTG GTGGTGGGTG TGATCGCGCG 1320  
ACTCTGTGTC TGCCCTTCTGG TGGTGGTGGT GGTGCTCATG TCCCGATACC ATCGGCGCAA 1380  
GGCCCGCAGC ATGACCCAGA AATATGAGGA GGAGCTGACC CTGACCCAGG AGAACTCCAT 1440  
40 CGGAGGCTG CATTCCTCAT ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT 1500  
GAGAGCCGAG GGCCACCCCTG ATAGTCTCAA GGACAACAGT AGCTGCTCTG TGATGAGTGA 1560  
AGAGCCCGAG GGCCCGAGT ACTCCAGCT GACCAAGGTG AGGAGATAG AAACACAGAC 1620  
TGAAGTCTG TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGC ATGAAGGCAT 1680  
CAAAACAGCC ATGAACCAT TTGTTGAGGA GAATGGGACC CTACGGGCCA AGCCCAAGCG 1740  
45 CAATGGCATC TACATCAATG GGCGGGGACA CTTGGTCTGA CCCAGGCTG CCTCCCTTCC 1800  
CTAGGCTGG CTCTTCTGTG TGACATGGGA GATTTTAGCT CATCTTGGGG GCCTCCTTAA 1860  
ACACCCCATC TCTTGGGGA AGATGCTCCC CATCCCACTG ACTGCTTGAC CTTTACCTCC 1920  
AACCCTTCTG TTCATCGGGA GGGCTCCACC AATTGAGTCT CTCCCACCAT GCATGCAGGT 1980  
CACTGTGTGT GTGCATGTGT GCCTGTGTGA GTGTGACTG ACTGTGTGTG TGTGGAGGGG 2040  
50 TGAAGTCCG TGGAGGGGTG ACTGTGCTCG TGGTGTGTAT TATGCTGTCA TATCAGAGT 2100  
AAGTGAATG TGTGTATGT GCCACGGGAT TTGAGTGGT GCGTGGGCAA CACTGTGAGG 2160  
GTTTGGCGTG TGTGTATGT GGTGTGTGT GACCTCTGCC TGAAGGAAGA GGTATTCTCT 2220  
CAGACCCAGC AGCAGTATTA ATGATGCAGA GGTGGAGGA GAGAGGTGGA GACTGTGGCT 2280  
CAGACCCAGG TGTGCGGGCA TAGCTGAGC TGGAACTGCT CTCGGGTGTC AGGGAACTCT 2340  
55 TCTCCTACCA TTTCGGAGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA 2400  
GAGGCTTGAA CTGTTACAGA AGCCCTCTGC CCTCTGGTGG CCTCTGGGCC TGCTGCATGT 2460  
ACATATTTC TGTAAATATA CATGCGCGG GAGCTTCTTG CAGGAATACT GCTCCGAATC 2520  
ACTTTTAAT TTTTCTTTT TTTTCTTCTG CCCTTTCAT TAGTGTATT TTTTATTAT 2580  
TTTATTTTT ATTTTCTTT AGAGTTTGTG TCCAGCCTGG ACGATATAGC CAGACCTCTG 2640  
CTGTAAAAAA ACCAAAACCC AAAAAAATA AAAAAAATA

Seq ID NO: 66 Protein sequence  
Protein Accession #: AAH10423

65 1 11 21 31 41 51  
MFLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDEV TVVLGQDAKL PCFYRGDSGE 60  
QVGQVAVARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNVAQA 120  
DEGEYECRVV TFPAGSFQAR LRLRVLPVPL PSINPGPALE EQGLTLAAS CTAEGSPAPS 180  
70 VTWDEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL IQDQRITHIL 240  
HVSFLAEASV RGLEDQNLWE IGREGAMLC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL 300  
GFPLTTEHS GIYVCHVSNE FSRDSQVTV DVLDPOEDSG KQVDLVASV VVVGVIAALL 360  
FCLLVVVVVL MSRYHRRKAQ QMTQRYEEL TLTRENSIRR LHSHTDPRS QPEESVGLRA 420  
EGHPDLSKDN SSCSVMSEEP EGRSYSTLT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ 480  
75 AMNHVQENG TLRAKPTGNG IYINGRHLV

80 Seq ID NO: 67 DNA sequence  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274..1782

1 11 21 31 41 51  
CGCGGGGCGC GAGTCCGCG GGGCCTCGCG GGACGCGGGC AGTGCAGAGA CCGCGGCGCT 60  
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120  
GTGAAAGGAA AGGAAGATCA TTTTCATGCT TGTGATAAAA GGTTCAGACT TCTGCTGATT 180

5  
10  
15  
20  
25  
30

CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
TGCCATAAGT GAGAAGCAAA CTTCTCTGAT AACATGCTTT TGGGAAGTGC AGGAAAAATTA 300  
AATGTGGGCA CCAAGAAAGA GGTAGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360  
TGGGTGTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTCTG GGTCACTTCT 480  
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACACTCCCAT TCCTCATCAA 540  
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600  
CTGCCCTCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660  
ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG 720  
TATAAAAGAC AAGAAACCCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780  
ATTCCTCTCG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
TCAGGCTCTC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900  
ATTGGAAAGG GTCGTATGAG GGAAGTTTGG ATGGGAAAGT GGGGTGCGGA AAGGTAGCT 960  
GTGAAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020  
ACAGTGTGTA TGAGGACATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080  
GGGTCTGGA CCAAGTTGTA CTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
TATCTGAAGT CCACCACCT AGACGCTAAA TCAATGCTGA AGTTAGCTTA CTCTCTGTC 1200  
AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260  
CATCGAGATC TGAAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320  
GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
ACTCGAGTTC GCACCAAGC CTATATGCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440  
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTTGGGAG 1500  
GTTGTAGAGA GATGTATATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560  
CTAGTCCCA GLPCLVQRTI AKQIQMVKQI GKGRYGEVVM GKWRGEKVAV KVFFTEEAS 1620  
CGCCCTCAT TCCCAACCCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAACTC 1680  
ATGACAGAA GCTGGGCTCA CAATCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740  
ACACTTGCCA AAATGTCAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800  
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTGTCTTC CCAGTGGGTT CAGACCTCAC 1920  
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
TCTGTTGTA GCGGAGAAA CCGTTGGTA ACTTGTCAA GATATGATGC AT

Seq ID NO: 68 Protein sequence

Protein Accession #: NP\_001194

35  
40  
45

1 11 21 31 41 51  
MLLSRAGKLN VGTIKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60  
DSGLFVVTSGLGLEGSDPQ CRDTPIPHR RSIECCTERN ECKDLHPTL PPLKNRDFVD 120  
GEIRERALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
EQSQSSSGSS GLPCLVQRTI AKQIQMVKQI GKGRYGEVVM GKWRGEKVAV KVFFTEEAS 240  
WFRTEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTILDAKS 300  
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSNILV KKNGTCCIAV LGLAVKFISD 360  
TNEVDIPFNT RVGTRKYMPP EVLDESILNRN HFQSYIMADM YSFLILNEWV ARRCVSGGIV 420  
EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS 480  
RLTALRVKKT LAKMSSESDI KL

Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 166..1737

50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
TTGGGGGTTT ATTCTCTTCC CTTCTAACTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60  
AGTGCAGTAG TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCTCA ACTCAAGCAA 120  
TCCTCCCAAC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180  
TTAAAGCTTT GTTCCAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240  
GCGGTAGCTG TTTCAATTTT CTTCGTGAA GTCTTCACT ACAGCATCAT CAAGACATTT 300  
GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360  
ATAATCTCAA TCTGTGTGTT TGTCTTAA CA TTTTCAGCTC CCCTCGCCAC AGTCTGAGC 420  
AATCGTTTTC GACACCGTCT GGTAGTATG TTGGGGGGGC TACTTGTGAG CACCGGGATG 480  
GTGGCGCGCT CCTTCTCACA AGAGGTTTCT CATATGTAG TCGCATCGG CATCATCTCT 540  
GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600  
AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT 660  
TTGCAACCCG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CTCTCTCTC 720  
TTGGGGCTAC TACAGTTAAA CATTGTATC TTCGGAGCAC TGCTCAGACC CATCTTTATC 780  
AGAGGACCCG CGTCACCGAA AATAGTCATC CAGGAAATC GGAAGAAGC GCAGTATATG 840  
CTTGAAATG AGAAAAACAG AACCTCAATA GACTCCATTG ACTCAGAGT AGAAGTAACT 900  
ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCACATG 960  
CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAGGCCCC GCTATTAGAC 1020  
TTCTCATTTT TGAAGAGAAA AAGTTTATT TGTATGAT TATTGTGCT CTTTGAACA 1080  
CTGGGATTCT TTGCACCTTC CTGTATATC ATTCTCTG GCAATTAGT GGGCATTGAC 1140  
CAGGACCGCG CTGCTTTTAT ATTATCTACG ATGGCCATTG CAGAAGTTTT CGGAAGGATC 1200  
GGAGCTGGTT TTGTCCTCAA CAGGGAGCCC ATTCGTAAGA TTTACATTGA GCTCATCTGC 1260  
GTCATCTTAT TGACTGTGTC TCTGTTTGCC TTTACTTTTG CTACTGAATT CTGGGGTCTA 1320  
ATGTCATGCA CATATTTTTT TGGGTTTATG GTTGAACAA TAGGAGGGAC TCACATTCCA 1380  
CTGCTTGCTG AGGATGATGT CGTGGGCATT GAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440  
ATCTTCATTC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGTGGAC 1500  
CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCTGCGCAG CTGGCATGGC CCGGCTGCT 1560  
GTGTGCTCG CCTGCTGAG ACCGTGTAAG ATGGGACTGT GCCAGCATCA TCACTCAGGT 1620  
GAAACAAAGG TAGTGAGGCA TCGTGGGAAG ACTTTACAGC ACATACCTGA AGACTTTCTG 1680  
GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAATGGAGCC GGTATGACAC 1740  
ACTTTCTTAC AACACAGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCAACGGGG 1800  
ACACAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAACTACA TTTTAAAGG 1860

5  
10  
15  
20  
25

```

AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGT TTGTTTGT TTGTTTAAAGC 1920
TTTTTTTTTT TGTCTGTTTT TAAAGCCAAA ACAAAAACA ACCAAGCACT CTCCATATA 1980
TAAATCTGGC TGTATTCAAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTTACA 2040
TTCCGATATT AAAATAGTGA CATGAAGTGG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100
TAAATGATT TCTTTTTTCT TTTTCTTCT TCCTATGGTC TTGCTGTAAT AAACACTCT 2160
CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAATGAA ATTGGCCAGT C

```

Seq ID NO: 70 Protein sequence  
Protein Accession #: Eos sequence

10  
15  
20  
25

```

1      11      21      31      41      51
|      |      |      |      |      |
MTQNKLKLC S KANVYTEVPD GGNWNAVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESN 60
SRISWIIISIC VFVLTFSAPL ATVLNRFH RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120
IGIISGLGYC FSFLPTVTIL SQYFGKRRI VTAFASTGEC PAVFAPAPAI MALKERIGWR 180
YSLLFVGLLQ LNVIFGALL RPIFIRGPAS PKIVIQENRK EAQVMLENEK TRTSIDSIDS 240
GVELTTSFKN VPTHNLLELE PKADMQQVLV KTSRPPSEKK APLLDPSILK EKSFIYALF 300
GLPATLGFFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
IELICVILLT VSLFATTFAT EFWGLMSCSI PFGFMVGTIG GTHIPLLAED DVVGIEKMSS 420
AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
RHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

```

Seq ID NO: 71 DNA sequence  
Nucleic Acid Accession #: NM\_004694  
Coding sequence: 166..1737

30  
35  
40  
45  
50  
55  
60  
65

```

1      11      21      31      41      51
|      |      |      |      |      |
TTGGGGGTTT ATTCTCTTCC CTCTAACTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60
AGTGCAGTAG TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCCTCA ACTCAAGCAA 120
TCTCCCAACC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180
TTAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
GGGGTAGCTG TTTCAATTTT CTTCGTTGAA GTCTTCACCT ACGGCATCAT CAAGACATTT 300
GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
ATAATCTCAA TCTGTGTGTT TGTCTTAAAC TTTTCAGCTC CCTCGCCAC AGTCTTGAGC 420
AATCGTTTCG GACACCGTCT GGTAGTGATG TTGGGGGGGC TACTTGTGAG CACCGGGATG 480
GTGGCCGCTC CTCTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540
GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600
AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT 660
TTCGACACAG CAATCATGGC TCTGAAGGAG CGCATTTGCT GGAGATACAG CCTCCTCTTC 720
GTGGGCTTAC TACATTTAAA CATTGTCTATC TTGGGAGCAC TGCTCAGACC CATCATATC 780
AGAGGACCAG CGTCAACGAA AATAGTCATC CAGGAAAATC GGAAGAAGC GCAGTATATG 840
CTTGAAGATG AGAAAAACAG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT 900
ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCAGACATG 960
CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020
TTCTCCATTG TGAAGAGAAA AAGTTTATT TGTATGCAAT TATTTGGTCT CTTTGCAACA 1080
CTGGGATTCT TTGACCTTTC CTGTATCATC ATTCTCTGCG GATTAGTCT GGGCATTGAC 1140
CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGGCCATTG CAGAAGTTT CCGAAGGATC 1200
GGAGCTGGTT TTGTCTCAA CAGGAGCCCC ATTCGTAAGA TTTACATTGA GCTCATCTGC 1260
GTCACTTATG TGAAGTGTG TGTGTTTGCC TTTACTTTTG CTACTGAATT CTGGGGTCTA 1320
ATGTCACTGA GCATATTTT TTGGTTTATG GTTGGAAACA TAGGAGGACT CACATTCCAC 1380
TGCTGCTGTA AGATGATGTC GTGGGCATTG CAGAAGATGT CTCTCAGCAG TGGGGTCTAC 1440
ATCTTCATTC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCTGCGCAG CTGGCATGGC CCTGGCTGCT 1560
GTGTGCTCG CCCTGTGTAG ACCGTGTAAG ATGGGACTGT GCCAGCGTCA TCACTCAGGT 1620
GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACITTACAGG ACATACCTGA AGACTTTCTG 1680
GAAATGATC TTGCAAAAAA TGAGCACAGA GTTCAGTGC AAATGGAGCC GGTATGACAC 1740
ACTTCTTAC AACACAGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAACGGGG 1800
ACCAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTT CAAAACCTACA TTTTAAAGGG 1860
AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGT TTGTTTGT TTGTTTAAAGC 1920
TTTTTTTTTT TGTCTGTTTT TAAAGCCAAA ACAAAAACA ACCAAGCACT CTCCATATA 1980
TAAATCTGGC TGTATTCAAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTTACA 2040
TTCCGATATT AAAATAGTGA CATGAAGTGG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100
TAAATGATT TCTTTTTTCT TTTTCTTCT TCCTATGGTC TTGCTGTAAT AAACACTCT 2160
CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAATGAA ATTGGCCAGT C

```

Seq ID NO: 72 Protein sequence  
Protein Accession #: NP\_004685

70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
MTQNKLKLC S KANVYTEVPD GGNWNAVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESN 60
SRISWIIISIC VFVLTFSAPL ATVLNRFH RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120
IGIISGLGYC FSFLPTVTIL SQYFGKRRI VTAFASTGEC PAVFAPAPAI MALKERIGWR 180
YSLLFVGLLQ LNVIFGALL RPIFIRGPAS PKIVIQENRK EAQVMLENEK TRTSIDSIDS 240
GVELTTSFKN VPTHNLLELE PKADMQQVLV KTSRPPSEKK APLLDPSILK EKSFIYALF 300
GLPATLGFFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
IELICVILLT VSLFATTFAT EFWGLMSCSI PFGFMVGTIG GLTFHLLKM MSWALQKMSS 420
AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
RHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

```

Seq ID NO: 73 DNA sequence  
Nucleic Acid Accession #: NM\_002184.1  
Coding sequence: 256..3012

1 11 21 31 41 51  
 5 GAGCAGCCAA AAGGCCCGCG GAGTCGCGCT GGGCCGCCCC GGGCAGCTG AACCGGGGGC 60  
 CGCGCTGCCC AGGCCGACGG GTCTGGCCCA GCCTGGCGCC AAGGGGTTG TGCGCTGTGG 120  
 AGACGGGAG GGTGAGGCG GCGCGGCCCT AGTGAAACCC AATGGAAAA GCATGACATT 180  
 TAGAAGTAGA AGACTTAGCT TCAAAATCCCT ACTCCTTAC TTACTAATT TGTGATTG 240  
 AAATATCGC GCAAGATGTT GACGTTGAC ACTTGGGTAG TGCAAGCCTT GTTTATTTC 300  
 CTCACCACTG AATCTACAGG TGAACCTTCTA GATCCATGTG GTTATATCAG TCCTGAATCT 360  
 CCAGTTGTAC AACTTCATTC TAATTTCACT GCAGTTTGTG TGCTAAAGGA AAAATGTATG 420  
 10 GATTATTTTC ATGTAAATGC TAATTACATT GTCTGGAAAA CAAACCATTT TACTATTCTC 480  
 AAGGAGCAAT ATACTATCAT AAACAGAAAC GCATCCAGTG TCACCTTTAC AGATATAGCT 540  
 TCATTAAATA TTCAGCTCAC TTGCAACATT CTTACATTG GACAGCTTGA ACAGATGTT 600  
 TATGGAATCA CATATAATTC AGGCTTGCCCT CCAGAAAAAC CTAAAAATTT GAGTGTGATT 660  
 15 GTGACGAGG GGAAGAAAAA GAGGTGTGAG TGGGATGGTG GAAGGGAAAC ACACCTGGAG 720  
 ACAAACTTCA CTTTAAATC TGAATGGGCA ACACACAAGT TTGCTGATTG CAAAGCAAAA 780  
 CGTGACAGCC CCACCTCATG CACTGTTGAT TATTCTACTG TGTATTTTGT CAACATTGAA 840  
 GTCTGGGTAG AAGCAGAGAA TGCCCTTGGG AAGGTTACAT CAGATCATAT CAATTTTGAT 900  
 CCTGTATATA AAGTGAAGCC CAATCCGCCA CATAATTTAT CAGTGATCAA CTCAGAGGAA 960  
 20 CTGTCTAGTA TCTTAAATTT GACATGGACC AACCCAGTA TTAAGAGTGT TATAATACTA 1020  
 AAATATAACA TTCAATATAG GACCAAGAT GCCTCAACTT GGAGCCAGAT TCCTCTCTGAA 1080  
 GACACAGCAT CCACCTGATG TTCAATCACT GTCCAAGACC TTAACCTTT TACAGAAATAT 1140  
 GTGTTTAGGA TTCGCTGTAT GAAGGAAGAT GGTAAAGGAT ACTGGAGTGA CTGGAGTGAA 1200  
 GAAGCAAGTG GGATCACCTA TGAAGATAGA CCATCTAAAG CACCAAGTTT CTGGTATAAA 1260  
 25 ATAGATCCAT CCCATACCA AGGCTACAGA ACTGTACAAC TCGTGTGGAA GACATTGCCT 1320  
 CCTTTTGAAG CCAATGGAAA AATCTTGGAT TATGAAGTGA CTCTCAAG ATGGAAATCA 1380  
 CATTTACAAA ATTACACAGT TAATGCCACA AAACGTACAG TAAATCTCAC AAATGATCGC 1440  
 TATCTAGCAA CCCTAACAGT AAGAAATCTT GTTGGCAAAT CAGATGCAGC TGTTTTAACT 1500  
 ATCCCTGCCT GTGACTTCA AGCTACTCAC CCTGTAATGG ATCTTAAAGC ATTCCTCCAA 1560  
 30 GATAACATGC TTTGGGTGGA ATGGACTACT CCAAGGGAAT CTGTAAAGAA ATATATACTT 1620  
 GAGTGTGTG TGTATCAGA TAAAGCACCC TGTATCAGC ACTGSCAACA AGAAGATGGT 1680  
 ACCGTGCATC GCACCTATT TAAAGGGAAC TTAGCAGAGA GCAATGCTA TTTGATAACA 1740  
 GTTACTCCAG TATATGCTGA TGACCCAGGA AGCCCTGAAT CCATAAAGGC ATACCTTAAA 1800  
 CAAGCTCCAC CTTCCAAAGG ACCTACTGTT CGGACAAAAA AAGTAGGAA AAACGAAGCT 1860  
 35 GTCTTAGAGT GGGACCAACT TCCTGTTGAT GTTCAGATG GATTTATCAG AAATTATACT 1920  
 ATATTTTATA GAACCATCAT TGGAAATGAA ACTGCTGTGA ATGTGGATTG TTCCACACA 1980  
 GAATATACAT TGTCTCTTT GACTAGTGAC ACATTGTACA TGGTACGAAT GGCAGCATA 2040  
 ACAGATGAAG GTGGGAAGGA TGGTCCAGAA TTCACTTTAA CTACCCCAA GTTTGCTCAA 2100  
 GGAGAAATG AAGCCATAGT CGTGCTGTT TGCTTAGCAT TCCTATTGAC AACTCTTCTG 2160  
 40 GGAGTGTCTG TCTGCTTAA TAAGCGAGAC CTAATTAAAA AACACATCTG GCCTAATGTT 2220  
 CCAGATCCTT CAAAGAGTCA TATTGCCAG TGGTCACTC ACACCTCTCC AAGGCACAA 2280  
 TTTAATTCAA AAGATCAA GTATTGATG GCAATTTTCA CTGATGTAAG TGTGTGGAA 2340  
 ATAGAAGCAA ATGACAAAA GCCTTTTCCA GAAGATCTGA AATCATTTGA CCTGTTCAA 2400  
 AAGGAAAAA TTAATCTGA AGGACACAGC AGTGGTATTG GGGGGTCTTC ATGCATGTCA 2460  
 45 TCTCTAGGC CAAGCATTTT TAGCAGTGAT GAAATGAAT CTTACAAAA CACTTGGAGC 2520  
 ACTGTCCAGT ATTCTACCGT GGTACACAGT GGCTACAGAC ACCAGTTTCC GTCAGTCCAA 2580  
 GTCTTCTCAA GATCCGAGTC TACCCAGCCC TTGTTAGATT CAGAGGAGGC GCCAGAAGAT 2640  
 CTACAAATAG TAGATCATGT AGATGGCGGT GATGGTATT TGCCAGGCA ACAGTACTTC 2700  
 AAACAGAACT GCAGTCAGCA TGAATCCAGT CCAGATATTT CACATTTTGA AAGGTCAAAG 2760  
 50 CAAGTTTCAT CAGTCAATGA GGAAGATTTT GTTAGACTTA AACAGCAGAT TTCAGATCAT 2820  
 ATTTCACAAT CCGTGGATC TGGGCAATG AAAATGTTTC AGGAAGTTTC TGCAGCAGAT 2880  
 CGTTTGGTC CAGGTACTGA GGGACAAATG GAAAGATTG AAACAGTTGG CATGGAGGCT 2940  
 GCGACTGATG AAGGCATGCC TAAAGTTAC TTACCAGCA CTGTACGGCA AGGCGGCTAC 3000  
 ATGCCTCAGT GAAGGACTAG TAGTTCTGTC TACAACCTCA GCAGTACCTA TAAAGTAAAG 3060  
 CTAATATGAT TTTATCTGTG AATTC

Seq ID NO: 74 Protein sequence  
 Protein Accession #: NP\_002175.1

1 11 21 31 41 51  
 60 MLTLQWVVO ALFIPLTTES TGEILLPCGY ISPESPVVQL HSNFTAVCVL KEKCMDYFHV 60  
 NANYIVWKTN HFTIPKEQYT IINRTASSVT PTDIASLNQ LTCNLTFGQ LEQNVYGITI 120  
 ISGLPPEKPK NLSCIVNEKG KMRCEWDGGR ETHLETNFTL KSEWATHKFA DCKAKRDTPT 180  
 65 SCTVDYSTVY FVNIEVWVEA ENALGKVTSD HINFDPVYKV KPNPPHNLVS INSEELSSIL 240  
 KLWNPSPK SVIILKYNQ YRTKDASTWS QIPPEDTAST RSSFTVQDLK PFTEYVFRIR 300  
 CMKEDKGWY SDWSEEASGI TYEDRPSKAP SFWKIDPSH TGGYRTVQLV WKTLPPEAN 360  
 GKILDYEVTL TRWKSHLQNY TVNATKLTVN LTNDRYLATL TVRNLVGKSD AAVLTIPACD 420  
 FQATHFVMDL KAPPKDNMLW VEWTTPRESV KKYILEWCVL SDKAPCITDW QQEDGTVHRT 480  
 70 YLRGNLAESK CYLITVFPVY ADGPGSPESI KAYLKQAPPS KGPTVRTKKV GKNEAVLEWD 540  
 QLPVDVQNGF IRNYTIFYRT IIGNETAVNV DSSHTYETLS SLTSDTLYM RMAAYTDEGG 600  
 KDGEPTFTT PKFAQGEIEA IVVPVCLAPL LTTLLGLVFC FNKRDLIKHH IWPVDPDSK 660  
 SHIAQSPHT PPRINFPNSKD QMYSNGNFTD VSVVEIAND KKPFPEDLKS LDLFKKEKIN 720  
 TEGHSSGIGG SSCMSSSRPS ISSSDENESS QNTSSTVOYS TVVHSGYRHO VPSVQVPSRS 780  
 75 ESTQPLDSE ERPEDLQVLD HVDGGDLILP RQYQPKNCES QHESSPDISH PERSKQVSSV 840  
 NEEDFVRLKQ QISDHISQSC GSGQMKMFQE VSAADAFGPG TEGQVERFET VGMEAATDEG 900  
 MPKSYLQTV RQGGYMPQ

Seq ID NO: 75 DNA sequence  
 Nucleic Acid Accession #: NM\_022131  
 Coding sequence: 11..2878

1 11 21 31 41 51  
 80 TGCTGCGAGG ATGCTGCCTG GCGCGCTGTG CTGGGTGCCG CTCCTGCTGG CGCTGGGCGT 60



5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75

GGGGAGCGCG AGCGGCGGTG GCGGGGACAG CCGGCAGCGC CGCCTCCTCG CGGCTAAAGT 120  
 CAATAAGCAC AAGCCATGGA TCGAGACTTC ATATCATGGA GTCATAACTG AGAACAAATGA 180  
 CACAGTCATT TTGGACCCAC CACTGGTAGC CCTGGATAAA GATGCACCGG TTCCTTTTGC 240  
 AGGGGAAATC TGTGCGTTCA AGATCCATGG CCAGGAGCTG CCTTTGAGG CTGTGGTGCT 300  
 CAACAAGACA TCAGGAGAGG GCGCGCTCCG TGCCAAGAGC CCCATTGACT GTGAGTTGCA 360  
 GAAGGAGTAC ACATTTCATCA TCCAGGCCTA TGACTGTGGT GCTGGGCCCC ACGAGACAGC 420  
 CTGGA AAAAG TCACACAAGG CCGTGGTCCA TATACAGGTG AAGGATGTCA ACGAGTTTGC 480  
 TCCACCTTC AAAGAGCCAG CCTACAGGC TGTGTGACG GAGGGCAAGA TCTATGACAG 540  
 CATTCTGCAG GTGGAGGCCA TTGACGAGGA CTGCTCCCA CAGTACAGCC AGATCTGCAA 600  
 CTATGAAATG GTACACACAG ATGTGCTTT TGCCATCGAC AGAAATGGCA ACATCAGGAA 660  
 CACTGAGAAG CTGAGCTATG ACAAACAACA CCAGTATGAG ATCTGTGTGA CCGCTACGA 720  
 CTGTGGACAG AAGCCCGCTG CTCAGGACAC CTTGTGTCAG GTGGATGTGA AGCCAGTTTG 780  
 CAAGCCTGGC TGGCAAGACT GGACCAAGAG GATTGAGTAC CAGCCTGGCT CCGGAGCAT 840  
 GCGCCTGTTT CCCAGCATCC ACCTGGAGAC GTGCGATGGA GCGGTGTCTT CCCTCCAGAT 900  
 CGTCACAGAG CTGCAGACTA ATTACATTGG GAAGGGTGTG GACCGGAGGA CCTACTCTGA 960  
 GAAATCCCTT CAGAGCTTAT GTGGAGCCTC CTCTGGCATC ATTGAOCTCT TGCCATCCCC 1020  
 TAGCGCTGCC ACCAACTGGA CTGCAGGACT GCTGTGGAC AGCATGTAGA TGATCTTCAA 1080  
 GTTTGACGGC AGGCAGGGTG CCAAAATCCC CGATGGGATT GTGCCAAGA ACCTGACCGA 1140  
 TCAGTTACAC ATCACCATGT GGATGAAACA CGGCCCCAGC CCTGGTGTGA GAGCCGAGAA 1200  
 GGAAACCATC CTCTGCAACT CAGACAAAC CGAAATGAAC CGGCATCACT ATGCCCTGTA 1260  
 TGTGCACAC TGCAGCCTCG TCTTTCTCTT GCGGAAGGAC TTGACACAGG CTGACACCTT 1320  
 TCGCCCCGCG GAGTTCCTACT GGAAGCTGGA TCAGATTGTG GACAAAGAGT GGCACCTACTA 1380  
 TGTCTCAAT GTGGAGTTTC CTGTGGTAAC CTATACATG GATGAGCAAA CATATGAACC 1440  
 ATACCTGTGT ACCAAGACT GGCCCATTTCA TCCATCTCAC ATAGCCATGC AACTCAAGT 1500  
 CGCGCTGTGT TGGCAGGAG GAGAAGTCAC CAAACACAG TTTGCTCAGT TCTTTATCGG 1560  
 AAGCCTGCCC AGTCTCACCA TCCGCCCTGG CAAATGGAA AGCCAGAAGG TGATCTCCTG 1620  
 CCTGCAGGCC TGCAAGGAAG GCGTGACAT TAATTCTTG GAAAGCCTTG GCCAAGGAAT 1680  
 AAGATATCAC TTCAACCCCT CGCAGTCCAT CCTGTGTATG GAAGGTGACG ACATTGGGAA 1740  
 CATTAAACGT GCTCTCCAGA AAGTCTCCTA CATCAACTCC AGGCAGTTCC CAACGGCGGG 1800  
 TGTGCGGCGC CTCAAAGTAT CCTCCAAAGT CCAGTGCTTT GGGGAAGACG TATGCATCAG 1860  
 TATCCCTGAG GTGATGCTCT ATGTGATGGT CCTCCAGGCC ATCCAGCCCC GGATCACCTT 1920  
 CCGGGGCACA GACCACTTCT GGAGACCTGC TGCCCACTTT GAAAGTGCCA GGGGAGTGAC 1980  
 CCTCTTCCCT GATATCAAGA TTGTGAGCAC CTTCGCCAAA ACCGAAGCCC CCGGGGACGT 2040  
 GAAAACCAACA GACCCCAAT CAGAAGTCTT AGAGGAAATG CTTCAAACT TAGATTTCTG 2100  
 TGACATTTTG GTATCGGAG GGGACTTGA CCAAGGACG GAGTGCTTGG AGCTCAACCA 2160  
 CAGTGAGCTC GACCAACGAC ACCTGGATGC CACTAATTCT ACTGCAGGCT ACTCCATCTA 2220  
 CGGTGTGGGC TCCATGAGCC GCTATGAGCA GGTGCTACAT CACATCCGCT ACCGCACTG 2280  
 GCGTCCGGCT TCCCTTGAGG CCCGGCGTTT CCGGATTAAG TGCTCAGAAC TCAATGGGG 2340  
 CTACACTAGC AATGAGTTCA ACTTGGAGGT CAGCATCCTT CATGAAGACC AAGTCTCAGA 2400  
 TAAGGAGCAT GTCAATCATC TGATTGTGCA GCCTCCCTTC CTCCAGTCTG TCCATCATCC 2460  
 TGAGTCTGAC AGTAGCTACC AGCAGATTTC AGTGGTCCCC AGCATTGCCA CAGTGGTCAT 2520  
 CATCATCTCC GTGTGATGC TTGTGTTGT GGTGGCCATG GGTGTGTACC GGGTCCGGAT 2580  
 CGCCACACG CACTTCATCC AGGAGACTGA GGCTGCCAAG GAATCTGAGA TGGACTGGGA 2640  
 CGATTCTGCG CTGACTATCA CAGTCAACCC CATGGAGAAA CATGAAGGAC CAGGGCATGG 2700  
 GGAAGATGAG ACTGAGGGAG AAGAGGAGGA AGAAGCCGAG GAAGAAATGA GCTCCAGCAG 2760  
 TGGCTCTGAC GACAGGAGG AGGAGGAGGA AGGAGGAGG ATGGGCAGAG GCAGACATGG 2820  
 GCAGAAATGA GCCAGGCAAG CCCAGCTGGA GTGGGATGAC TCCACCTCC CCTACTAGTG 2880  
 CCCAGGGGTG TGCTGCCTGG CCCACATGTC CCTTTTGTAA ACCCTGACCC AGTGATGCC 2940  
 CATGTCTATC ATACCTCACC TCTGATGTCT GTGACATGTC TGGGAAGGCC TTCTCCAGCT 3000  
 TCCTGGAGCC CACCTTTAA GCCTTGGGCA CTCCCTGTGT TTCATCCATG GGGAGGTCC 3060  
 AAGAAGCCCA GATAGGCCAT CAGTGAGGAC TTCAGGGTAG ACTTTGTCT GTAGCCTCCA 3120  
 CTTCTGCCCT AAGTTCCCA GCATCCTGAC TACCTGTCTG CAGAGTTTGC CTTTGTITTT 3180  
 TCCTGCAGGG AAGAAGGCC ACCTTTGTGT CACTCACCTC CCCAGGCTCA GAGTCCCAA 3240  
 GGCCCTGGGG TTCCAATCTA CTGTGCGTCT CTCCACACA GACCAGTAGG TTCTCCTATG 3300  
 CTGACTCCAG GTTGCTTCA ACAAGGAGGG TGGTTGAAT TCACACAGT AAGGTCTTAG 3360  
 TGTTAACAG TGTAAAGAA AGTCTTGTG GAGGCAGAAC TAAAGTTTAA GGGAAAGGTA 3420  
 CACACATTCT CTCTCTCTCT CTCTCTCTGT CTATCTAGTT CCCAGCTTG GAGAGCCTTT 3480  
 CCCCTGTCTT CTTTCTGAG CCATATAAGC TTATAAGAAA AGTCCCAAAC CAAGAAATAGG 3540  
 TCCTTGGCCA CAAGCAGGGT CTGATCCCC ATCAGAGCTA TCTGAGCCTG CCTGTCTGGG 3600  
 CACCTGCTGC AACCATGAGC CTACCTGCC AGGGGCACTC AGCAACAGA ACCACAGGGC 3660  
 CCAGGAGGCA TTCCACACAG GCACTGCCCC AGGACAAAC AACAAAGGCA GTCACAAACA 3720  
 GGACAAACAG GACACAAAC AACACAAAC AAGGACAGTC AACCAAGCC TAGAGCCAGA 3780  
 AAGCAGATGG AAGTCTAAT GAGTCAAAAC GTAGGCTTCA TGGTGGGTGG AGTGGGGTGG 3840  
 GCTGGGCTCC CCCAGSACAG AGGGGACCTT GAGGTGGCA AGGCTCTCAC CACTCAGCCT 3900  
 TATGTCCCT TATCTCCTAT CTCCCTCTT GAGAAATAC ACGCTTCTG CATGTATTAG 3960  
 AAACGCAGCA GCTCCACCAA GTCTACAATG AAAGTTTGAA ATTAACTGC AAGGAATTAG 4020  
 AAGCATATTT GCAATCATG CAGCTTCTT TTTCTTCTG TCATAAAGG AGGAACACTT 4080  
 TAGATAGAGG GCAAAATAT CTGAAACCT AATTCTTTC TTTTGTGAT AAGGAATCT 4140  
 TTTCCATCTC CATCTAACA TGCAACACCT GTGAAGAGAA TTGTTTCTAT AGTAACTGGT 4200  
 CTGTGATCTT TTGTGCCAA GAGAATAGCA GGCAAGAAAT AGGGCCTTGA CAGAAATTC 4260  
 ACGAGCTCT GAGAACATGT TTGTTTCGAA TGTCTGATTC CTCTTTGTCA TCAATGTGTA 4320  
 TGCTCTGTCC CCATCCTCA CTCCTCTCA AGCTCACACC AATTGGTTTG GCACAGGCAC 4380  
 AGAGCTGGTC CCTAGTTAAG TGGCATTAT GTTAAAAAA A

Seq ID NO: 76 Protein sequence  
 Protein Accession #: NP\_071414

80  
 1 11 21 31 41 51  
 MLPGRLCWVP LLLALGVGSG SGGGDSRQR RLLAAKVNKH KPWIIETSYHG VITERNDTVI 60  
 LDPLVALDK DAPVPFAGEI CAPKIHQOEI PFEAVVLNKT SGEGLRLAKS PIDCELOKEY 120  
 TFIIQAYDCG AGPHETAWKK SHKAVVHIQV KDVNEFAPTF KEPAYKAVVT EGKIYDSILQ 180  
 VEAIDEDCSF QYSQICNYEI VTIDVPFAID RGNIRNTEK LSYDKQHQYE ILVTAYDCGQ 240  
 KPAAQDTLVQ VDVKPVCKPG WQDWTKRIEY QPGSGSMPLF PSIHLETCDG AVSSLIQIVTE 300

5 LQTNVYIGKGC DRETYSEKSL QKLCGASSGI IDLLPSPSAA TNWTAGLLVD SSEMIKFDG 360  
 ROGAKIPDGI VPKNLTQDFT ITMMWKHGPS PGVRAEKETI LCNISDKTEMN RHHYALYVHN 420  
 CRVLFLLRKD FQADQTFRPA EFWHKLQDQC DKEWHYVYIN VEFVVTLYM DGATYEPYLV 480  
 10 TNDWPIHPSH IAMQLTVGAC WQGGSEVTKPQ FAQFFHGSLSA SLTIRPGKME SQKVISCLOA 540  
 CKEGLDINSL ESGLQGIKYH FNPSQSILVM EGGDIGNINR ALQKVSYINS RQFPFAGVRR 600  
 LKVVSKVQCF GEDVCISIFE VDAYVMVLQA IEPRIITLRT DHFWRPAAQF ESARGVTLPF 660  
 DIKIVSTFAK TEAPGDVTKIT DPKSEVLEEM LHNLDPCDIL VIGGDLDPQ ECLELNHSEL 720  
 HQRHLDATNS TAGSYIYGVG SMSRYEQVLH HIRYRNWRPA SLEARRPRIK CSELNTRYTS 780  
 15 NEFNLEVISIL HEDQVSDKEH VNHLIVQPPF LQSVHHPESR SSIQHSSVVP SIATVVIIS 840  
 VCMLEVVVAM GVYRVRIAEQ HPIQETEAAR ESEMWDSDSA LTITVNPMEK HEGPGHGEDE 900  
 TEGEEEEEEA EEMSSSSGSD DSEEEEEEEG MGRGRHGQNG ARQAQLEWDD STLPY

Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482..3007

1 11 21 31 41 51  
 20 AACTGAGCTA ACAAGAAATA CTAGAAAAGG AGGAAGGAGA ACATTGCTGC AGCTTGGATC 60  
 TACAACCTAA GAAAGCAAGA GTGATCAATC TCAGCTCTGT TAAACATCTT GTTTACTTAC 120  
 TGCATTACGC AGCTTGCAAA TGGTTAACTA TATGCAAAA AGTCAGCATA GCTGTGAAGT 180  
 ATGCCGTGAA TTTTAAITGA GGGAAAAGG GACAATTGCT TCAGGATGCT CTAGTATGCA 240  
 CTCTGCTTGA AATATTITCA ATGAAATGCT CAGTATTCTA TCTTTGACCA GAGGTTTAA 300  
 25 CTTTATGAAG CTATGGGACT TGACAAAAG TGATATTGA GAAGAAAGTA CGCAGTGGTT 360  
 GGTGTTTTCT TTTTITTAAT AAAGGAATTG AATTACTTTG AACACCTCTT CCAGCTGTGC 420  
 ATTACAGATA ACGTCAGGAA GAGTCTCTGC TTTACAGAAT CGGATTTTCA CATATGACAA 480  
 CATGAAGCTG TGGATTCTAT TCTTTTATTC ATCTCTCTCT GCCTGTATAT CTTTACACTC 540  
 CCAAACTCCA GTGCTCTCAT CCAGAGGCTC TTGTGATTCT CTTTGCAATT GTGAGGAAAA 600  
 30 AGATGGCACA ATGCTAATAA ATTGTGAAGC AAAAGGTATC AAGATGGTAT CTGAAATAAG 660  
 TGTGCCACCA TCAGACCTT TCCAATAAG CTTATTAAAT AACGGCTTGA CGATGCTTCA 720  
 CACAATAGC TTTCTGGGCT TTACCAATGC TATTCAATA CACCTTGGAT TTAACAATAT 780  
 TGCAGATATT GAGATAGGTG CATTTAATGG CCTTGGCCTC CTGAAACAAC TTATATCAA 840  
 TCACAATTCT TTAGAAATTC TTAAGAGGGA TACTTTCCAT GGACTGGAAA ACCTGSAATT 900  
 35 CCTGCAAGCA GATAACAATT TTATCAGAGT GATTGAACCA AGTGCCCTTA GCAAGCTCAA 960  
 CAGACTCAAA GTGTAAATTT TAAATGACAA TGCTATTGAG AGTCTTCTC CAAACATCTT 1020  
 CGGATTGTTT CTTTAAACCC ATCTAGATCT TCGTGGAAAT CAATTACAAA CATTGCCTTA 1080  
 TGTGTTGTTT CTCGAACACA TTGGCCGAAT ATTGGATCTT CAGTTGGAGG ACAACAATG 1140  
 GGCCTGCAAT TGTGACTTAT TGCAATTAAA AACTTGGTTG GAGAACATGC CTCCACAGTC 1200  
 40 TATAATTGGT GATGTTGTCT GCAACAGCCC TCCATTTTTT AAAGGAAGTA TACTCAGTAG 1260  
 ACTAAAGAAG GAATCTATTT GCCCTACTCC ACCAGTGTAT GAAGAACATG AGGATCCTTC 1320  
 AGGATCATT CATCTGGCAG CAACATCTTC AATAAATGAT AGTCGCATG CAACTAAGAC 1380  
 CACGTCCATT CTAACACTAC CCACCAAGC ACCAGGTTTG ATACCTTATA TTACAAGCC 1440  
 ATCCACTCAA CTTCAGGAC CTTACTGCC TATTCTTGT AACTGCAAAG TCCTATCCCC 1500  
 45 ATCAGGACTT CTAATACATT GTCAGGAGCG CAACATTGAA AGCTTATCAG ATCTGAGACC 1560  
 TCTCCGCAAA AATCTTAGAA AGCTCATTCT AGCGGGAAT ATTATTACA GTTTAATGAA 1620  
 GTCTGATCTA GTGGAATATT TCACCTTGA AATGCTTAC TTGGGAAACA ATGATATGA 1680  
 AGTTCITGAA GAAGGATCGT TTATGAACCT AACGAGATTA CAAAACCTCT ATCTAAATGG 1740  
 TAACCACTG ACCAAATTA GTAAAGGCAT GTTCCTTGGT CTCATAATC TTGAATACIT 1800  
 50 ATATCTTGAA TACAATGCCA TTAAGGAAT ACTGCCAGAA ACCTTTAATC CAATGCCTAA 1860  
 ACTTAAAGCT CTGTATTAA ATAACAACCT CCTCCAAGTT TTAACCAAC ATATTTTTTC 1920  
 AGGGGTTCTT CTAACTAAGG TAAATCTTAA AACAAACAG TTAACCCATC TACCTGTAAG 1980  
 TAATATTTTG GATGATCTTG ATTACTAAC CCAGATTGAC CTTGAGGATA ACCCTGGGA 2040  
 CTGCTCCTGT GACCTGGTTG GACTGCAGCA ATGGATACAA AAGTTAAGCA AGAACACAGT 2100  
 55 GACAGATGAC ATCTCTGCA CTTCCCCGG GCATCTCGAC AAAAGGAAT TGAAGGCCCT 2160  
 AAATAGTGA ATCTCTGTC CAGGTTTAGT AAATAACCA TCCATGCCAA CACAGACTAG 2220  
 TTACCTTAGT GTCAACACTC CTGCAACAAC AACAAATACG GCTGATACTA TTTTACGATC 2280  
 TCTTACGAC CTTGTGCCAC TGTCTGTCT AATATTGGGA CTTCTGATTA TGTTCATCAC 2340  
 TATTGTTTTT TGTGCTGAC GATAGTGTGT TCTTGTCTT CACCGCAGGA GAAGATACAA 2400  
 60 AAAGAAACAA GTAGATGAGC AATGAGAGA CAACAGTCT GTGCATCTTC AGTACAGCAT 2460  
 GTATGGCCAT AAAACACTC ATCAACTAC TGAAGACCC TCTGCTTAC TCTATGAACA 2520  
 GCACATGGTG AGCCCATGG TTCAATGTCTA TAGAAGTCCA TCCTTTGGTC CAAAGCATCT 2580  
 GGAAGAGGAA GAAGAGGGA ATGAGAAAGA AGGAAGTGAT GCAAAACATC TCCAAGAGAG 2640  
 TCTTTGGAA CAGGAAATC ATTCACTAC CACAGGGTCA AATATGAAAT ACAAAACAC 2700  
 65 GAACCAATCA ACAGAATTTT TATCCTTCCA AGATGCCAGC TCATTGTACA GAAACATTTT 2760  
 AGAAAAGAA AGGGAACCTC AGCAACTGG AATCAGAGAA TACCTAAGGA AAAACATTGC 2820  
 TCAGCTCCAG CCTGATATGG AGGCACATTA TCCTGGAGCC CACGAAGAGC TGAAGTTAAT 2880  
 GGAACATTA ATGTACTCAC GTCCAAGGAA GGTATTAGTG GAACAGACAA AAAATGAGTA 2940  
 TTTTGAACCT AAAGCTAATT TACATGCTGA ACCTGACTAT TTAGAGTCC TGGAGCAGCA 3000  
 70 AACATAGATG GAGAGTTTGA GGCCTTTCG AGAAATGCTG TGATTCGTGT TTAAGTCCAT 3060  
 ACCTGTAA TAAGTGCTT ACCTGAGTGT GTCATCAATC AGAACCTAAG CACAGCAGTA 3120  
 AACATGGGG AAAAAGAAAG AAGAAGAAA GAAACTCAGG GATCACTGGG AGAAGCCATG 3180  
 GCATTATCTT CAGCAATTT AGTCTGTCCC AAATAAATC AATCCTTGCA TGTAAATC

Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 80 MKLNIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCCEEK DGTMLINCEA KGIKMWSEIS 60  
 VPPSRFPQLS LNNGLTMLH TNDPGLTNA ISIHGFPNNI ADIEIGAFNG LGLLKQLHIN 120  
 HNSLEIKED TFHGLENLFP LQADNNFITV IEPFAFSKLN RLKVLILNDN AIESLPPNIF 180  
 RFVPLTHLD RGNQLQTLPY VGFLFHIGRI LDQLLEDNKW ACNCDLLQLK TWLENMPPQS 240  
 IIGDVVNCSP PFFKGSILSR LKKESICPTP FVYEEHEDPS GSLHLAATSS INDSRMSTKT 300  
 TSILKLPTKA PGLIPIYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP 360

PPONPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG 420  
 NHLTKLSKGM FLGLNLEYL YLEYNAIKEI LPTGFNPMFK LKVLVYNNNL LQVLPPHIFS 480  
 GVPLTKVNLK TNQFTHLPVS NILDDLILIT QIDLEDNPDW CSDCLVGLQQ WIKLSKNTV 540  
 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSPMTQTS YLMTVTPATT TNTADTILRS 600  
 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM 660  
 YGHKTHHTT ERPSASLYEQ HMVSPMVHVV RSPSPGPKHL EEEEEERNEKE GSDAKHLQRS 720  
 LLEQENHSPIL TGSNMKYKTT NQSTEFLSFO DASSLYRNIL EKERELQQLG ITEYLKRNIA 780  
 LQCPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ 840  
 T

Seq ID NO: 79 DNA sequence  
 Nucleic Acid Accession #: NM\_016640.2  
 Coding sequence: 39..1358

1 11 21 31 41 51  
 GCTTAAGTTG ACCTCTGGGT CCGGAATCGC GGGCAAGAT GCGCGCGGCC AGGTGTTGGA 60  
 GGCTTTTGCT ACACGGTCCG AGGCTTTCAT TGCAACCCGC GGCTAATGCC GCCGCCACGG 120  
 CTACAGAAAC GACCTCCCAA GAGTTCGCGG CGACCCCGGT CGCGCGGTAC CGCCCGATTG 180  
 TGGCTTCCAT GACAGCCGAC AGCAAAGCTG CACGGCTGCG CGCGATCGAG CGCTGGCAGG 240  
 CGACCGTGCA CGCTGCGGAG TCGGTAGACG AGAAGCTGCG AATCCTCACC AAGATGCAGT 300  
 TTATGAAGTA CATGCTTTAC CCGCAGACCT TCGCGCTGAA TCGCGACCGC TGTACCAAGT 360  
 ACTTCACCAA GACCGTGTTC CTGTGCGGTC TGGCGCGGCC CCCAGCGGAG CCCGAGCCCG 420  
 AGCCCGAACC CGAACCTGAA CCTGCGCTGG ACCTCGCGCG GCTGCGTGGG GTCCGCTGGG 480  
 ACTGCTGCTG GCAGGAGCAC TTCTACTGCG GCGCGAGCGG GCGCGTGCAC CGTTACGAGG 540  
 AGAGCGAGGT CATATCTTTG CCTTCTGCG ATCAGCTGGT GTCAACCCCTC GTGGGCTTCC 600  
 TCAGCCCAAC CAACCCGGCC CTGGCGCTGG CCGCCCTCGA TTATAGATGC CCAATTCATT 660  
 TTTACTGGGT GCGTGGTGAA GAAATTATTC CTCTGCTGCA TCGAAGAGGT CGAATTGATG 720  
 ACTTGCAGTA CCAGATAGAT GATAAACCAA ACAACAGAT TCGAATATCC AAGCAACTCG 780  
 CAGAGTTTGT GCCATTGGAT TATTCTGTTT CTATAGAAAT CCCCACTATA AAATGTAAAC 840  
 CAGACAAACT TCCATTATTC AAACGGCAGT ATGAAAACCA CATATTTGTT GGCTCAAAAA 900  
 CTGCAGATCC TTGCTGTTAC GGTCAACCCC AGTTTCATCT GTTACCTGAC AAATTAAGAA 960  
 GGGAAAGGCT TTTGAGACAA AACTGTGCTG ATCAGATAGA AGTTGTTTTT AGAGCTAATG 1020  
 CTATTGCAAG CCTTTTGTCT TGGACTGGAG CACAAGCTAT GTATCAAGGA TTCTGGAGTG 1080  
 AAGCAGATGT TACTCGACCT TTTGCTCTCC AGGCTGTGAT CACAGATCGA AAATACTTTT 1140  
 CCTTTTCTG CTACCACTTA AATACTTTGG CACTGACTAC ACAAGCTGAT CAAATAAACC 1200  
 CTCGTAAAAA TATATGTTGG GTTACACAAA GTAAGCCTCT TTATGAAACA ATTGAGGATA 1260  
 ATGATGTGAA AGGTTTTAAT GATGATGTTT TACTTCAGAT AGTTCACTTT CTACTGAATA 1320  
 GACCAAAAGA AGAAAAATCA CAGCTGTTGG AAAACTGAAA AAGCATATTT GATTGAGAAC 1380  
 TGTGGGAATA TTTAAATTTT ACTGAAGGAA CAATAATGAT GAGATTGTGA ACTGTCAACT 1440  
 ATTAATACAT TTGATTTTGG AGACAAAAAA AAAAAAATAA AA

Seq ID NO: 80 Protein sequence  
 Protein Accession #: NP\_057724.1

1 11 21 31 41 51  
 MAAARCWRLP LRGPRLSLHT AANAATATE TTSQDVAAAT VARYPPIVAS MTADSKAARL 60  
 RRIERWQATV HAAESVDEKL RILTKMQFMK YMVYPTPAL NADRWYQYFT KTVFLSGLPP 120  
 PPAEPEPEPE PEPEPALDLA ALRAVACDCL LQHFYLRRL RRVRHYESEE VISLFLDLQL 180  
 VSTLVGLLSP HNPALAAAAAL DYRCPVHFWY VRGEELIPRG HRRGRIDDLR YQIDDKPNNQ 240  
 IRISQLAEF VPLDYSVPIE IPTIKCKPDK LPLFKROYEN BIFVGSKTAD PCCYGHTQFH 300  
 LLPDKLRRLR LLRQNCADQI EVVFRANAIA SLFAWTGAQA MYQGFNSEAD VTRFFVSQAV 360  
 ITDGKYFSFF CYQLNTLALT TQADQNNPRK NICWGTQSKP LYETIEDNDV KGFNDVLLQ 420  
 IVHFLNLRPK EESQQLLEN

Seq ID NO: 81 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..2070

1 11 21 31 41 51  
 ATGAGCGGTG CCGGGGTGGC GGCTGGGACG CGGCCGCCCA GCTCGCGGAC CCGGGGCTCT 60  
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTC TGAGGCCGCA GAGCCCGCAG 120  
 CTCAGGCAGA CGCAGCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 GAAAACAAGG GTGAGCGGCG GCGGGGCCCT AGGCCGCGCC TGCCTCCCA GGCACACTCA 300  
 AACTGCGCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360  
 GGGGGAACAC AGGACGGGGA GCGCTCCAG ACTGTCTTGG CCCACCTGGC TGCACCTGCC 420  
 CCTGTATGCC AACCCAGTGG GTACAGTTTC TGGGGGACCT GGACAGATGC CGTACTCTCT 480  
 AGCCGTGGCT GSAAGATGTT ATGCAGCCAA GCACAGCAGG TGCTGCTCTC GGGGAGCCCA 540  
 GGGCCTGAGG TCAATTGACG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CTGCGCTGTC TAGATCTTGG 660  
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCCAGGGGAT ATGCACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 CGAGCAACCA TGGGGAACAA GGGAGGAAGC AGAGTCTGTT TTCCTTGCCA CTGTGCCAAG 840  
 GCACTTCCCC ATCTGACAGC CGGCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATATCTTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA 960  
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCAGGGA 1020  
 GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
 CTGTTCTGGG CCAAAGTGGG CCAAGTGGG CAGCCCCAGC CCGTCACTGG TGGGAGCCTG 1140  
 GACAGGACAC GGGAGAGGGC CATGCTTTCC CTGCGGACCT GCTGTTCCAT GTGTCCCAAG 1200  
 CCTCTCTGCT TCCAGATGG CCGCTCAGGA AACCACTTT CCAGGGGCTC TGCTCCCTTG 1260  
 GCGCTCTGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGCG 1380
GGCGTAGCG CCGACTCTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
TCCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCCGA AGGCGGACCT GGAAGAGGAG 1560
CCCTTACTTC ACAACAGCAA GCTGGACAAA GTTCTGTTGG TACAAGGGCA GGCCAGAAAG 1620
GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC 1680
AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCCTGC CCCTTCCCTT GCGAAAGCCC 1740
ACCACACTTA GGCAGTGCAG AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCGAG 1800
ACCCAAGAGC TGGCGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
CCGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAAA GGCTCCACCC 1920
AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CTGCCCCGCA 1980
CTGAAGCAGA CCCCAGAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
AAACGGCGCC TGCATCGCTC AGTGCTTTGA

```

Seq ID NO: 82 Protein sequence  
Protein Accession #: FGENESH predicted

1 11 21 31 41 51

```

MSGAGVAAAT RPPSSPTPGS RRRRQRPSPVQ VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
QQQHSEMLAK LHEBIEHLKR ENKGEFARGP RPALPPQAH S TLPLPQHRNT AINSSTRLGS 120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180
GPEVIAGRWV ATGCSPLDLP PSRAEMGRNP WDSFPCPARSL PQIAAVARPR ISSPMALSPH 240
MLGAQGIWTH SIQGSPLAIW AATMGTGKGS RVLFPCHLSK ALPHDPDSGPH PAQDPGLNSQ 300
AHFPLSLGLG LTFSGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGGP FPSRCNSSE 360
LFWAKCGPSR QPQCSAGDA DRTREEAMLS LGTCCSMCPK PSCFPDGPSP NHLRSASAPL 420
GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPKGKRGLA GGSADTVRSP ADSLSMSSFQ 480
SVKISINSAN SQGKARPPQG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQSQARK 540
EKAEASNAGN ACGMSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLQ 600
TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP FVAERAILPA 660
LKQTPKWNFA ERQKRLQAMQ KRRLHRSVL

```

Seq ID NO: 83 DNA sequence  
Nucleic Acid Accession #: NM\_005264.1  
Coding sequence: 557..1954

1 11 21 31 41 51

```

GAATTCGGGC CAGAAGAAAT CTGGCCTCGG AACACGCCAT TCTCCGCGCC GCTTCCAATA 60
ACCACTAACA TCCTTAACGA GCATCCGAGC CGAGGGCTCT GCTCGGAAAT CGTCTGGGCC 120
CAACTCGGCC CTTCGAGCTC TCGAAGATTA CGCATCTAT TTTTITTTTC TTTTITTTCT 180
TTTCTAGAGC CAGATAAAGT GAGCCCGGAA AGGGAAGSAG GGGGCGGGGA CACCAITGCC 240
CTGAAAGAAAT AATAAGTAA ATAAACAAAC TGGCTCCTCG CCGCAGCTGG ACGCGTCCG 300
TTGAGTCAGG GTTGGGTGGG ACCTGAACCC CTAAAAGCGG AACCGCCTCC CGCCTCGGCC 360
ATCCCGGAGC TGAGTCGCGG GCGGCGGTGG CTGCTGCCAG ACCCGGAGTT TCCTCTTTCA 420
CTGGATGGAG CTGAACCTTG GCGGCGCAGA GCAGCACAGC TGTCCGGGGA TCGCTGCAGC 480
CTGAGCTCCC TCGGCAGAGC CCAGCGGGCG CTGCGGATTI TTTTGGGGGG GCGGGGACCA 540
GCGCCGCGGC GGCACCATGT TCTTGGCGAC CCGTACTTTC GCGCTGCGCC TCTTGGACTT 600
GCTCTGTGCG GCGCAAGTGA GCGGCGGAGA CCGCTGGAT TGGGTGAAAG CCACTGATCA 660
GTGCTGAAG GAGCAGAGCT GCAGCACCAA GTACCGCAGC CTAAGGCAGT GCGTGGCGGG 720
CAAGGAGACC AACTTCAGCC TGGCATCCGG CCTGGAGGCC AAGGATGAGT GCGCGACGCG 780
CATGGAGGCC CTGAAGCAGA AGTCGCTCTA CAACTGCGCG TGCAAGCGGG GTATGAAGAA 840
GGAGAAAGAA TGCTCTCGCA TTTACTGGAG CATGTACCAG AGCCTGCAGG GAAATGATCT 900
GCTGGAGGAT TCCCATATG AACCAATTAA CAGCAGATTG TCAGATATAT TCGGGTGGT 960
CCCATTCATA TCAGATGTTT TTCAGCAAGT GGAGCACATT CCCAAAGGGA ACAAATGCTT 1020
GGATGCAGCG AAGGCTGCGA ACCTCGACGA CATTGCAAG AAGTACAGGT CGGCTACAT 1080
CACCCCGTGC ACCACAGCG TGTCCAACGA TGTCTGCAAC CGCCGCAAGT GCCACAAGGC 1140
CTTCCGCGAG TTCTTTGACA AGGTCCCGGC CAAGCACAGC TACCGAATGC TCTTCTGCTC 1200
CTGCGCGGAC ATCGCCTGCA CAGAGCGGAG GCGACAGACC ATCGTGCCGT TGTGCTCCTA 1260
TGAGAGAGAG GAGAAGCCCA ACTGTTTGAA TTGCGAGGAC TCCTGCAAGA CGAATTACAT 1320
CTGCAGATCT CGCCTTGCGG ATTTTITTTAC CAACTGCCAG CCAGAGTCAA GGTCTGTGAG 1380
CAGCTGTCTA AAGGAAACT ACCTGACTG CCTCTCGGCC TACTCGGGGC TTATTGGCAC 1440
AGTCATGACC CCCAATACA TAGACTCCAG TAGCCTCAGT GTGGCCCCAT GGTGTGACTG 1500
CAGCAACAGT GGGAAACGAC TAGAAGAGTG CTTGAAATTT TTGAATTTCT TCAAGGACAA 1560
TACATGTCTT AAAAATGCAA TTCAAGCCTT TGGCAATGGC TCCGATGTGA CCGTGTGGCA 1620
GCCAGCCTTC CAGTACAGA CCACCACTGC CACTACCACC ACTGCCCTCC GGGTTAAGAA 1680
CAAGCCCCCT GGGCCAGCAG GGTCTGAGAA TGAATTTCCC ACTCATGTTT TGCCACCGTG 1740
TGCAAAATTA CAGGCACAGA AGCTGAAATC CAATGTGTG GGCATACAC ACCTCTGTAT 1800
TTCAATGGT AATTATGAAA AAGAAGGTCT CGTGCTTCC AGCCACATAA CCACAAAATC 1860
AATGGCTGCT CCTCAAGCT GTGGTCTGAG CCCACTGCTG GTCTGTGGT TAACCGCTCT 1920
GTCCACCTTA TTATCTTTAA CAGAAACATC ATAGCTGCAT TAAAAAATA CAATATGGAG 1980
ATGTAAGAG ACMAAACCA AGTTATCTGT TTCTGTCTCT CTGTATAGC TGAATTTCCA 2040
GTTTAGGAGC TCAGTTGAGA AACAGTTCCA TTCACTGGA ACATTTTTTT TTTCTCTTT 2100
AAGAAAGCTT CTTGTGATCC TTGCGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC 2160
AACTCAGAA GGCCTTGGGA TATGCTGTAT TTAAAGGGA CAGTTGTGAA CTTGGGCTGT 2220
AAGCAAACT GGGGCTGTGT TTTCGATGAT GATGATCATC ATGATCATGA GTATTTTAAC 2280
AGTTTTACTT CTGGCCTTTC CTAGCTAGAG AAGGAGTTAA TATTTCTAAG GTAACCTCCA 2340
TATCTCTCTT AATGACATTG ATTTCTAATG ATATAAATTT CAGCCTACAT TGATGCCAAG 2400
CTTTTTTGCC ACAAGAAGA TTCTTACCAA GAGTGGGCTT TGTGAAACA GCTGGTACTG 2460
ATGTTCACTT TTATATATGT ACTAGCATT TCCACGCTGA TGTATTGTA CTGTAAACAG 2520
TTCTGCACCT TTGTACAAAA GAAAAACCA CCGGAATTC

```

Seq ID NO: 84 Protein sequence  
Protein Accession #: NM\_005264.1

	1	11	21	31	41	51	
5	MFLATLYPAL	PLLDLLLSAE	VSGGDRLCDV	KASDQCLKEQ	SCSTKYRTLK	QCVAGKETNF	60
	SLASGLEAKD	ECRSAMEALK	QKSLYNCRCK	RMKKEKNCL	RIYWSMYQSL	QGNDDLEDSF	120
	YEPVNSRLSD	IFRVVPFISD	VFQVVEHIPK	GNNCLDAAKA	CNLDIDCKKY	RSAYITPCTT	180
	SVSNDVNCRR	KCHKALRQFF	DKVPAKHSYG	MLFCSCRDIA	CTERRRQTIV	PVCSYEEREK	240
	PNCLNLQDSC	KTNYICRSRL	ADFFTNQDPE	SRSVSSCLKE	NYADCLLAYS	GLIGTVMTPN	300
10	YIDSSSLVA	PWCDCSNNGN	DLEELKPLN	FFKONTCLKN	AIQAFNGNSD	VTWQPAFPV	360
	QTTTATTTTA	LRVKNKPLGP	AGSENEIPTH	VLPPCANLQA	QKLKSNVSGN	THLCISNGNY	420
	EKEGLGASH	ITTKSMAAPP	SCGLSPLLVL	VVTALSTLLS	LTETS		
	Seq ID NO: 85 DNA sequence						
	Nucleic Acid Accession #: XM_027172.1						
15	Coding sequence: 143..1405						
	1	11	21	31	41	51	
20	GGTGGAGACA	CCGCTCAGG	GCTCGGTGCA	CAGTGGACAT	TTGGGGAGCG	TTGTGGGTGA	60
	CCCCACACAC	GGCACTGGGA	ATGCAGGGGA	GAGGGGGCCA	AGGGGGAAAG	GGGCCAGAGT	120
	GTGGGCTTTG	GATTCAGGAG	GGATGGATTG	CAGTCCCTAGC	TTGCCACTTA	TTAGGACTCC	180
	TGAGAGCAGC	CTCCATGAGG	CCCTGGACCA	GTGCATGACC	GCCCTGGACC	TCTTCTCTAC	240
	CAACCACTTC	TCAGAAGCAC	TCAGCTACCT	CAAGCCGAGA	ACCAAGGAAG	GCAATGTACCA	300
25	CTCACTGACA	TATGCCACCA	TCCTGGAGAT	GCAGGCCATG	ATGACCTTTG	ACCCCTCAGGA	360
	CATCCTGCTT	GCGGGCAACA	TGATGAAGGA	GGCAGAGATG	CTGTGTGAGA	GGCAGCGGAG	420
	GAAGTCTTCT	GTAACAGATT	CCTTCAGCAG	CCTGGTGAAC	CGCCCCACGC	TGGGCCAATT	480
	CACTGAAGAG	GAATCCACG	CTGAGGCTG	CTATGCAGAG	TGCCTGTCTG	AGCGAGCAGC	540
	CCTGACCTTC	CTGCAGGCTT	CCTCACACGG	AGGGGCAGTC	AGGCCAGAG	CCTTGCATGA	600
30	TCCCTCTCAC	GCCTGCAGCT	GCCACCTGG	GCCAGGCGGT	CAGCATCTTT	TCCTCTCTGCA	660
	GGAGGAGAAC	ATGCTGAGCT	TCATCAAAGG	CGGCATCAAA	GTTCGAAACA	GCTACCAGAC	720
	CTACAAGGAG	GAGAGCAGCT	TTGTTCAATC	CTCACAATAC	TGCAAGGGTG	AGAACCAACC	780
	GCACCTTTGAA	GGAGGAGTGA	AGCTTGGTGT	AGGGGCCTTC	AACCTGACAC	TGTCCATGCT	840
	TCCTACTAGG	ATCCTGAGGC	TGTTGGAGTT	TGTTGGGTTT	TCAGGAAACA	AGGACTATGG	900
35	GCTGCTGAG	CTGGAGGAGG	GAGCGTCAGG	GCACAGCTTC	CGCTCTGTGC	TCTGTGTCAT	960
	GCTCCTGCTG	TGCTACCACA	CCTTCTCTAC	CTTCGTGCTC	GGTACTGGGA	ACGTCAACAT	1020
	CGAGGAGGAC	GAGAGCTCTT	TGAAGCCCTA	CCTGAACCGG	TACCCCTAAGG	GTGCCATCTT	1080
	CCTGTTCTTT	GCAGGGAGGA	TTGAAGTCAT	TAAAGGCAAC	ATTGATGCAG	TGAGTGATGG	1140
	GGGTCCGGGC	CGGGGCTGGG	GATCCCTCGG	GGTCTCCAG	ACCAGCAGGA	AGTCAGGCAC	1200
40	ATGTGACATA	CTCAGGGACA	GGATAGACTG	GGGGGCGGGG	GGGGGCCAAG	AGAGAACCAA	1260
	CCAGAGAGCA	GGGGCAGGAG	AGGCCCTTCT	GGCAGAGCAG	CCTGGGAAGA	CAAGGGAGGA	1320
	GGAGGCATT	TGTTGCTCTG	GGATTGAC	TGGGAGATAT	AGGACTGCAG	CATTGCACTG	1380
	GAGGAGGAGT	GAGGAGGAGT	CTTGAGGGAG	GCAGAGGTTA	GGAAAGCCCA	TCTGTTTAGG	1440
	GCATGACGAT	TAGGCTGGAG	TCTGGTACCT	CCCTCTCATT	ATAGCTCTCT	CCTGCTCTTT	1500
45	CATTTTGTGA	CTAAAAACCA	GAGTCTTAGG	CGGGGGCTGT	ATTGAGCCCC	AACGTCTATG	1560
	AAGACTTAGG	AGGTAAAAAC	AGGACTGGAG	GCCAGATCTC	CTGGCTCTGT	GGGCCCCACC	1620
	TGAGCTCAGC	ACAGGCTGGG	ACCACTATGC	CCTGGAGGAG	TCCCGGTCTG	CTGTGGTGT	1680
	GGGAGGTTG	GAGGATGCAG	AGGGGTTGGG	GCTGGGTGGG	CACCCGCTAG	GCTGACCAGA	1740
	AGGTGCTGTC	AGGCCATCCG	GCCTTTCGAG	GAGTGTCTGT	AGGCCAGCA	GCACTGGAAG	1800
50	CAGTTCCACC	ACATGTGCTA	CTGGGAGCTG	ATGTGGTGCT	TCACCTACAA	GGGCCAGTGG	1860
	AAGATGTCTT	ACTTCTACGC	CGACCTGCTC	AGCAAGGAGA	ACTGCTGTCT	CAAGGTGGGC	1920
	TGATGCCACG	TGTTAGGGGG	ATTGGGTGAC	CAGGGCTGAC	TGTGTGCTCT	CAGACCACGG	1980
	GCCAAATCCC	TAACTGAACA	CAGATGTCTC	AGCTGGAATC	TAAACATAAC	CTTAAATCTT	2040
	AATAGGACTC	AGGCTTGAA	GGAACTAAAG	ACCACAAGAG	AACTTCTGA	ACCACATGT	2100
55	GTCAACAAGA	GATTTCTAGT	CACAAAGGAC	AGAAACATGG	CTCCCTCTGT	CCAGTAGAAC	2160
	TGTTTCTGTG	GTAGAAATGT	TCTACTATG	CATGCCCCAA	ATATGGTAGT	CACCAGCCAC	2220
	ATGTGCTAGC	TGAGCACATG	AAATGTGCTT	AGTGCAACTG	GGAAACTGAT	TGTTTTCAGT	2280
	TTTATTTAAT	TTTAATTAAC	TAAATGTTAA	ATTAAATAG	CCATGTAGGG	CTTGTGGCCA	2340
	CTATATTGGA	CTATGCAGGT	CCAAAACACA	AAAGGCTCAT	ATRACTGAAC	ATTCTTGGCA	2400
60	CATCCGACTT	CAGGTAGGGC	TGGATCCAGG	AAITCAAATG	ATGTGTCTGT	GCTTGGTCTT	2460
	TCCATTGTG	GCTGTGCTCT	CTCCTATGAC	ATCTTTGTTT	CTGCTGCATC	TTTGACAGGA	2520
	GGTCTCTCCC	ATGTGACAGG	CAAGGTGGCC	ACGGGCTGCT	TCTACTCATA	TCCTCCCTTT	2580
	GGTTTCAACC	AGAGTCCCAC	AGTTTGAGCC	TCACTGGTCT	GACTTGTCTC	CTGCCAATGC	2640
	CTGGAACAGA	GGGGTGGGAA	GATTCTCAT	GGGCTGAGAG	TAGGAGAGGG	GTGGTTCCAC	2700
65	AGAAGAAAAAT	GATGCACCCA	GAAATAGTGG	AGGGATTAA	AAGATGCCAT	ACAGGCCAAA	2760
	CAAGGCCAAA	CAGATGCCCG	CCTACCAAAG	ATGAAATTTA	TCATGGTAAG	TATTGAAATA	2820
	AGTGTAGACT	TGTACCATCA	TAGTAATGAT	AGTGCAGAAA	TTGGAACCAA	GAGTCTTACA	2880
	ACCACCTAGC	TCAGCAAAAG	TCTAATCTGT	TATTTGTAAG	TACACAGGAC	ATGTGTCTTC	2940
	ATGGCTTCAT	CCCTCTGCCA	TAGCAGACAT	TGCTAATCAA	TCCTCTGCCA	TGAGCCTAGC	3000
70	TGTGACCTTA	GATACCTTCC	CTGCAAGGCT	CCAGGCAGCC	GTTAGAAGCT	ACCCACATTT	3060
	GCACCTGTTA	GGAGACCTGT	CATCTGCATC	TGGTCCCTCC	CCCTCTCTGT	CATGGAGGTC	3120
	TCTTCTGCTG	CCCTGCTGCG	GGACCAAGCT	GAAGGGGAAT	TCTCTGGGTC	TGGGGCAGGT	3180
	GGGGCTGGGG	AAGGGAGCAG	GCTTCTACTG	AGCTCTCAAC	ATGCTGCGCA	CCTGTCTATG	3240
	CCTCCACACC	ACACCCAGTG	AGGAGAAGTT	ATTATCTCCA	TTGGGCACAT	GAGGGCCACT	3300
75	GATGCTAAGC	GAGGACTGTG	ACTTCCCAAC	CCACATGGCT	GTTGGTGACA	GACACCGGAT	3360
	TTGAGGACAG	TCCTGTGTGA	CTCAGAGGCC	TCTGCTTCTC	TCTGTCTCTT	AGAGTCTCTC	3420
	TGAGGAGTGC	GGGCTTGCCC	TGAGCCCAAC	CTGCTGTTGA	AGGTGCTTCC	TCAGGCCAG	3480
	CTCCCATGGC	CCCCACACCC	CCTCCTCATC	ACCTCCTACT	CCCAAAAAGG	ACAAAGCCTC	3540
	AGGGAACCTT	TTTTCTTTT	TTAGAGACAG	GGTCTTGCTA	TGTTGGTCAG	GCTAGTCTTG	3600
80	AACTCCTGGG	CCCAAGCAAT	CTTCCCACTT	CTGCCTCCTA	AAGTGTCTGG	ATTCTGGGCC	3660
	TTAGGGGAAC	TTTTTGAACT	GAAAGTGACT	CTGGAAGCCT	TCCTGTAGAG	TGAGGTGGGT	3720
	GGCTGGGGCT	AACCATATGA	GGAAGGAGAG	ACCTGGTGGG	GGCACACAGC	TGCTATATAG	3780
	AGGAACAGAA	GGTGGGCCAG	GCCTCCACGC	TGTCAGGAAA	TCTGGCTCAG	TCCCCAGACC	3840
	GCTGTGTGGC	TTTGGGGTGG	CCAGTCCCTC	TCTCTCTGCA	ACACTCTCTT	CATGAGGACT	3900
	TCTGTGAAAA	ATGGGGGTTG	TAACTCTCTG	AGTCTCTGGG	CCCCACCAT	TTCTAATCTC	3960

5  
10  
15  
20  
25  
30  
35  
40

CAGAACTTGG CCACCACAGA CTCACCAAC TTCTAGTCTT GGGGCTGGG CCTCTGGCCA 4020  
TTGCCATAGG CACCACCTGC TCTGTGCAGG CAGCGCCCCC CTCTGCCAGG ATCCTCCGAG 4080  
GTCAGCTGCT GGGTCTGACC GGCAGACCTT GGTGAGCGA CGGATGAACG GAGTATGCAG 4140  
ACACAGGCTT GCCTGTGAGC AGATGGGGGA CCCCTGCCAG AGTCAGCAGC GGCCCCCATA 4200  
AGCCTGCCAC GCTTGCATTT ATTTAGTACA GATGTAATGA CAAAGGCCTA AAGCAAATC 4260  
CATTTGTGGC TAAATTAACAT TGTGCCCCC CCAGAAAGAG CAGTCTCCG CATGATGATT 4320  
AAAGGCCAGG TTCCGAGGCC TAAGTAAACC AACTTATCTA GATCAATTC CTTACTTCTT 4380  
GTTATCTACT CTGAGAGAAT TCAGCTGCCT TCAGCCAAAT CCTTCCCGA AGCTTTTGCA 4440  
AAACCTCOGA GCCTTCCAAG GTTTGCTTCT TTCTGTAATT TTTCTACCA CCTGACCTA 4500  
TCTCTCGAG TCAGCCCTGT GGAGGCTTT GTGTTTCCCC CAGTGCTGGC AGCCTAGAGG 4560  
CTGAGATGGC CAGAAACAAG GTGGTGACAG TGGGTGCTC AGGCTTGGG AAACCCAAGG 4620  
AGCTAAAGGC ATGCCAGGC AACCAAGAG GACAGGAAGG CTTCTGAGGA GAGACCTCTG 4680  
AGGTGGGTCT TGSAGAGGAA GGACTTAGGG AGGCAGAGTG GAGGAAGTGA GAGGACACCC 4740  
CAAGCCAAGA GGGCGGCAGG ACCAAAGGCT CAGAAGCCAG GCGCTGCAG AGGGGCTGTG 4800  
TGCCACAGGG TGAAGAGTTT GTGTGGCAGA AGGCAGGGG GCTTGCATCA GGGGTGACAG 4860  
CTGCTCTTTT GTCCAGCAGT AGCCCTGTGA CATCCCTGGA GAGCTGGGGC GTCCACAATC 4920  
CTAAGTCACA GCCCCATCC TAACCTTGGT GGTGCACTGA GGGTGAAGTG TCTGTGGGCA 4980  
GGAGGGAAGA CTCTTGGAGA TGAGCCTGGT GAAGGATAA TGGCATCCG GGCAGAGGAG 5040  
GAGCACAGGC AGAGGCTTGG GGAGAGTTTA AGGAGTGTAG GGGAGGAAT GGCAGAAGAT 5100  
GAGCCAGAAA AAGAAAGGTT AGGGCAGGCT CTGGAGGACA TGAGTGGCTG TTTGGGCTTT 5160  
ATCCAGCAGT GGGGAGCAGT TGGCAGGCTT TGGCTTAGA TAGGTGCTT AGAAAGCCCA 5220  
CCAGCAGTTG CTGGGCCACC CCGCTGGCTG GGTCTGTTC TAAGGCAGGA AATACAAGCA 5280  
TGAGCAGGAA AAGACCCCTT CAAGGCTCAC GTCTAGTGG GGAGACAAGA AACACAGATG 5340  
GGCAATATAA CACGATGCTT GGTTCAGTA AGTGCAGTGA AGAACAGCG AGGCTGGATG 5400  
CAGGGAGTGA TGGGAGGGGC TTTGTAAGGG GAGGTGCGGG GAAGCCTGTC TCAGAGGACA 5460  
CCAGAAATGA GCGCAGGAGC AGCACGTGGC AGTCACATGG CAGGCCGTTA GGGCAGAGGG 5520  
AGCTGGGCGG GGCACAGCAG GGCAGGAGTG TGTGTGATGT GTCTGGGAA CCGCCCTGAG 5580  
GCGCTGCTGT GGTGTGAGTG CTGCAGGTGT CAAGGAAAT GTAGGAGATG TCTCCTGAGT 5640  
GTGATGGAAT ATAAACAGAT TTCCAGAAGG AACTGACATG ATCTGACTTA AAAAGGTGAG 5700  
TGTGCGAAT GGCTTGCAGG GGACAGGAGT GGGAGCAGGG AGATAGGAGA CAATGTGTAC 5760  
CAGGACAGCA GAAAGACATC CCGGTAGCC TGGAACAGGG AGACGGTGTG GAGATGGTGG 5820  
CAGTCCGATA ATGAGAGCGG TAGGGCAAGG CCAGCAGGAT CCTAGAGTGA GACGGGAGGT 5880  
AAAGTCACCG GGAATGGTG TCTCCACGTC AGGGGCAAGG GAAAGGAGA GGACAAGGT 5940  
GACCCGGGAG GTTAAAGATG GGACCGGGC CAGACGAGT GGTCTATGCC TGTATCTCTA 6000  
GCATTTTGGG AGGCTGAGGC GGGCGGATAG CTTGAGGTCA GGAGTTTGAA ACCAGCCTGG 6060  
CCAAATGCTT GAAACCCCTT CTCTACTAAA ATATACAAAA ATTAGCCTGG CGTGGTGGTG 6120  
CATGCTGCA GTCCAGCTA TTCAGGAGGC TGAGGCAACA AGAATCGCTT GAACTGGGA 6180  
GGCGGAGGTT GCACTGAGCC GAGATCGGC CATAGCACTC CAGCCTTAGC CTGGGCGACA 6240  
GAGCGAGACC ACATC

Seq ID NO: 86 Protein sequence  
Protein Accession #: XP\_027172.1

45  
50

1 11 21 31 41 51  
MDSSPSLPLI RTPESSLHEA LDQCMALDL FLTNQFSEAL SYLKPRTKES MYHSLTYATI 60  
LEMQMMTFD PQDILLAGNM MKEAQLCQR HRRKSSVTD FSSLVNRPTL GQFTEEEIHA 120  
EVCYAECLLQ RAALTFLQSS SHGGAVRPRA LHDPSHACSC PPGPGRQHLF LQDENMVSPF 180  
IKGGIKVRNS YQTYKELDSL VQSSQYCKGE NHPHFEQGVK LGVGAFLNLT SMLPTRLRL 240  
LEFVFGSGNK DYGLQLLEEG ASGHSFRSVL CVMILLCYHT FLTFVLGTGN VNIIEAEKLL 300  
KPYLNRYPKG AIFLFFAGRI EVIKGNIDAV SDGGPGRGWG SLGVSTSRK SGTCDILDR 360  
IDWGRGGQBE RTNQRAGAGE ALLAEQPGKT REEEAFVVPF ILTGRTYTA LQWREVEGGA

55  
60

Seq ID NO: 87 DNA sequence  
Nucleic Acid Accession #: AB007921  
Coding sequence: 143..1363

60  
65  
70  
75  
80

1 11 21 31 41 51  
GGTGAGACA CCGCCTCAGG GCTCGGTGCA CAGTGGACAT TTGGGGAGCG TTGTGGGTGA 60  
CCCCACACA GGCACCTGGA ATGCAGGGGA GAGGGGGCCA AGGGGGAAG GGGCCAGAGT 120  
GTGCTCTTG GATTACAGAG GATGAGATTC CAGTCTAGC TTGCCACTTA TTAGGACTCC 180  
TGAGAGCAGC CTCATGAGG CCTTGACCA GTGCATGACC GCGCTGGACC TCTTCTCTAC 240  
CAACCACTTC TCAGAAGCAC TCAGCTACCT CAGCCCAAGA ACCAAGGAAA GCATGTACCA 300  
CTCACTGACA TATGCCACCA TCCTGGAGAT GCAGGCCATG ATGACCTTTG ACCCTCAGGA 360  
CATCTGCTT GCGGGCAACA TGATGAAGGA GGCACAGATG CTGTGTCAGA GGCACCGGAG 420  
GAAGTCTTCT GTAACAGATT CCTTCAGCAG CCGGTGAAC GCGCCACAGC TGGGCCAATT 480  
CACTGAAGAG GAAATCCAGC CTGAGGTCTG CTATGCAGAG TGCCCTGCTGC AGOGAGCAGC 540  
CCTGACCTTC CTGCAGGTT CCTCACAGG AGGGGCACTC AGGCCAGAG CCTTGCACTGA 600  
TCCTCTCTAC GCGTCAGCT GCCCACCCTG GCCAGGCGGT CAGCATCTTT TCCTCCTGCA 660  
GGAGAGAAAC ATGGTGAGCT TCATCAAAAG CCGCATCAAA GTTGAAACA GTTACCAGAC 720  
CTACAAGGAG CTGAGCAGCC TTGTTCACTC CTCACAATAC TGCAAGGGTG AGAACCACCC 780  
GCATTTGAA GGAGGAGTGA AGCTTGGTGT AGGGGCTCTT AACCTGACAC TGTCCATGCT 840  
TCCTACTAGG ATCCTGAGGC TGTGGAGTT TGTGGGTTT TCAGAAACA AGGACTATGG 900  
GCTGCTGCAG CTGAGGAGG GAGCGTCAGG GCACAGCTTC CGCTCTGTGC TCTGTGTCAT 960  
GCTCTGCTG GCTTACCACT CTTCTCTCAC CTTCTGCTC GTTACTGGGA ACGTCAACAT 1020  
CGAGGAGGCC GAGAGCTCT TGAAGCCCTA CCTGAACCGG TACCCTAAGG GTGCCATCTT 1080  
CCTGTTCTTT GCAGGGAGGA TTGAAGTCAT TAAAGGCAAC ATTGATGCAG TGAGTGATGG 1140  
GGGTCCGGGC CGGGGCTGGG GATCCCTCGG GGTCTCCAG ACCAGCAGGA AGTCAGGCAC 1200  
ATGTGACATA CTCAGGAGCA GGATAGACTG GGGGCGGGGG GGGGGGCCAA GAGAGAACCA 1260  
ACCAAGAGAGC AGGGGCAAGG GAGGCCCTTC TGGCAGAGCA GCGTGGGAAG ACAAGGGAGG 1320  
AGGAGGCATT TGTGGTGCTT GGGATTITGA CTGGGAGATA TAGGACTGCA GCATTGCACT 1380  
GGAGGGAGGT GGAGGGAGGT GCTTGAGGGA GGCAGAGGTT AGGAAAGCCC ATCTGTTTAG 1440  
GGCATGACGA TTAGGCTGGA GTCTGTGACC TCCCTCCAT TATAGCTCTC TCCTGCTCTT 1500

	TCATTTTGGT	ACTAAAAACC	AGAGTCCTAG	GCGGGGGCTG	TATTTGAGCC	CAACGTCATG	1560
	TAAGACTTAG	GAGGTAAAC	CAGGACTGGA	GGCCAGATCT	CCTGGCTCCT	GGGGCCCCAC	1620
	CTGAGCCTAG	CACAGGCTG	GACCACTATG	CCCTGGAGGA	GTCCCGGTCT	GCTGTGGTGT	1680
	TGGGAGGTTG	GGAGGATGCA	GAGGGGTTGG	GGCTGGGTGG	GCACCCGTCA	GGCTGACCAG	1740
5	AAGGTGCTG	CAGGCCATCC	GGCGTTTCGA	GGAGTGCTGT	GAGGCCACGC	AGCACTGGAA	1800
	GCAGTCCAC	CACATGTGCT	ACTGGGAGCT	GATGTGGTGC	TTCACTACA	AGGCCAGTGT	1860
	GAAGATGTCC	TACTTCTACT	CCGACCTGCT	CAGCAAGGAG	AACGTCTGGT	CCAAGGTGGG	1920
	CTGATGCCAC	GTGTTAGGGG	CATTGGGTGA	CCAGGGCTGA	CTGTGTGCCT	CCAGACCACG	1980
10	GGCCAAATCC	CTAAGTGAAC	ACAGATGTCT	CAGCTGGAAT	CTAAACATAA	CCTTAAATTC	2040
	TAATAGGACT	CAGGCTTGGG	AGGAACTAAA	GACCACAAGA	GAAACTTCTG	AACCACAATG	2100
	TGTCACAAG	AGATTTCTAG	TCACAAAGGA	CAGAAACATG	GCTCCCTCTG	TCCAGTAGAA	2160
	CTGTTTCTGT	GGTAGAAATG	TTCTACTTAT	GCACCTGCCA	AATATGGTAG	TCACCAGCCA	2220
	CATGTGCACA	CTGAGCAGAT	GAAATGTGCC	TAGTGCACCT	GGGAAACTGA	TTGTTTTCAG	2280
15	TTTTATTAA	TTTTAATTAA	CTAAATGTTA	AATTTAAATA	GCCATGTAGG	GCTTGTGGCC	2340
	ACTATATTGG	ACTATGCAGG	TCCAAAACAC	AAAGGGCTCA	TATAACTGAA	CATTCTTGGC	2400
	ACATCOGACT	TCAGGTAGGG	CTGGATCCAG	GAATTCAAAT	GATGTGCTCT	GGCTTGGTCT	2460
	TTCCATTGTG	GGCTGTGCTC	TCTCCTATGA	CATCTTTGTT	TCTGCTGCAT	CTTTGCAGGA	2520
	AGGTTCTCTC	CATGTGACAG	GCAAGGTGGC	CACGGGCTGC	TTCTACTCAT	ATCCTCCCCCT	2580
20	TGGTTTCAAC	CAGACTCCCA	CAGTTTGAGC	CTCACTGGTC	TGACTTGTCA	CCTGCCAATG	2640
	CCTGGAACAG	AGGGGTGGGA	AGATTCTCTA	TGGGCTGAGA	GTAGGAGAGG	GGTGGTTCCA	2700
	CAGAAGAAA	TGATGCACCC	AGAAATAGTG	GAGGATTAA	CAAGATGCCA	TACAGGCAAA	2760
	ACAAAGCCAA	ACAGATGCCC	GCTTACCAAA	GATGAAATTT	ATCATGTGTA	GTATTGAAAT	2820
	AAGTGTAGC	TTGTACCATC	ATAGTAATGA	TAGTGCAGAA	ATTGGAACCA	AGAGTCTTAC	2880
25	AACCACTAG	CTCAGCAAA	GTCTAATCTG	TTATTGTGTA	ATACACAGGA	CATGTGTCTT	2940
	CATGGCTTCA	TCCCTGCCCC	ATGGCAGACA	TTGCTAATCA	ATCCTCTGCC	ATGAGCCTAG	3000
	CTGTGACCTT	AGATACCTTC	CCTGCAAAAG	TCCAGGCAGC	CGTTAGAACT	GACCCACATT	3060
	GGCACCTGTT	AGGAGACCTG	TCACTGTGCAT	CTGGTCCCTC	CCCCCTCTCT	GCATGGAGGT	3120
	CTCTCCGTA	GGCTTGCCTG	GGGACCAAGC	TGAAGGGGAA	TTCTCTGGGT	CTGGGGCAGG	3180
30	TGGGGCTGGG	GAGGGGAGCA	GGCTTCTACT	GAGCTCTCAA	CATGTCTGGC	ACCTGTCTAT	3240
	TCCTCCACAC	CACACCCAGT	GAGGAGAAAT	TATTATCTCC	ATTGGGCACA	TGAGGGCCAC	3300
	TGATGCTAAG	CGAGGACTGT	GACTTTCCCA	CCCACATGGC	TGTTGGTGAC	AGACACCGGA	3360
	TTTGAGGACA	GTCTGTGTGT	ACTCAGAGGC	CTCTGCTTCT	CTCTGTCTCC	TAGAGTCTCT	3420
	CTGAGGAGTC	GGGGCTTGCC	CTGAGCCAC	CCTGTCTGTT	AAGGTGCTTC	CTCAGGCCCA	3480
35	GCTCCCATGG	CCGCCACACC	CCCTCCTCAT	CACCTCCTAC	TCCCAAAAAG	GACAAAGCCT	3540
	CAGGGAACCT	TTTTTCTTTT	TTTAGAGACG	GGGTCTTGCT	ATGTTGGTCA	GGCTGGTCTT	3600
	GAACTCTCTG	GCCCAAGCAA	TCTTCCCGCC	TCTGCTCTCT	AAAGTGCTGG	GATTCTGGGC	3660
	CTTAGGGAAC	CTTTTGAAC	TGAAAGTGAC	GCTCGAAGCC	TTCTGTGAGA	GTGAGGTGGG	3720
	TGGCTGGGGC	TAAACCATAT	GGGAAGGAGA	GACCTGGTGG	GGGCACACAG	CTGCTATATA	3780
40	GAGGAACAGA	AGGTGGGCCA	GGCCTCCACG	CTGTGAGGAA	ATCTGGCTCA	GTCCCCAGAG	3840
	CGCTGTGTGG	CTTTGGGGTG	GCCAGTCCCT	CTCTCTCTGC	AACACTCTCC	TCATGAGGAC	3900
	TTCTGTGAAA	AATGGGGGTT	GTAACCCCTCT	GAGTTCTGGG	GCCCCACCCA	TTTCTAATCT	3960
	CCAGAACTTG	GCCACCAACG	ACTCCACCAA	CTTCTAGTCC	TGGGGCCTGG	GCCTCTGGCC	4020
	ATTGCCATAG	GCACCACTGT	CTCTGTGCAG	GCAGCGCCCC	CCTCTGCCAG	GATCCTCCGA	4080
45	GGTCAGCTGC	TGGTCTGAGC	CCGCAGACCC	TGGCTGAGCG	ACGGATGAAC	GGAGTATGCA	4140
	GACACAGGCT	TGCTTGTGAG	CAGATGGGGG	ACCCTTGCCA	GAGTCAGCAG	CGGCCCCCAT	4200
	AAGCCTGCCA	CGCTTGCAAT	TATTTAGTAC	AGATGTAATG	ACAAAGGCCT	AAAGCAAACT	4260
	CCATTGTGGG	GTAATTAAAC	TTGTGCCCCC	CCCAGAAAGA	GCAGTCTCTC	GCATGATGAT	4320
	TAAAGGCCAG	GTTCGAGGCG	CTAAGTAAAC	CACTTATCT	AGATCAATTC	CCTTACTTCT	4380
50	TGTTATCTAC	TTGAGAGAGG	TTGAGCTGCC	TTGAGCCAAA	TCCTTTCCCG	AAGCTTTTGG	4440
	AAAACCTCCG	AGCCTTCCAA	GGTTTGCTTC	TTTCTGTAAT	TTTTCTCACC	ACCCTGACCT	4500
	ATCTCCTGCA	GTGAGCCCTG	TGGAGGCTTT	TGTTTTCCTC	CCAGTGCTGG	CAGCCTAGAG	4560
	GCTGAGATGG	CCAGAAACAA	GGTGGTGACA	GTGGGCTGCT	CAGGCTTGGG	GAAACCCAGG	4620
	GAGCTAAAGG	CATGCCCAAG	CAACCAAGAA	GGACAGGAAG	GCTTCTGAGG	AGAGACCTCT	4680
55	GAGGTGGGTC	TTGGAGAGGA	AGGACTTAGG	GAGGCAGAGT	GGAGGAAGTG	AGAGGACACC	4740
	CCAGCCAAAG	AGGGCGGCAG	GACCAAGGCG	TCAGAAAGCA	GGGGCTGCA	GAGGGGCTGT	4800
	GTGCCACAGG	GTGAAGAGTT	TGTGTGGCAG	AAGGCGAGGG	GGCTTGCAATC	AGGGGTGACA	4860
	GCTGCTCTTT	TGTCCAGCA	TAGCCCTCTG	ACATCCCTGG	AGAGCTGGGG	CGTCCACAA	4920
	TCTAAGTCA	AGCCCCATC	CTAACCTCTG	TGGTGCACTG	AGGGTGAGCT	GTCTGTGGGC	4980
60	AGGAGGGAAG	ACTCTTGGAG	ATGAGCCTGG	TGAAGGGATA	ATGGCATCCC	GGGCCGAGGA	5040
	GCAGCACAGG	CAGAGGCTGT	GGGAGAGTTT	AAGGAGTGTA	GGGGAGGAAA	TGGCAGAGAA	5100
	TGAGCCAGAA	AAAGAAAGGT	TAGGGCAGGT	CCTGGAGGAC	ATGAGTGGCT	GTTTGGGCTT	5160
	TATCCAGCAG	TGGGGAGGCC	TTGGCAGGCT	TGTGGCTTAG	ATAGGTGCTT	TAGAAAGCCC	5220
	ACCAGCAGTT	GCTGGGCCAC	CCCGCTGGCT	GGGTCTGTTT	CTAAGGCAGG	AAATACAAGA	5280
65	ATGAGCAGGA	AAAGAACCCC	TCAAGGCTCA	CGTCTAGTGT	GGGAGACAAG	AAACACAGAT	5340
	GGGCAATATA	ACAGATGTCT	TGGTTCCAGT	AAGTGCACTG	AAGAACACAG	GAGGCTGGAT	5400
	GCAGGGAGTG	ATGGAGGGGG	CTTTGTAAGG	GGAGGTGGGG	GGAAGCCTGT	CTCAGAGGAC	5460
	ACCAGATATG	AGCGCAGGAG	CAGCACGTGG	CAGTCAATGT	GCAGGCCGTT	AGGGCAGAGG	5520
	GAGCTGGGCA	GGGCACAGCA	GGGCAGGAGT	GTGTTTGATG	TGTCTCTGGA	ACCGCCCTGA	5580
70	GGCGTCTGT	TGGCTGGAGT	GCTGCAGGTG	TCAAGGAAAT	TGTAGGAGAT	GTCTCTTGAG	5640
	TGTGATGGAA	TATAACCAGA	TTTCCAGAA	GAACTGACAT	GATCTGACTT	AAAAAGGTCA	5700
	GTGTGGGAAA	TGGCTTGAG	GGGACAGGAG	TGGGAGCAGG	GAGATAGGAG	ACAATGTGTA	5760
	CCAGGACAGC	AGAAAGACAT	CCCGGTAGC	CTGGAACAGG	GAGACGGTGT	GGAGATGGTG	5820
	GCAGTCCGAT	AATGAGAGCC	GTAGGGCAGG	GCCAGCAGGA	TCCTAGAGTG	AGACGGGAGG	5880
75	TAAAGTCA	GGGACTTGGT	GTCTCCAGT	CAGGGGCAAG	GGAAAGGGAG	AGGACAAGGG	5940
	TGACCCCGGA	GGTTAAAGAT	GGGACCGGGG	CCAGACGCAG	TGGCTCATGC	CTGTAATCCT	6000
	AGCACTTTGG	GAGGCTGAGG	CGGGCGGATG	GCTTGAGGTC	AGGAGTTTGA	AACCGGCTTG	6060
	GCCAAACATGG	TGAACCCCGG	TCTCTACTAA	AATATACAAA	AATTAGCCCTG	CGGTGGTGGT	6120
	GCATGCCCTGC	AGTCCCAAGT	ATTGAGGAGG	CTGAGGCGAC	AAGAAATCGCT	TGAACCTGGG	6180
80	AGGCGGAGGT	TGCAGTGAGC	CGAGATCCCG	CCATAGCACT	CCAGCCCTAG	CCTGGGCGAC	6240
	AGAGCGAGAC	CACATC					

Seq ID NO: 88 Protein sequence  
Protein Accession #: BAA32297.1

```

1      11      21      31      41      51
5      |      |      |      |      |      |
VETPPQGSVH SGHLGSVVD PHTGTGNAGE RGPRGKGARV LALDSGGMDS SPSLPLIRTP 60
ESSLHEALDQ CMTALDLFLT NQFSEALSYL KPRTKESMYH SLTYATILEM QAMMTFDPQD 120
ILLAGNMKEG AQMLCQRHRR KSSVTDSESS LVNRPFLGQF TEEIHAIEVC YAECLLQRAA 180
LTFLQGSSSHG GAVRPRALHD PSHACSCPPG PGRQHLFLQ DENMVSFIKG GIKVRNSYQT 240
YKELDSLVSQS SQYCKGENHP HFEGGVKLG VAFNLTL SML PTRILRLLEF VGFSGNKDYG 300
LLQLEEGASG HSFRSVLCVM LLLCYHTFLT FVLGTGNVNI EAEKLLKPY LNRYPKGAIF 360
10     LFFAGRIEVI KGNIDAVSDG GPGRGWSLGS VSQTSRKSQT CDILRDRIDW GRGGGPRENQ 420
PESRGRRGPS GRAAWEDKGG GGICGAWDFD WEI

```

Seq ID NO: 89 DNA sequence  
Nucleic Acid Accession #: AF007170  
Coding sequence: 73..1725

```

1      11      21      31      41      51
20     |      |      |      |      |      |
AAGGAGGCGC CCTCCGGGAA AAGCGACGCG AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
CTGGACCACT GCATGACCGC CCTGGACCTC TTCCTCACCA ACCAGTTCTC AGAAGCACTC 120
AGCTACTCTCA AGCCCAAGAA CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
CTGGAGATGCG AGCCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240
ATGAAGGAGG CACAGATGCT GTGTGAGAGG CACCGGAGGA AGTCTTCTGT AACGATTCC 300
TTGAGCAGCG TGTGTAACCG CCCCAAGCTG GGCCATTCA CTGAAGAAGA AATCCACGCT 360
25     GAGGTCTGCT ATGTCAGATG CCTGCTGCAG CGAGCAGCCC TGACCTTCTT GCAGGACGAG 420
AACATGTTGA GTTTCATCAA AGGCGGCATC AAAGTTGAA ACAGCTACCA GACCTACAAG 480
GAGCTGGACA GCCTTGTTCG GTCTTCACAA TACTGCAAGG GTGAGAACCA CCGCACTTT 540
GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600
AGGATCCTGA GGCTGTGGA GTTTGTGGGG TTTTCAGAA ACAAGACTA TGGGCTGCTG 660
30     CAGCTGGAGG AGGAGAGCTC AGGGCAGAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720
CTGTGCTTACC ACTGCTGCTC CACCTTCTGT CTCGGTACTG GGAACGTCAA CATCGAGGAG 780
GCCGAGAGGC TCTTGAAGCC CTACCTGAAC CGGTACCCCTA AGGCTGCCAT CTTCCTGTTT 840
TTTGACGAGA GGATTTGAAT CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900
GAGTGCTGTG AGGCCAGACA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
35     ATGTGTTGCT TCACCTACAA GGGCCAGTGG AAGATGTCTT ACTTCTAGC CGACCTGCTC 1020
AGCAAGGAGA ACTGCTGCTC CAAGGCCACC TACATTACA TGAAGCCGCG CTACCTCAGC 1080
ATGTTTGGGA AGGAGGACCA CAAGCCGCTC GGGGACGAGC AAGTGGAAAT ATTTGAGCT 1140
GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
CGAAAGTCCC GCGCTACTT CTCTCCAAAC CCTATCTCGC TGCCAGTGCC TGCTCTGGAA 1260
40     ATGATGTACA TCTGGAACGG CTACGCGCTG ATTGGGAAGC AGCCGAACT CACGGATGGG 1320
ATACTTGAGA TTACTACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCGAGA GAACGAGTAC 1380
TCAGTGGATG ACGAGTGCTT GGTGAAATG TTGAAAGGCC TGTGCTGTA ATACCTGGGC 1440
CGTGCTCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAA GAAGATTAAA 1500
TATGACCACT ACTGATGCC AAAGCCCTG CTGGAGCTGG CCTGTGCTGT TATGGAGCAA 1560
45     GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAACTA CAAGAATTAC 1620
TCCATGGAGT CAGGACACA CTTTGAATC CAGGACGACA CACTCCAAAG CAAGTCTTCC 1680
CTAGAGACA CAAGCAGATC CATGCTTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGT 1740
CCGGCTGGA AGACAGAGC AGCTGGACAG AGCTCTGTA AACATTCAA AATACCCCT 1800
CCCCCTGCCG TGCCCTGCTT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860
50     TGTATCCGCT CAGAAGCCGA GCTGGCATTT TCACCACTGT AGCCAGGGC CTTTGGCAAG 1920
GGCAGAGCAG CTGGAGCCCT CTGCTGCCCC TATCACACAT ACGGCTACTT GCTTTTCACT 1980
GTGATGTTTA AGAAGATGTA TGAACAGTTT ACATTTTCTT TAGAAATACA TTGATGGGAT 2040
CACAGTTGGC TTTAAAAACC AACACAATC AACCACTGT AAGTCTTTGT CTTACCTAT 2100
TATCATCTGG AGGTAATCT CTTTATATGA TGTAGCCAAA GGGCAATTG CTTTCAAAT 2160
55     TCAGCAAGTT CTCAGCTGT GTGACGGAAG GTCCCTCAGA GGACCTGAGG AATGCCTGGG 2220
AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTTGGGC ATGAGGATGT ACACAGACAC 2280
CCACTACCTT ACTACTACA CTTCAATTCA CTCCTTTTGT AAATTTCCAA TTTAAAAATC 2340
AAGCAGCTCT TTTTGTAGG ATAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
60     AGTAGAAATG GGCAGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
AAATTTGGGG GGCAGGAGGA GTTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
CTGAAACCCAC TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTTCAAGSTA 2580
CAATTTGCTTA CTGACAGCAT TTTGTATAA ACTGTTATTC TTGAAAAAAA AAAAAAAA 2640
AA

```

Seq ID NO: 90 Protein sequence  
Protein Accession #: AAC39582.1

```

1      11      21      31      41      51
70     |      |      |      |      |      |
KEAASGKSDR RTPESLHEA LDQCMTALDL FLTNQFSEAL SYLKPRTKES MYHSLTYATI 60
LEMQAMMTFD PQDILLAGNM MKEAQMLCQR HRRKSSVTD SSSLVNRPFL GQFTEEEIHA 120
EVCYAECLLQ RAALTFLQDE NMVSFIKGGI KVRNSYQTYK ELDSLVSQSS YCKGENHPHF 180
EGGVKLGUGA FNLTSLMLPT RILRLLEFVG FSGNKDYGLL QLEEGASGHS FRSVLCVMLL 240
LCYHTFLTFF LGTGNVNIIE AEKLLKPYLN RYPKGAIFLF FAGRIEVIKG NIDAAIRFFE 300
75     ECCEAQQHWK QFHMCYHEL MWCFTYKQGW KMSYFYADLL SKENCWSKAT YIYMKAAYLS 360
MFGKEDHKPF GDDEVELFRA VPGLKLKLAG KSLPTEKFAI RKSRRYPSSN PISLPVPALE 420
MMYIWNQYAV IGKQPKLTDG ILEIITKAE MLEKGPENEY SVDDECLVLK LKGLCLKLYG 480
RVQBAEENFR SIASANEKIK YDHYLPNAL LELALLLMEQ DRNEBAIKLL ESAKQNYKTY 540
80     SMESRTHFRI QAATLQAKSS LENSRRSMVS SVSL

```

Seq ID NO: 91 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 31..906



1 11 21 31 41 51  
CGGGTCGACC CACGCGTCCG GGGAGAAAGG ATGGCCGGCC TGGCGGCGCG GTTGGTCTCG 60  
CTAGCTGGGG CAGCGGCGCT GGCAGAGCGG TCCAGGGGCG ACCGTGAGCC GGTGTACCGC 120  
5 GACTGCGTAC TGCAGTGGCA AGAGCAGAAC TGCTCTGGGG GCGCTCTGAA TCACTTCCGC 180  
TCCCGCCAGC CAATCTACAT GAGTCTAGCA GGCTGGACCT GTCGGGACGA CTGTAAGTAT 240  
GAGTGTATGT GGGTCACCGT TGGGCTCTAC CTCCAGGAAG GTCACAAAGT GCCTCAGTTC 300  
CATGGCAAGT GGCCCTTCTC CCGGTTCTCG TTCTTTCAAG AGCCGGCATC GGCCGTGGCC 360  
TCGTTTCTCA ATGGCCTGGC CAGCCTGGTG ATGCTCTGCC GCTACCGCAC CTTCGTGCCA 420  
10 GCCTCTCCCC CCATGTACCA CACCTGTGTG GUCTTCGGCT GGGTGTCCCT CAATGCATGG 480  
TTCTGGTCCA CAGTYYTCCA CACCAGGGAC ACTGACCTCA CAGAGAAAAT GGACTACTTC 540  
TGTGCTCCA CTGTCTCCT ACATCAATC TACCTGTGCT GCGTCAGCCT CATCCGCTTC 600  
GACTATGGCT ACAACCTGGT GGCCAACGTG GCTATTGGCC TGGTCAACGT GGTGTGGTGG 660  
15 CTGGCCTGGT GCCTGTGGAA CCAGCGGCGG CTGCCTCAGG TGCAGCAAGT CGTGGTGGTG 720  
GTCTTGTGTC TGCAGGGGCT GTCCCTGTCT GAGCTGTCTG ACTTCCCACC GCTCTTCTGG 780  
GTCCCTGGAT CTGGCAGATC CTGGCACATC AGCACCATCC CTGTCCAGCT CCTCTTTTTC 840  
AGCTTTCTGG AAGATGACAG CTGTACCTG CTGAAGGAAT CAGAGGACAA GTTCAAGCTG 900  
GACTGAAGAC CTGGAGCGA GTCTGCCCA GTGGGATCC TGGCCCGCC CTGCTGGCCT 960  
20 CCCTTCTCCC CTCAACCTT GAGATGATT TCTCTTTTCA ACTTCTTGAA CTGGACATG 1020  
AAGGATGTGG GCCAGAAATC ATGTGGCCAG CCCACCCCTT GTTGGCCCTC ACCAGCCTTG 1080  
GAGTCTGTTC TAGGAAAGGC CTCCAGCAT CTGGGACTCG AGAGTGGGCA GCCCCTCTAC 1140  
CTCCGTGAGC TGAATCTGGG TGGAACTGAG TGTGCTCTTA GCTCTACCGG GAGGACAGCT 1200  
GCCTGTTTCC TCCCATCAG CTCTCTCCCC ACATCCCCAG CTGCCTGGCT GGGTCTTGAA 1260  
25 GCCCTCTGTC TACCTGGGAG ACCAGGGACC ACAGGCCCTA GGGATACAGG GGGTCCCTT 1320  
CTGTATACAC CCCCCACCTT CCTCCAGGAC ACCACTAGGT GGTGCTGGAT GCTTGTCTTT 1380  
TGGCAGCCCA AGGTTCAAGG CGATTCTCCC CATGGGATCT TGAGGGACCA AGCTGCTGGG 1440  
ATTGGGAAGG AGTTTCAACC TGACCTTGGC CTTAGCCAGG TTCCAGGAG GCCTCACCAT 1500  
ACTCCCTTTC AGGGCCAGG CTCCAGCAAG CCCAGGGCAA GGATCCTGTG CTGCTGTCTG 1560  
30 GTTGAAGGCC TGCCACCGTG TGTCCGGAGT GTGGCCGAG CTGAGTGCAT AGGTGACAGG 1620  
GCCGTGAGCA TGGGCTCTGG TGTGTGTGAG CTCAGGCAC T AGGTGCGCAG TGTGGAGACG 1680  
GGTGTGTGTC GGGTCCCGAC GTGGCTTCAA AGTGTGTGTG GTGCAGGGGG TKGGTGTGTT 1740  
AAGCGTGGGT TAGGGGAACG TGTGTGCGCG TGCTGGTGGG CATGTGAGAT GAGTGACTGC 1800  
CGGTGAATGT GTCCACAGTT GAGAGGTTGG AGCAGGATGA GGGAACTCTG TCACCATCAA 1860  
35 TAATCACTTG TGGAGCGCCA CTGGGCCCAA GACGCCACCT GGGCGGACAG CAGGAGCTCT 1920  
CCATGGCCAG GCTGCTCTGT TGCAATGTTCC CTGTCTGGTG CCCCTTTGCC CGCCTCTTGC 1980  
AAACCTCACA GGGTCCCGAC ACAACAGTGC CCTCCAGAAG CAGCCCTCG GAGGACAGG 2040  
AAGGAAATG GGGATGGCTG GGGCTCTCTC CATCCTCCTT TTCTCCTTGC CTTCGCATGG 2100  
CTGGCCTTCC CCTCCAAAAC CTCCATTCCC CTGCTGCCAG CCCCTTTGCC ATAGCCTGAT 2160  
40 TTTGGGGAGG AGGAAGGGGC GATTGTAGGG AGAAGGGGAG AAAGCTTATG GCTGGGTCTG 2220  
GTTTCTTCCC TTCCAGAGG GTCTTACTGT TCCAGGGTGG CCCAGGGGCA GGCAGGGGCC 2280  
ACACTATGCC TGGCCCTCTG TAAAGGTGAC CCCTGCCATT TACCAGCAGC CTGGCATGT 2340  
TCCTGCCCCA CAGGAATAGA ATGGAGGGAG CTCCAGAAAC TTTCATCCCC AAAGGCAGTC 2400  
TCCGTGGTGG AAGCAGACTG GATTTTGTCT CTGCCCCTGA CCCCTTGCTC CTCTTTGAGG 2460  
45 GAGGGGAGCT ATGCTAGGAC TCCAACTCA GGGACTCGGG TGGCCTGCGC TAGCTTCTTT 2520  
TGATACTGAA AACTTTTAAG GTGGGAGGGT GGCAGGGGAT GTGCTTAATA AATCAATTCC 2580  
AAGCCTCAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 92 Protein sequence  
Protein Accession #: Eos sequence

50 1 11 21 31 41 51  
MAGLAARLVL LAGAAALASG SQGDREPVYR DCVLQCEBQN CSGGALNHFR SRQPIYMSLA 60  
55 GWTCDRDKY ECMVTVGLY LQEGHKVPQF HGKNWPSRFL FQEPASAVA SFLNGLASLV 120  
MLCRYRFPV ASSPMYHTCV AFAWVSLNAN FWSVTFHTRD TDLTERMDYF CASTVILHSI 180  
YLCCVTVGL QHPVVSFAFR ALLLLMLTVH VSYLSLIRFD YGNLVANVA IGLNVNVNWL 240  
ANCLNNQRL PHVRKCVVVV LLLQGLSLLE LLDFPPLFW LDAHAIWEIS TIPVHVLFFS 300  
FLEDDSLYLL KESEDKPKLD

Seq ID NO: 93 DNA sequence  
Nucleic Acid Accession #: NM\_033419.1  
Coding sequence: 18..980

65 1 11 21 31 41 51  
CGAGCCAGGG AGAAAGGATG GCGGCGCTGG CCGGCGGTT GGTCTGCTA GCTGGGGCAG 60  
CGGCGCTGGC GAGCGGCTCC CAGGGCGACC GTGAGCCGGT GTACCGGAC TGGTACTGTC 120  
70 AGTGCGAAGA GCAGAACTGC TCTGGGGGCG CTCTGAATCA CTTCCGCTCC CGCCAGCCAA 180  
TCTACATGAG TCTAGCAGGC TGGACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG 240  
TCACCGTTGG GCTCTACCTC CAGGAAGGTC ACAAGTGCC TCACTTCCAT GGCAGTGGC 300  
CCTTCTCCCG GTTCTCTGTC TTTCAAGAGC CGGCATCGGC CGTGGCCTCG TTTCTCAATG 360  
GCCGTGCCAG CCTGGTATG CTCTGCCGCT ACCGCACCTT CGTGCCAGCC TCCTCCCCCA 420  
TGTACCACAC CTGTGTGGCC TTGCGCTGGG TGTCCCTCAA TGCAATGGTC TGGTCCACAG 480  
75 TTTTCCACAC CAGGGACACT GACCTCACAG AGAAAATGGA CTACTTCTGT GCCTCCACTG 540  
TCATCTTACA CTCAATCTAC CTGTGCTCGG TCAGGACCGT GGGGCTGCAG CACCCAGCTG 600  
TGGTCACTGC CTTCGGGCTC CTCTGCTGCT TCATGCTGAC CGTGCACTGT TCCTACCTGA 660  
GCCTCATCCG CTTCGACTAT GGCTACAACC TGGTGGCCAA CGTGGCTATT GGCCTGGTCA 720  
80 ACGTGGTGTG GTGGCTGGCC TGTGCTGGG GGAACAGCG CGGCTGCTCT CACGTGGGCA 780  
AGTGGTGGT GGTGGTCTTC CTGTGTCAGG GGTGTCCCT GCTCGAGCTG CTGACTTCC 840  
CACGCTCTT CTGGGTCTCG GATGCCCATG CCATCTGGCA CATCAGCACC ATCCCTGTCC 900  
ACGTCCTCTT TTTCACTTT CTGGAAGATG ACAGCCTGTA CCGTCTGAAG GAATCAGAGG 960  
ACAAGTTCAA GCTGGACTGA AGACCTTGGA GCGAGTCTGC CCCAGTGGGG ATCCTGCCCC 1020  
GCCTCTGCTG GCTTCCCTTC TCCCTCAAC CCTTGAGATG ATTTCTCTT TTCAACTTCT 1080  
TGAACCTGGA CATGAAGGAT GTGGGCCAG AATCATGTGG CCAGCCACCC CCTGTGTGGC 1140

5 CCTCACCAGC CTTGGAGTCT GTTCTAGGGA AGGCCTCCCA GCATCTGGGA CTCGAGAGTG 1200  
 GGCAGCCCTT CTAGCTCCTG GAGCTGAAGT GGGGTGGAAC TGAGTGTGCT CTTAGCTCTA 1260  
 CCGGAGGAGC AGCTGCCTGT TTCCTCCCA TCAGCCTCCT CCCCACATCC CCAGCTGCCT 1320  
 GGCTGGGTCC TGAAGCCCTC TGCTACCTG GGAGACCAGG GACCACAGGC CTTAGGGATA 1380  
 CAGGGGGTCC CTTCTGTGTA CCACCCCCCA CCTCCTCCA GGACACCACT AGGTGGTGCT 1440  
 GGATGCTTGT TCTTTGGCCA GCCAAGGTTT ACCTGATGCA TCCCATGGG ATCTTGAGGG 1500  
 ACCAAGCTGC TGGGATTGGG AAGGAGTTTC ACCCTGACCA TTGCCCTAGC CAGGTTCCTA 1560  
 GGAGGCCTCA CCATACTCCC TTTCAGGSCC AGGGCTCCAG CAAGCCAGG GCAAGGATCC 1620  
 10 TGTGCTGCTG TCTGGTTGAG AGCCTGCCAC CGTGTGTCGG GAGTGTGGGC CAGGCTGAGT 1680  
 GCATAGGTGA CAGGGCCGTG AGCATGGGCC TGGGTGTGTG TGAGCTCAGG CTTAGGTGCG 1740  
 CAGTGTGAGG ACGGGTGTG TCAGGGAAGA GGTGTGGCTT CAAAGTGTGT GTGTGCAGG 1800  
 GGTGGGTGTG TTAGCGTGGG TTAGGGGAAC GTGTGTGCGC GTGCTGTGGG GCATGTGAGA 1860  
 TGAGTGAAGT CCGGTGAATG TGTCCACAGT TGAGAGGTTG GAGCAGGATG AGGGAATCCT 1920  
 15 GTCACCATCA ATAATCACTT GTGGAGCGCC AGCTCTGCCC AAGCGCCAC CTGGGCGGAC 1980  
 AGCCAGGAGC TCTCCATGGC CAGGCTGCCT GTGTGCATGT TCCCTGTCTG GTGCCCTTTT 2040  
 GCCCGCTCC TCACAACTTC ACAGGTTCCC CACACAACAG TGCCCTCCAG AAGCAGCCCC 2100  
 TCGGAGGCAG AGGAAGGAAA ATGGGGATGG CTGGGCTCTC CTCATCTCTT CTTTCTCTCT 2160  
 TGCCTTCGCA TGGCTGGCCT TCCCTCCAA AACCTCCAT CCGCTGCTGC CAGCCCTTTT 2220  
 20 GCCATAGCCT GATTTTGGGG AGGAGGAAGG GCGSATTGA GGGAGAAGGG GAGAAAGCTT 2280  
 ATGGCTGGGT CTGGTTTCTT CCTTCCAGG AGGGTCTTAC TGTTCACAGG TGGCCCCAGG 2340  
 CAGGCGAGG AGCCGCTATG GCCTGCGCCC TGTAAGAGT GACCCCTGCC ATTACACAG 2400  
 AGCCCTGGCA TGTCTCTGCC CCACAGGAAT AGAATGGAGG GAGCTCCAGA AACTTTCAT 2460  
 25 CCAAGAGGCA GTCTCCGTGG TTGAAGCAGA CTGGATTTT GCTCTGCCCC TGACCCCTTG 2520  
 TCCCTCTTTG AGGAGGGGGA GCTATGCTAG GACTCCAAAC TCAGGGACTC GGGTGCCTG 2580  
 CGTAGCTTC TTTTGATACT GAAAACTTTT AAGGTGGGAG TGTGGCAAGG GATGTGCTTA 2640  
 ATAAATCAAT TCCAGCCTC AAAAAAAAAA AAAAAAAAAA AA

Seq ID NO: 94 Protein sequence  
 Protein Accession #: NP\_219487.1

30 1 11 21 31 41 51  
 MKDVGPESCG QPTPCWPSPA LESVLGKASQ HLGLESQQLP YLLELNWGGT ECALSSSTGRT 60  
 AACFLPISLL PTSPARWLGP EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTTRWCKMLV 120  
 35 LWPAKVHGDG PHGILRDQAA GIGKEFHPDH CPSQVPRRP HTPFQGGSSG KPRARILCCC 180  
 LVESLEPCVG SVQAEICGD RAVSMGLGVC ELRPRCAVWR RVLGSKRCGF KVCVCRGWVC

Seq ID NO: 95 DNA sequence  
 Nucleic Acid Accession #: XM\_090469  
 Coding sequence:

40 1 11 21 31 41 51  
 45 ATGGGGTTTG GAGACACAGG AACCGTGGAA GGGAGCCTAG GAACGTGGAA AGATAGCTCC 60  
 TGCCGCGTGC TGGACAGGAC GCAGGTGAAC AAGCCCTGCC TGCTGGAGGC TGCCAGCAC 120  
 AGCCCAACCC CCTTGCAATG ACAGTCGGTC AACAGCCACC CATCAGGTGC TCATCAGAAA 180  
 CCACCTGAAG TGAATAATGT TGGAGCCAGT CAAGGTTTGC TGACAATGGA AACAAACAG 240  
 TCCCTGGCAC AAGGCACAGG CTGCTCAGTG TGCTGGGAGG TGAACGGCCC AGGGTTGGAA 300  
 50 ATGTCTCTTC CTGAGTGTCT CAGTGTCTGAT GCTGGCCAGG TGGAGCAGAG AAGACAATG 360  
 AACTCCGAG ATACTGACTG GGAAGTCTAG GAGGGACAGG GAAGTCTAGA TTTCCCGGTG 420  
 GCTGCCACCC AGGAAGACAC TTTCTTTTGA AAAGACATCA AGCACAAGAG TACGTTACAG 480  
 CAATCAGTTC AGCAGCAGAA TTGCATTATC AGCCCCAGAG AAAAAACCTG TGGGAATGTC 540  
 AGGGCACCTT GCGGCCACCC AAGGCGAGAG GCCCGCTTGC CCTCAGCAG GCGCTGGGG 600  
 55 CTCAGCCGCA GCCCGGCCCC GTCCCAAGT ACACCCATGG CGCCCTTCCC GACCTCTGAC 660  
 CGCGAGCTAG ACGGCCCAGG CCGGCCCCCC GGGCTGCGGA GCTCGGCAGC AGCCCCCTAC 720  
 TGCTGCCCCG CGGCTCCAGA AGCCCAAGAA CTCTCTTCTC TGCTGCCCTT TTATCCAGAT 780  
 GGCAGCCAC CACCTAAGGA CATCTGCAAG ACGCTCCAGC ACAAGGCACC TGGGAAGAGA 840  
 60 CTGCATCAAG AATCACCAGG TTCAATTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900  
 TGTATCAAG GGGCTCTGGG TGTGGCTGCT GAAGCAGCAT TTCATTACA GTTTTCCAGT 960  
 GAATGA

Seq ID NO: 96 Protein sequence  
 Protein Accession #: XP\_090469

65 1 11 21 31 41 51  
 MGFGDQGTVE GSLGTSKDS CRVLDRTQVN KPCLLEAAKH SPHPLHGQSV NSHPSGARQK 60  
 PPEVIMFGAS QGLLTMETNQ SLAQGTGCSV CWEVNGPGL MSPLGVLSD AGQVEHRRQM 120  
 70 NSADTDWTE EGPGSLDAFV AAHQEDTFPL KDIKHTSTFR QSVQONCIY SPREKPCGNV 180  
 RAPCAPPRRE APLALSRPWR LSRSPAPSPR TPMAPPTSD RELDAPGPPP GLRSSAAAPH 240  
 CLPAAPPAQK LPFLPLPYD GSPPPKDILQ TLQHKAPGR LHQESPGSFP IGLCNRTAEP 300  
 CLKGALGVAA EAFHLQFSS E

Seq ID NO: 97 DNA sequence  
 Nucleic Acid Accession #: NM\_003474.2  
 Coding sequence: 37..3036

75 1 11 21 31 41 51  
 80 CACTAACGCT CTTCTAGTC CCGGGGCCAA CTCGGACAGT TTGCTCATT ATTGCAACGG 60  
 TCAAGCTGG CTTGTGCCAG AACGGCGCGC GCGCGACGCA CGCACACACA CGGGGGGAAA 120  
 CTTTITTAAT AATGAAAGGC TAGAAGAGCT CAGCGCGCGC GCGGGCCGTG CGCGAGGGCT 180  
 CCGGAGCTGA CTCGCCGAGG CAGGAATCC CTCGGTTCGC GACGCCCGGC CCCGCTCGGC 240  
 GCGCGCTGG GATGGTGCAG CGCTCGCCGC CGGGCCGAG AGCTGTGCA CTGAAGCCGG 300

	GCGACGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
	GCCGGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
	GCTGATGAAG	TTGTCACTGC	CTCTGTTGG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
	TTGCACTCCA	AGAAATCATCC	AGAAGTGCTG	AATATTGCGA	TACAAACGGG	AAGCAAAGAA	540
5	CTGATCATAA	ATCTGGAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCACGTGT	720
	TCTGGTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGTCTTAGA	ACCAATGAAA	780
10	AGTGCAACCA	ACAGATACAA	ACTCTTCCCA	GCGAAGAAGC	TGAAAGCGT	CCGGGGATCA	840
	TGTGGATCAC	ATCAACAAC	ACCAAACCTC	GCTGCAAGA	ATGTGTTTCC	ACCACCTCT	900
	CAGACATGGG	CAAGAAGGCA	TAAAGAGAG	ACCCCTAAGG	CAACTAAGTA	TGTGGAGCTG	960
	GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGCGATTAA	TAGAGATTGC	TAATCACGTT	GACAAGTTTT	ACAGACCACT	GAACATTGG	1080
	ATCGTGTGG	TAGGCGTGG	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
15	CCATTACCA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	1200
	TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTCC	AAGGGACCAC	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCAT	GGACCATTC	1320
	GACAAATCCC	TGGTGCAGC	CGTGACCCCTG	GCACATGAGC	TGGCCACAA	TTTCGGGATG	1380
	AATCATGACA	CATGGAACAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
20	ATCATGAACG	CTTCCACCGG	GTACCCATTT	CCCATTGGTG	TCAGCAGTTG	CAGCAGGAAG	1500
	GACTTGGAGA	ATGCGCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACTT	GCCGGAAGTC	1560
	AGGGAGTCTT	TGGGGGCCCA	GAAGTGTGGG	AACAGATTGG	TGGAAGAAGG	AGAGGAGTGT	1620
	GACTGTGGGG	AGCAGAGAGA	ATGTATGAAT	CGCTGCTGCA	ATGCCACCAC	CTGTACCCCTG	1680
	AAGCCGGAAG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCACST	GAAGCTGCA	1740
25	GGAAACAGGT	GCAGGGACTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
	AGCCCTCACT	GCCCAAGCCAA	CGTGTACCTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
	GGCTACTGCT	ACAAATGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTGAC	ACTCTGGGGA	1920
	CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTCG	AGGTGATCCT	1980
	TATGGCAACT	GTGGCAAAAT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
30	AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2100
	GTTTCCATAG	AAACAAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
	CACGTGTACT	TGGGCGATGA	CATGCCGGAC	CCAGGGCTTG	TGCTTGACAG	CACAAAGTGT	2220
	GCAGATGGAA	AAATCTGCCT	GAATCGTCAA	TGTCAAAATA	TTAGTGTCTT	TGGGGTTTAC	2280
	GAGTGTGCAA	TGCACTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
35	GAGGCCCACT	GGGCACCTCC	CTTCTGTGAC	AAGTTTGGCT	TGGAGGAAG	CACAGACAGC	2400
	GGCCCCATCC	GCGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATTCGTGT	GACCATCCTG	2460
	TGTTCTCTTG	CTGCGGGAAT	TGTGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGTCTG	2520
	TTTACAAATA	AGAAGACCAAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
	CGTGGCTTCC	AACCTGTGCA	GGCTCACCTC	GGCCACCTTG	GAAGAAGSCT	GATGAGGAAG	2640
40	CCGCCAGATT	CCTACCCACC	GAAGGACAAT	CCCAGGAGAT	TGCTGCASTG	TCAGAATGTT	2700
	GACATCAGCA	GACCCCTCAA	CGGCCCTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
	CTTCCCTCCC	TCCACCGGGC	CCCAAGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
	AAGCCTAGCC	TTAGGCGAGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880
	CCTGCAGATC	CTCTGGCCAG	AACAACCTGG	CTCACTCATG	CCTTGGCCAG	GACCCACGGA	2940
45	CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
	GTGCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CGACACCTT	TTTTCAACAG	3060
	TGAAGACATA	AGTTTGCACT	ATCTTTTCACT	TCCAGTTGGA	GTTTTTTGT	CCAACTTTTA	3120
	GGATTTTTTT	TAATGTTTAA	AACATCATTA	CTATAAGAAC	TTTGAGCTAC	TGCCGTGAGT	3180
	GCTGTGCTGT	GCTATGGTGC	TCGTCTACT	TSCACAGGTA	CTGTAAAT	ATTAATTAT	3240
50	GCAGAATGTT	GATTACAGTG	CAGTGGCTG	TAGTAGGCAT	TTTTACCATC	ACTGAGTTT	3300
	CCATGGCAGG	AAGCTTGTG	GTGCTTTAG	TATTTTATG	AACITGAAAT	ATCCTGCTTG	3360
	ATGGGATCTC	GGACAGGATG	TGTTTGTCTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
	CCAACTACCC	CCAAGCTGTG	TTATGGTACC	AGATGCAGCT	CAAGAGATCC	CAAGTAGAAT	3480
	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
55	TGTGTTTGGC	TTTCAGGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCCAGGG	3600
	ACACCTGGGA	GAATATCTGC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
	AGGAATCTTA	AGGTGTAGCC	ACACAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCCCTGAG	CTGACCAGCC	GTGAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
	GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTGCTG	TCCTTTCTAG	AGCACTGCCA	3840
60	CCAGTAGGTT	ATTAGCTTG	GAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCAGGCA	3900
	CTGCAAAACG	CCACCTCCCT	ATAGTGTCTG	GAGCTGAGCA	AATCACCACA	AACGTGAATA	3960
	CAATGATCCT	GTATTGAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAATA	TTTTCAGATG	4020
	TGAACCATTA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAA	4080
	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTATGGG	4140
65	TATAGTTTAT	GTCTGTATC	ATTATTGTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCTTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTCTT	TAAACACTTG	CAACCTACCT	GTGAGCATC	ACAGAAATGT	ATAAGGAAAT	4320
	CAACTTGTCT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTGAA	4380
	CTCTTCACTC	TTCAATGGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGCTCT	TAAAGTACT	4440
70	AATGGCATGA	GAAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCCTA	TGCTTTTGAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCTTCCAGA	AAACAAAAC	GCATTTCACT	TTCCGGGTGT	4680
	TCCCACTGTT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
75	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTCCAA	CTGATATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAAAT	TCTTTAAAT	GCTGGAATAA	AATACTGCTG	4860	
	AGATACATAC	AGAATTACTG	TAACTGATTA	CACCTGTGTA	TTGACTATAA	GCCAAACATA	4920
	TATATATCTT	TAAAAAGGTT	TACAGAATTT	TATGGTGCA	TACGTGGGCA	TTGTCTTTT	4980
80	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCT	CCAATTATTA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAA	AA				

Seq ID NO: 98 Protein sequence  
Protein Accession #: NP\_003465

1 11 21 31 41 51  
MAARPLPVSP ARALLLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSG DLWIPVKSFD 60  
SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHY 120  
5 YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPK KLSVRGSCG 180  
SHHNTFNLAA KNVFPSPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLKVKQR 240  
LIEIANHVDK FYRPLNIRIV LVGVEVWMDM DKCSVSQDPF TSLHEFLDNR FMKLLPRKSH 300  
DNAQLVSGVY FQGTIGMAP IMSMCTADQS GGIWMDHSDN PLGAAVTLAH ELGHNFGMNH 360  
10 DTLDRGCSQ MAVEGGCGIM NASTGYPFPM VFSSCSRKDL ETSLEKGMV CLFNLPEVRE 420  
SFGGQKCGNR FVEEGECDC GEPEECMNR CNATTCTLRP DAVCAHGLCC EDCQLKPAGT 480  
ACRDSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVGY CYNGICQTHE QQCVTLMGPG 540  
AKPAPGICFE RVNSAGDPYG NCGKVSXSSF AKCEMRDAKC GKIQCQGGAS RPIVGTNAVS 600  
IETNIPLQGG GRILCRGTHV YLGDDMPDPG LVLATKCAD GKICLNRQCC NISVFGVHEC 660  
15 AMQCHGRGVC NNRKINCHCEA HWAPPFCDKF GFGGSTDSP IRQADNQLT IGILVTILCL 720  
LAAGFVVYLK RKTILRLFT NKKTIEKLR CVRPSRPPRG PQPCQAHGLH LGKGLMRKPP 780  
DSYPPKDNFR RLQCCQNDVI SRPLNGLNVP QPQSTQRVLP FLHRAFRAPS VFARPLPAKP 840  
ALRQAGTCK PNPPQKPLPA DPLARTTTLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900  
RSTHTAYIK

20 Seq ID NO: 99 DNA sequence  
Nucleic Acid Accession #: NM\_003714  
Coding sequence: 135..1043

1 11 21 31 41 51  
25 GAGGAGGAGG GAAAAGCGGA GCAAAAAGGA AGAGTGGGAG GAGGAGGGGA AGCGGCGAAG 60  
GAGGAAGAGG AGGAGGAGGA AGAGGGGAGC ACAAAGGATC CAGGTCTCCC GACGGGAGGT 120  
TAATACCAAG AACCATGTGT GCCGAGCGGC TGGGCCAGTT CATGACCCCTG GCTTTGGTGT 180  
30 TGGCCACCTT TGACCGCGCG CGGGGAGCCG ACGCCACCAA CCCACCCGAG GGTCCCCAAG 240  
ACAGGAGCTC CCACGAGAAA GGCCGCGCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT 300  
GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG CGGTGTTTGA ATGTTTCGAG AACAACTCTT 360  
GTGAGATTGG GGGCTTACAT GGGATTGCA TGACTTTCT GCACAACGCT GGAATAATTG 420  
ATGCCACGG CAAGTCATT ATCAAAGACG CCTTGAATG TAAGGCCAC GCTCTCGCG 480  
35 ACAGGTTCCG CTGCATAGC CGGAAGTGCC CGGCCATCAG GGAATGTGT TCCAGTTGC 540  
AGCGGGAATG CTACCTCAAG CACGACCTGT CGCGGCTGC CCAGGAGAAC ACCCGGGTGA 600  
TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660  
ACTTGTCTGT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTT 720  
AGTGTGAGCA GAACCTGGGA AGCCTGTGCT CCATCTTGAG CTCTGCACC TCGGCCATCC 780  
40 AGAAGCCTCC CACGCGGCC CCGAGCGGCC AGCCCCAGT GGACAGAAC AAGCTCTCCA 840  
GGGCCACCA CGGGGAAGCA GGACATCACC TCCAGAGCC CAGCAGTAGG GAGACTGGCC 900  
GAGGTGCCAA GGGTGAGCGA GGTAGCAAGA GCCACCCAAA CGCCCATGCC CGAGGCAGAG 960  
TCGGGGGCTT TGGGCTCAG GGACCTCCG GAAGCAGCGA GTGGGAAGAC GAACAGTCTG 1020  
AGTATTCTGA TATCCGAGG TGAATGAAA GGCCTGGCCA CGAAATCTTT CCTCCACGCC 1080  
45 GTCCATTTTC TTATCTATGG ACATTCCAAA ACATTTACCA TTAGAGAGGG GGGATGTCTC 1140  
ACGAGGATT CTGTGGGAC TGTTGACTTC ATCGAGGTGT GTGTTCCGCG AACGGACAGG 1200  
TGAGATGGAG ACCCTTGGGG CCGTGGGGTC TCAGGGGTGC CTGGTGAATT CTGCACTTAC 1260  
ACGTACTCAA GGGAGCGCGC CCGGCTTATC CTGTAACCTT TGCTCTCTTT CCATCTGTGG 1320  
AGTCAGTGGG TGTCCGCGC TCTGTTGTGG GGGAGGTGAA CCAGGGAGGG GCAGGGCAAG 1380  
50 GCAGGGCCCC CAGAGCTGGG CCACACAGTG GGTGCTGGGC CTCGCCCCGA AGCTTCTGGT 1440  
GCAGCAGCCT CTGGTCTGT CTCCGCGGAA GTCAGGGCG CTGGATTCCA GGACAGGAGT 1500  
GAATGTAAAA ATAAATATCG CTTAGAAATG AGGAGAAGGG TGGAGAGGAG GCAGGGGCGG 1560  
AGGGGTGGCT TGGTGCCAAA CTGAAATTC GTTTCTTGTG TGGGGCCTTG CGGTTACAG 1620  
CTCTTGGCGA GGTGGGAGGG AGGAGTGTCA TTTCTATGT TAATTCTGA GCCATTGTAC 1680  
55 TGCTGGGCT GGGGGGACA CTGTCCAAG GAGTGGCCCC TATGAGTTTA TATTTTAAAC 1740  
ACTGCTTCAA ATCTCGATT CACTTTTTTT ATTTATCCAG TTATATCTAC ATATCTGTCA 1800  
TCTAAATAAA TGGCTTTCAA ACAAAGCAAC TGGGTCTATTA AAACAGCTC AAAGGGGGTT 1860  
TAAAAAAAAA AAACACAGCC CATCCTTTGA GCCTGATTTT TCTTTTTTTT AAGTTCTATT 1920  
TTAAAGCTA TCAAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCCTGCC 1980  
60 CACTTGGGG AAACCTTATA CCCAGAGGAA AATACACACC TGGGGAGTAC ATTTGACAAA 2040  
TTTCCCTTAG GATTTCGTTA TCTCACCTTG ACCCTCAGCC AAGATTGCTA AAGCTGCGTC 2100  
CTGCCGATT CAGGAGACCC AGCTGGAAAC CTGGCTTCTC CATGTGAGGG GATGGGAAAG 2160  
GAAAGAGAG AATGAAGACT ACTTAGTAAT TCCATCAGG AAATGCTGAC CTTTACATA 2220  
AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA 2280  
65 TTTAGCAATA AGGAGAGGAG TCCAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340  
GGGAGAGGAA GAAAGAGAG AGAGAAAAGA GCCTGCTGCC

Seq ID NO: 100 Protein sequence  
Protein Accession #: NP\_003705

70 1 11 21 31 41 51  
MCAERLQGFQ TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRSLQNT AEIQHCLVNA 60  
GDVGGGVFEC FENNSCEIRG LHGICMTFLH NAGKFDAGK SPFKDALCK AHALRRHFGC 120  
75 ISRKCPAIRE MVSQIQRECY LKHDLCAAA ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180  
CGEEVKCAIT HSVQVQCEQN WGSLSILSF CTSAIQKPFT APPERQFQVD RTKLRSRAHGG 240  
EAGHHLPEPS SRETGRGAKG ERGSKSHFNA HARGRVGGLG AQGPSGSSEW EDEQSEYSDI 300  
RR

80 Seq ID NO: 101 DNA sequence  
Nucleic Acid Accession #: NM\_005940  
Coding sequence: 23..1489

1 11 21 31 41 51

5 AAGCCAGCA GCCCGGGG GATGGCTCC GGCCGCTGG CTCGAGCG CGCCGCGCG 60  
 CGCCCTCTG CCCCGATGC TGCTGCTGCT GCTCCAGCG CGCCGCTGC TGGCCCGGGC 120  
 TCTGCCGCG GACGTCCACC ACCTCCATGC CGAGAGGAG GGGCCACAGC CTGGCATGC 180  
 AGCCCTGCC AGTAGCCCG CACCTGCCCC TGCCACGCG GAAGCCCCC GGCTGCCAG 240  
 CAGCTCAGC CCTCCCGCT GTGGCGTGC CGACCATCT GATGGGCTGA GTGCCCGCA 300  
 CGACAGAAG AGGTTCTGTC TTTCTGGCG GCGCTGGAG AAGACGACC TCACCTACAG 360  
 GATCCTTCGG TTTCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACA TGGCAGAGGC 420  
 CCTAAAGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCAG AGGGCCGTGC 480  
 10 TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGAC GACCTGCCGT TTGATGGGCC 540  
 TGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGG ATGTCCACTT 600  
 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACAGGGC ACAGACTGCG TCAGGTGGC 660  
 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCA AGGCCCTGAT 720  
 TCGCGCTTC TACACCTTTC GCTACCCACT GAGTCTCAG CCAGATGACT GCAGGGCGT 780  
 15 TCAACACCTA TATGGCCAGC CTGGGCCAC TGTCACCTCC AGGACCCAG CCCTGGGCC 840  
 CCAGGCTGG ATAGACACA ATGAGATTGC ACCGCTGGAG CCAGACGCC CGCCAGATGC 900  
 CTGTAGAGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTT TCTTCAAGC 960  
 GGGCTTTGTG TGGCGCTTCC GTGGGGGCA GCTGCAGCCC GGCTACCCAG CATGGCCCTC 1020  
 TCGCCACTGG CAGGCACTGC CCAGCCCTGT GGACGCTGCC TTGAGGATG CCAGGGGCA 1080  
 20 CATTTGGTTC TTCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAGC CAGTCTCTGG 1140  
 CCCCAGCCC CTCACCGAGC TGGGCTGGT GAGGTTCGCG GTCCATGCTG CCTTGGTCTG 1200  
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACCC 1260  
 CAGCACCCGG CGGTAGACA GTCCCGTGC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320  
 CTCTGAGATC GACGCTGCTT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGGCGGCGC 1380  
 25 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCTCTCTGT 1440  
 GGGTCTGAC TTCTTTGGCT GTGCCAGCC TGCCAACT TCTCTGAC CATGGCTTGT 1500  
 ATGCCCTCAG GGGTGTGAC CCCTGCCAG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560  
 ATCTTTGTGG CTGTGGGAC CAGGCATGGG ACTGAGCCCA TGTCTCTCTG AGGGGATGG 1620  
 GGTGGGTAC AACCAACATG ACAACTGCCG GAGGGGCCAC GCAGGTCTGT GTACCTGCC 1680  
 30 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740  
 GGGACCCGCT ATCAGGTCCC TGGCAACCT GGCCTGCCCT TCTCATCCCT GTCCCTCAG 1800  
 GTAGCACCAT GGCAGGACTG GGGGAACCTG AGTGTCTCTG CTGTATCCCT GTTGTGAGT 1860  
 TCCTTCCAGG GGTGGGACT GAAGCAAGGG TGCTGGGGCC CCATGCGCTT CAGCCCTGGC 1920  
 TGAGCAACTG GCGCTAGGG CAGGGCCACT TCCTGAGTTC AGGTCTTGGT AGGTGCTGC 1980  
 35 ATCTGTCTGC CTCTGGCTG ACAATCTCTG AAATCTGTTC TCCAGAATCC AGGCCAAAA 2040  
 GTTCACAGTC AATAGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGAGGCTG 2100  
 CAACATACCT CAATCTGTGC CCAGGCCGGA TCCTCTGAA GCCCTTTTGC CAGCACTGCT 2160  
 ATCTCCAAA GCCATTGTA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TCTTTTCTT 2220  
 TTTTAACT GAGGATTGTC ATTAACACA GTTGTCTTCT

40 Seq ID NO: 102 Protein sequence  
 Protein Accession #: NP\_005931

45 1 11 21 31 41 51  
 MAPAANLRS AARALLPML LLLQPPPLL ARALPPDVH LHAERRGPQ WHAALPSSPA 60  
 PAPATQEAPR PASSLRPPRC GVPDPDSGLS ARNRQKREVL SGRNEKTDL TYRILRFPWQ 120  
 LVQQRQVTM AEALKVMSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DPGGILAHA 180  
 FFPKTRHGD VHPDYDEWT IGDDQGTDL QVAHEFGHV LGLQHTTAAK ALMSAPYTFR 240  
 50 YPLSLSPDC RGVQHLVQRP WPTVTSRTPA LGPQAGIDTN EIALEPDAP PDACEASFDA 300  
 VSTIRGELFF FKAGFVRLR GGQLQPGYPA LASRWQGLP SPVDAAPEDA QGHWFQGA 360  
 QYVVDGEKP VLGPAPLTEL GLVRFVHAA LVNSPEKNI YFFRGRDYWR FHPSTRRVDS 420  
 PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFPD VKKALEGFP RLVGDPDFGC 480  
 AEPANTFL

55 Seq ID NO: 103 DNA sequence  
 Nucleic Acid Accession #: NM\_033151.2  
 Coding sequence: 351..4499

60 1 11 21 31 41 51  
 ACTGGGATA AGCAAGAAGA CTGATTTTAT GAGCAGGGGT TTGATACATC AAAGGAGATT 60  
 GCCCAGGATC AAGGGTGC GGTTGGGGT GGGTTGGGA GGGTGGTTAG AGAAGGTTTC 120  
 ACTAAGTGAT TTGGGCTGA GGCCTGAGAA GATGTTTAAA AAGAGGGATC AAGCACAGGC 180  
 65 TAAGGAGAGG AAAGAGCAGG CACCCAAACC TCTGCATGCG CCCAATATGC TCCTTGACAG 240  
 GTAGTGCCCC CTCTTCTGGC TGCTCAAGGC GAGATCTAAG CTTCTTCTAA CTCTGCTGT 300  
 CTTTTATAT TCTCTGATTC TGGGAAACGA AGAATTGGCA GGAAGTGAAT ATGACTAGGA 360  
 AGAGGACATA CTGGGTGCC AACTCTTCTG GTGGCCTCGT GAATCGTGGC ATGACATAG 420  
 CGGATGACAT GGTTCAGGA CTTATTATATA AAACCTATAC TCTCCAAGAT GGCCCTTGA 480  
 70 GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GAGGGGCAGC TGTCCACCG TGGGGGAAGT 540  
 ATGATGCTGC CTGAGAACCT ATGATTCCT TCGTCCCAA GCGAGGTTT CCGCCGCC 600  
 AGCCCTGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCTAGGCTC ACCCGCTCA 660  
 TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACCACT CCCTCCACTG TCAGTCCATG 720  
 ATGCCCTCAG CAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA GTCTCAAGGC 780  
 75 GAGGGATGA AAAAGCTTCA GTGCTCTG TGATGCTGAG GTTCCAGAGA ACAAGGTGA 840  
 TTTCTGATGC ACTTCTGGGC ATCTGCTTCT GCAITGCCAG TGTACTCGGG CCAATATTGA 900  
 TTATACCAA GATCCTGGAA TATTAGAAG AGCAGTTGGG GAATGTTGT CATGGAGTGG 960  
 GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC TCCTCCAGTT 1020  
 GGATCATCAA CCAACGCACA GCCATCAGGT TCGAGCAGC TGTTCTCTCC TTGCGCTTTC 1080  
 80 AGAAGCTCAT CCAATTAAG TCTGTAATAC ACATCACTC AGGAGAGGCC ATCAGCTTCT 1140  
 TCACCGTGA TGTAACTAC CTGTTGAAG GGGTGTGCTA TGGACCCCTA GTACTGATCA 1200  
 CCTGCGCATC GCTGGTCATC TGCAGCATTT CTCTACTT CATTTATTGA TACTGTCAT 1260  
 TTATTGCCAT CTATGCTAT CTCTGGTTT TCCACTGGC GGTATTCATG ACAAGAATGG 1320  
 CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGGACCA GCGATCCGT GTGACCATG 1380  
 AAGTCTCAC TTGATTAAG CTGATTAATA TGTACACATG GGAGAAACCA TTTGCAAAA 1440

5 TCATTGAAGA CCTAAGAAGG AAGGAAAGGA AACTATTGGA GAAGTGC GG CTGTGCCAGA 1500  
 GCCTGACAA TATAACCTTG TTCAATCATCC CCACAGTGGC CACAGCGGTC TGGGTCTCA 1560  
 TCCACACATC CTTAAAGCTG AAACCTCACAG CGTCAATGGC CTTACGATG CTGGCCTCCT 1620  
 TGAATCTCCT TGGGCTGTCA GTGTTCTTTG TGCTATTGCG AGTCAAAGGT CTCACGAATT 1680  
 CCAAGTCTCG AGTGATGAGG TTCAAGAAGT TTTTCTCTCA GGAGAGCCCT GTTTTCTATG 1740  
 TCCAGACATT ACAAGACCCC AGCAAAGCTC TGGTCTTTGA GGAGGCCACC TTGTATGCGC 1800  
 AACAGACCTG TCCCGGGATC GTCAATGGGG CACTGGAGCT GGAGAGGAAC GGGCATGCTT 1860  
 CTGAGGGGAT GACGAGGCT AGAGATGCCC TCGGGCCAGA GGAAGAAGGG AACAGCCTGG 1920  
 10 GCCAGAGATT GCACAAGATC AACCTGGTGG TGTCCAAGGG GATGATGTTA GGGGTCTGCG 1980  
 GCAACACGGG GAGTGGTAAG AGCAGCCTGT TGTCAAGCAT CCTGGAGGAG ATGCACTTGC 2040  
 TCGAGGGCTC GGTGGGGTGG CAGGGAAGCC TGGCCTATGT CCCCAGCAG GCCTGGATCG 2100  
 TCAAGGGGAA CATCAGGGAG AACATCTCTA TGGGAGGCGC ATATGACAAG GCCCGATACC 2160  
 TCCAGGTGCT CCACTGCTGC TCCCTGAATC GGGACCTGGA ACTTCTGCCC TTGGAGACA 2220  
 15 TGACAGAGAT TGGAGAGCGG GGCCTCAACC TCTCTGGGG GCAGAAACAG AGGATCAGCC 2280  
 TGGCCCGCGC CGTCTATTCC GACCGTCAGA TCTACCTGCT GGACGACCCC CTGTCTGCTG 2340  
 TGGAGCGCCA CGTGGGGAAG CACATTTTTG AGGAGTGCAT TAAGAAGACA CTCAGGGGGA 2400  
 AGACGGTCTG CCTGGTGACC CACCAGCTGC AGTACTTAGA ATTTTGTGGC CAGATCATTT 2460  
 TGTGGGAAA TGGGAAAATG TGTGAAAATG GAACTCACAG TGAGTTAATG CAGAAAAAGG 2520  
 20 GGAATATATG CCAACTTATC CAGAAGATGC ACAAGGAAGC CACTTCGGAC ATGTGTCAGG 2580  
 ACACAGCAA GATAGCAGAG AAGCCAAAGG TAGAAAGTCA GGCTCTGGCC ACCTCCCTGG 2640  
 AAGAGTCTCT CAACGGAAAT GCTGTGCGG AGCATCAGCT CACACAGGAG GAGGAGATGG 2700  
 AAGAAGGCTC CTTGAGTTGG AGGGTCTACC ACCACTACAT CCAGGCAGCT GGAGGTTACA 2760  
 TGGTCTCTGG CATAATTTTC TTCTTGTGG TGTGATCGT CTTCTTAACG ATCTCTAGCT 2820  
 25 TCTGGTGGCT GAGCTACTGG TTGGAGCAGG GCTCGGGGAC CAATAGCAGC CGAGAGAGCA 2880  
 ATGGAACCAT GGCAGACCTG GGCACATTG CAGACAATCC TCACTGTCTC TTCTACGAC 2940  
 TGGTGTACGG GCTCAAGGCC CTGCTCTCTA TCTGTGTTGG GGTCTGCTCC TCAGGGATTT 3000  
 TCACCAAACT CACGAGGAAG GCATCCACGG CCCTGCACAA CAAGCTCTTC AACAGGTTT 3060  
 TCCGCTGCCC CATGAGTTTC TTGACACCA TCCCAATAGG CCGGCTTTTG AACTGCTCG 3120  
 30 CAGGGGACTT GGAACAGCTG GACCACTCT TCCCATCTT TTGAGAGCAG TTCTGGTCC 3180  
 TGTCTTAAT GGTGATGCGC GTCTGTTGA TTGTAGTGT GCTGTCTCCA TATATCTGT 3240  
 TAATGGGAGC CATAATCATG GTTATTTGCT TCATTATTA TATGATGTTT AAGAAGGCCA 3300  
 TCGGTGTGTT CAAGAGACTG GAGAACTATA GCCGCTCTCC TTTATTCTCC CACATCCTCA 3360  
 35 ATTCTCTGCA AGGCCTGAGC TCCATCCATG TCTATGAAA AACTGAAGAC TTCATCAGCC 3420  
 AGTTTAAGAG GCTCACTGAT GCGCAGAATA ACTACCTGCT GTTGTCTCTA TCTTCCACAC 3480  
 GATGGATGGC ATTGAGGCTG GAGATCATGA CCAACCTTGT GACCTTGGCT GTTGCCTGT 3540  
 TCGTGGCTTT TGGCATTTTC TCCACCCCTT ACTCCTTTAA AGTCATGGCT GTCAACATCG 3600  
 TGCTGCAGCT GGGCTCCAGC TTCCAGGCCA CTGCCCGGAT TGGCTTGGAG ACAGAGGCCAC 3660  
 40 AGTTCAAGCT GTTAGAGAG ATACTGAGT ACATGAAGAT GTGTGTCTCG GAAGCTCCTT 3720  
 TACACATGGA AGGCACAAGT TGTCCCAGG GGTGCCACA GCATGGGAA ATCATATTTT 3780  
 AGGATTATCA CATGAAATAC AGAGACAACA CACCCACCGT GCTTCACGGC ATCAACCTGA 3840  
 CCATCCCGCG CCACGAAGTG GTGGGCATCG TGGGAAGGAC GGGCTCTGGG AAGTCTCCT 3900  
 TGGGCATGGC TCTCTCCGC CTGGTGGAGC CCATGGCAGG CCGGATCTCT ATTGACGGCG 3960  
 TGGACATTTG CAGCATGCGC CTGGAGGACT TGGGTGCAA GCTCTCAGT ATCCCTCAAG 4020  
 45 ATCCAGTGTCT GCTCTCAGGA ACCATCAGAT TCAACCTAGA TCCCTTTGAC CGTCACACTG 4080  
 ACCAGCAGAT CTGGGATGCC TTGGAGAGGA CATTCCTGAC CAAGGCCATC TCAAGTTCC 4140  
 CCAAAAAGCT GCATACAGAT GTGGTGAAGA ACGGTGAAA CTTCTCTGTG GGGGAGAGGC 4200  
 AGCTGCTCTG CATTGCCAGG GCTGTGCTTC GCAACTCCAA GATCATCCTT ATCGATGAAG 4260  
 CCACAGCCCTC CATTGACATG GAGACAGACA CCGTATCCA GCGCACAATC CGTGAAGCCT 4320  
 50 TCCAGGGCTG CACCGTGCTC GTCAATGCCC ACCGTGTAC CACTGTGCTG AACTGTGACC 4380  
 ACATCCTGGT TATGGGCAAT GGGAGGTTGG TAGAATTGTA TCGGCCGGAG GTACTGCGGA 4440  
 AGAAGCCTGG GCTATTGTTT GCAGCCCTCA TGGCCACAGC CACTTCTTCA CTGAGATAAG 4500  
 GAGATGTGGA GACTTCATGG AGGCTGGCAG CTGAGCTCAG AGGTTACAC AGGTGAGCT 4560  
 TCGAGGCCCA CAGTCTGCGA CTTCTTGTG TGGAGATGAG AACTTCTCCT GGAAGCAGGG 4620  
 55 GTAAATGTAG GGGGGTGGG GATTGTGGA TGGAAACCTT GGAATAGGCT ACTGTATGCC 4680  
 TCTCAAGACC TTAGAACCCC AGAACCATCT AAGACATGGG ATTCACTGAT CATGTGTTT 4740  
 TCTTTTAACT TTACATGCTG AATAATTTTA TAATAAGGTA AAGCCTTATA GTTTTCTGAT 4800  
 CTGTGTTAGA AGTGTGCAA ATGCTGTACT GACTTTGTAA AATATAAAAC TAAGGAAAAC 4860  
 TC

60 Seq ID NO: 104 Protein sequence  
 Protein Accession #: NP\_149163.2

1 11 21 31 41 51  
 65 MTRKRTYWVP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQRNP EAPGRAAVPP 60  
 WKYDAALRT MIPFRPKPRF PAPQPLDNAG LPSYLVSWL TPLMIQSLRS RLDENTIPPL 120  
 SVHDAADKNV QRLHRLWEEV VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFIASVLG 180  
 PILIIPKILE YSEEQGNVNV HGVGLCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS 240  
 70 FAFKLIQFK SVIHITSGEA ISFPTGDNVY LFEVGYGFL VLITCASLVI CSISSYFIIG 300  
 YTAFIAILCY LLVFPVAVFM TRMAVKAQHH TSEVSDQRIR VTSEVLTCIK LIRMYTWEKP 360  
 FAKIIEDLRK KERKLEKCG LVQSLTSITL FIIPVTAVAV WVLHTSLKL KLTASMAFSM 420  
 LASLNLRLS VFPVPIAVKG LTNSKSAVMR FRKPFLEQEP VFYVQTLDQD SKALVPFEAT 480  
 LSWQQTCPGI VNGALELERN GHASEGMTRP RDALGPEEKG NSLGPHELHI NLAVSKGMML 540  
 75 GVCQGTGSGK SSSLASILEE MHLLEGSGVG QGSLAYVPOQ AWIVSGNIRE NILMGAYDK 600  
 ARYLQVLHCC SLNRDLELLP FGDMTFIERG GLNLGGQKQ RISLARAVYS DRQIYLLDDP 660  
 LSAVDAHVGK HIFEECIKKT LRKTVVLVT HQLQYLEFCG QIILLENGKI CENGTHSEIM 720  
 QKKGKAYQLI QKMHEATSD MLQDTAKIAE KPKVESQALA TSLEESLNGN AVPERQLTQE 780  
 80 EEMEGLSLWS RVYHYHIAA GGYMVSCIIF FFFVLIVFLT IFSFWLSTYV LEQSGSTNSS 840  
 RESNGTMADL GNIADNPQLS FYQLVYGLNA LLLICVGVCS SGIFTKVTBK ASTALHNLKF 900  
 NKVFRCPMSF FDTIPIGRLL NCFAGDLEQL DQLLPISFEP FLVLSLMVIA VLLIVSVLSP 960  
 YILLMGAIIM VICFIYMMF KKAIGVFKRL ENYSRSLPFS HILNSIQGLS SIHVYKGTED 1020  
 FISQFKRLTD AQNNYLLFL SSTRWMLRL EIMTNLVTLA VALFVAFGIS STPYSPFKVMA 1080  
 VNIVLQLASS FQATARIGLE TEAQPTAVER ILQYMKMCVS EAPLHMEGTS CPQGWPOHGE 1140  
 IIFQDYEMKY RDNTPTVLHG INLTIRGHEV VGIVGRTGSG KSSLGMALFR LVEPMAGRIL 1200

IDGVDCISIG LEDLRSLKSLV IPQDPVLLSG TIRFNLDPPD RHTDQIWDIA LERTFLTKAI 1260  
SKFPKLLHTD VVENGNFVSF GERQLLCIAR AVLRLNSKIL IDEATASIDM ETDTLIQRTI 1320  
REAFQGCCTLV VIAHRVTTLV NCDHILVMGN GKVVEFDRPE VLRKKPGSLF AALMATATSS 1380  
LR

5

Seq ID NO: 105 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..4043

10 1 11 21 31 41 51  
| | | | |  
ATGACTAGGA AGAGGACATA CTGGGTGCCC AACTCTTCTG GTGGCCTCGT GAATCGTGGC 60  
ATCGACATAG GCGATGACAT GGTTCAGGA CTTATTATTA AAACCTATAC TCTCCAAGAT 120  
GGCCCTGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCACCG 180  
15 TGGGGGAAGT ATGATGTGTC CTTGAGAACC ATGATTCCCT TCCGTCCCAA GCGAGGTTT 240  
CTGCCCCCC AGCCCTCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300  
ACCCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCCTCCACTG 360  
TCAGTCCATG ATGCTCAGA CAATAATGTC CAAAGGCTTC ACCGCCTTTG GGAAGAAGAA 420  
GTCTCAAGGC GAGGAGTTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480  
20 ACAAGGTGTA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTA CTGCGG 540  
CCAATATTGA TTATACCAAA GATCCTGGAA TATTGAGAAG AGCAGTGGG GAATGTTGTC 600  
CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCGAAT GTGTGAAGTC TCTGAGTTTC 660  
TCCTCCAGT GCATCATCAA CCAACGCACA GCCATCAGGT TCCGAGCAGC GTTTTCTCCT 720  
25 TTTGCTTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780  
ATCAGCTTCT TCACCGGTGA TGTAAGTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840  
GTACTGATCA CTGCGCATC GCTGGTCATC TGCAGCATTT CTCTCTACTT CATTATTGGA 900  
TACTACTGAT TTATTGGCAT CTATGTCTAT CTCTGCTTTC TCCACTGGC GGTATTTCATG 960  
ACAGAAGTGG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT 1020  
30 GTGACCAAGT AAGTCTTCTC TTGCATTAA GTGATTAATA TGTACACATG GGAGAAACCA 1080  
TTTGCAAAAA TCATTGAAGG TATGGAAAGT CTGACTTTCT GCTCCAAACC TGGTGATGGC 1140  
ATGGCTTTCA GCATGCTGGC CTCTTTGAAT CTCTTGGC TGTCAGTGT CTCTGTGCTC 1200  
ATTGCACTCA AAGTCTTCTC GAATTTCAAG TCTGCACTGA TGAGGTTCAG GAAGTTTTC 1260  
CTCCAGGAGA GCGCTGTTT CTATGTCCAG ACATTACAAG ACCCCAGCAA AGCTCTGGTC 1320  
35 TTTGAGGAGG CCACCTTCTC ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG 1380  
GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCTTAGAGA TGCCCTCGGG 1440  
CCAGAGGAAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500  
AAGGGGATGA TGTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCTGTTGTCA 1560  
GCCATCTGG CTGTGAAGGC CTGCTCGAG GGCTCGGTGG GGGTGCAGGG AAGCCTGGCC 1620  
40 TATGTCCCCC AGCAGGCTG GATCGTCAG GGAACATCA GGAAGACAT CCTCATGGGA 1680  
GGGSCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740  
CTGGAACCTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCTC CAACCTCTCT 1800  
GGGGGGCAGA AACAGAGGAT CAGCTGGGCC CGCGCCCTCT ATTCCGACCG TCAGATCTAC 1860  
CTGCTGGAG GCGCTGTTT TGCTGTGGAC GCCCACTGGG GGAAGCACAT TTTTGAGGAG 1920  
45 TGCAATTAAG AGACATCTAG GGGGAAGAGG GTGCTCTGG TGACCCACCA GCTGCAGTAC 1980  
TTAGAATTTT GTGGCCAGAT CATTTTGTG GAAATGGGA AAATCTGTGA AAATGGAAC 2040  
CACAGTGAAT TAATGAGAAA AAAGGGGAAA TATGCCCAAC TTATCCAGAA GATGCACAAG 2100  
GAAGCCACTT CGACATGTT GCAGGACACA GCAAGATAG CAGAGAAGCC AAAGGTAGAA 2160  
AGTCAGGCTC TGGCCACTTC CCTGGAAGAG TCTCTCAACG GAAATGCTGT GCCGGAGCAT 2220  
CAGCTCACAC AGGAGGAGGA GATGAAGAA GGCTCCTTGA GTTGGAGGT CTACCAACAC 2280  
50 TACATCCAGG CAGCTGGAG TTACATGGTC TCTGCTATA TTTTCTTCT CTGTGTGCTG 2340  
ATCGTCTTCT TAACGATCT CAGCTTCTGG TGGCTGAGCT ACTGGTTGGA GCAGGGCTCG 2400  
GGGACCAATA GCGAGCGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGCAGAC 2460  
AATCTCAAC TGTCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCCTGCT CTCTCATCTG 2520  
55 GTGGGGTCT GCTCTCAGG GATTTTCACC AAAGTCAGG GGAAGGCATC CACGGCCCTG 2580  
CACACAAGC TCTTCAACA GGTTTTCCGC TGCCCATGA GTTCTTTGA CACCATCCCA 2640  
ATAGGCGCGC TTTTGAACCT CTTGCGAGGG GACTTGAAC AGCTGGACCA GCTCTGCCCC 2700  
ATCTTTTCAG AGCAGTTCCT GGTCTCTGCC TTAATGGTGA TCGCGCTCCT GTTGATTGTC 2760  
AGTGTGCTGT CTCATATAT CCTGTTAATG GGAGCCATA TCAATGGTTAT TTGCTTCATT 2820  
TATTATATGA TGTTCAGAA GGCCATCGGT GTGTTCAAGA GACTGGAGAA CTATAGCCGG 2880  
60 TCTCCTTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT 2940  
GGAAAACTG AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000  
CTGCTGTGT TCTATCTTC CACACGATGG ATGGCATTGA GGCTGGAGAT CATGACCAAC 3060  
CTGTGACCT TGGCTGTTGC CTTGTTGCTG GCTTTGGCA TTTCTCCAC CCCCTACTCC 3120  
TTTAAAGTCA TGGCTGTCAA CATGCTGCTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180  
65 CGGATTGGCT TGGAGACAGA GGCACAGTTC ACGGCTGTAG AGAGGATACT GCAGTACATG 3240  
AAGATGTGTG TCTCGAAGC TCCTTTACAC ATGGAAGGCA CAAGTTGTCC CCAGGGGTGG 3300  
CCACAGCATG GGGAAATCAT ATTTAGGAT TATCATGA AATACAGAGA CAACACACCC 3360  
ACCGTGCTCT ACGGCATCAA CCTGACCATC CGCGGCCAG AAGTGGTGGG CATCGTGGGA 3420  
70 AGGACGGCT CTGGGAAGTC CTCTTGGGC ATGGCTCTCT TCCGCTGGT GGAGCCCATG 3480  
GCAGGCGGGA TTCTCATGTA CGGCTGTGAC ATTGCAGCA TGGGCTTGA GGACTTGGG 3540  
TCCAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600  
CTAGATCCCT TTGACCGTCA CACTGACCAAG CAGATCTGGG ATGCTTGA GAGGACATTC 3660  
CTGACCAAGG CCATCTCAA GTTCCCAA AAGCTGCATA CAGATGTGGT GGAACCGGT 3720  
75 GGAACTCTCT CTGTGGGGGA GAGGACGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC 3780  
TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCTG 3840  
ATCCAGCGCA CAATCGTGA AGCCTTCCAG GGCTGCACCG TGCTGTCAT TGCCCAACCGT 3900  
GTCACCACTG TGCTGAACCTG TGACCATCT CTGTTATGG GCAATGGGAA GGTGGTAGAA 3960  
80 TTTGATCGGC CGGAGGTACT GGGGAAGAAG CCTGGGTCAT TGTTCGACG CCTCATGGCC 4020  
ACAGCCACTT CTTCCTGAG ATAA

Seq ID NO: 106 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP 60  
 5 WGKYDAALRT MIFFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RIDENTIPPL 120  
 SVHDASDQNV QRLHRLWEEV VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG 180  
 PILIIPKILE YSEEQGNVNV HGVLCLFALF LSECVKLSLF SSSWIINQRT AIRFRAVSS 240  
 FAFELIQFK SVIHITSGEA ISFPTGDNVY LPEGVCYGPL VLITCASLVI CSISSYFIIG 300  
 10 YTAFAIILCY LLVFPPLAVFM TRMAVKAQHH TSEVSDQRIR VTSEVLTCIK LIKMYTWEKP 360  
 FAKIIEGMES LTPCSKPGDG MAFSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRPKKFP 420  
 LQESPVFYVQ TLQDPSKALV FEATLSWQQ TCPGIVNGAL ELERNHASE GMTRPRDALG 480  
 PEEEGNSLGP ELHKINLVVS KGMMLGVCGN TSGSKSLLS AILEEMHLE GSVGVQGS LA 540  
 YVFPQAWIVS GNIRENIMLG GAYDKARYLQ VLHCCSLNRD LELLPFGDMT BIGERGLNLS 600  
 15 GGQKQRISLA RAVYSRQIY LLDDPLSAVD AHVGHIPFE CYKKTLRGKT VLVTHQLQY 660  
 LEPCGQIILL ENKICENGIT HSELMQKKGK YAQLIQMHK EATSDMLQDT AKIAEKPKVE 720  
 SQALATSLLE SLNGNAVPEH QLTQEEEMEE GSLSWRVYHH YIQAGGYMV SCIIFFVVL 780  
 IVPLTIPFSW WLSYWLQGS GTNSSRESNG TMADLGNAD NPQLSFYQLV YGLNALLLIC 840  
 VGVCSGGIFT KVTAKASTAL HNKLPNKVR CPMSFFDTIP IGRLLNCFAG DLEQLDQLP 900  
 20 IFSEQLVLSL LMVIAVLIV SVLSPIYLLM GAIIMVICFI YMMFKAIG VFKRLNYSR 960  
 SPLFSHILNS LQGLSIHYV GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALRLEIMTN 1020  
 LVTLAVALPV AFGISSTPYS PKVMVNVIL QCLASSFOATA RIGLETAQF TAVERILQYM 1080  
 KMCVSEAPLH MEGTSCPGW PQHGEIIPD YHMKYRDNTP TVLHGINTLI RGHEVGVIGV 1140  
 RTGSGKSSLG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN 1200  
 25 LDPEFRHTDQ QINDALERTF LTKAISKFPK KLHTDVVENG GNFSVGERQL LCIAARAVLRN 1260  
 SKIILIDEAT ASIDMETDPL IORTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMNGKQVVE 1320  
 FDRPEVLRKK PGSFLAALMA TATSSLR

Seq ID NO: 107 DNA sequence

Nucleic Acid Accession #: NM\_024022

Coding sequence: 202..1563

30 1 11 21 31 41 51  
 ACCGGGCACC GGAAGGCTCG GGTACTTTCG TTCTTAATTA GGTGATGCCG GTGTGAGCCA 60  
 35 GGAAGAGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGCC TACTATCTCT TCCGTGGTGG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCCGT AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTGTC ACCAGATGCA 300  
 40 GATGCTGTGT CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTGACACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCT CTCACTCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATGTCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGCTCACT AGCCAAATGT TGCTGTGCTC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 45 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GTGACTGCA TTACACCACT CAGTATATGT GAGGAGGGA 780  
 TGTGCTCTG TGCCAGTGGT TACCTTGCAG TGCACAGCCT GTGCTCATAG AAGGGGCTAC 840  
 AGCTCAGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCT AGTGGCCCTG GCAGGCCAGC 900  
 50 CTTCAGTTCC AGGGCTACCA CTTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCGCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGTGACAA TCCAGCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 55 GATGGAAGAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGG TGACGCTCC 1260  
 CCTGTCTGA ACCACGGGGC CGTCCCTTTG ATTTCCAAACA AGATCTGCAA CCACAGGGAG 1320  
 GTGTACGGTG GCATCATCTC CCCCTCCATG CTCTGCGCGG GCTACCTGAC GGGTGGGTG 1380  
 GACAGCTGCC AGGGGGACAG CGGGGGGCC CTGCTGTGTC AAGAGAGGAG GCTGTGGAAG 1440  
 TTAGTGGGAG GCACAGCTT TGGCATCGGC TGCAGAGAG TGAACAAGCC TGGGTGTGAC 1500  
 60 ACCGTGTCA CCTCTTCTC GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560  
 TGAAGAGGAA GGGGACAGAT AGCCACCTGA GTTCTGAGG TGATGAAGAC AGCCCGATCC 1620  
 TCCCTGAGAC TCCGTGTAG GAACCTGCAC ACAGCAGAC ACCCTTGGAG CTCTGAGTTC 1680  
 CGGCACCACT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTCAA 1740  
 65 GCTGCTTTT GTTTTGTGTT TTTTGTAGGT GGAGTCTCGC TCTGTTGCCC AGCCTGGAGT 1800  
 GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860  
 CCTCAGCTC CCCAGTAGCT GGGACCAAG GTGCCGCCA CCACACCCAA CTAATTTTGT 1920  
 TATTTTATG AGAGACAGGG TTTCAACATG TTGGCCAGGC TGCTCTCAAA CCCCTGACCT 1980  
 70 CAAATGATGT GCCTGCTTCA GCCTCCACA GTGCTGGGAT TACAGGCATG GGCCACCAAG 2040  
 CCTAGCTCA CGCTCCTTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAAGG 2100  
 GCGGCTTTC CCACTGTGTC ATCTGGTTT CTCTCCAGGG GTCTTGCAA ATTCTGTAGC 2160  
 AGATAAGCAG TATGTGACC TCACTGTCAA AGCTACCAAC AGCCACTCAG AAAAGACGCA 2220  
 75 CCAGCCCGA AGTGCAGAAC TGCAGTCACT GCACGTTTT ATCTCTAGGG ACCAGAACCA 2280  
 AACCACCTT TTTACTTTC AAGACTTATT TTCACTGTG GGGAGGTAA TCTAGGAATG 2340  
 ACTCGTTTAA GGCCTATTTT CATGATTCTT TTGTAGCATT TGGTGTCTGA CGTATTATTG 2400  
 TCCCTTGATT CCAATAATA TGTTCCTTTC CTCRAAAAAA AAAAAAAAAA 2460  
 AAAAA

Seq ID NO: 108 Protein sequence

Protein Accession #: NP\_076927

80 1 11 21 31 41 51  
 MGENDPPAVE APFSFRSLFG LDDLKISPA PDADAVAAQI LSLPLKFFP IIVIGIALI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCGVSDCKD GEDEYRCVRV GGQNAVQLVP 120  
 TAASWKMS DDWKHYANV ACAQLGPPSY VSSDNLRVSS LEGQFREFV SIDHLLPDDK 180  
 VTALHHSYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFGYH 240



LCGGSVITPL WIITAACHVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGKVCWT SGWGATEDGG DASPVLNHAA 360  
 VPLISNLIKCN HRDVGIGIIS PSMCLCAGYLT GGVDSQCGDS GGPLVCQERR LNKLVGATSF 420  
 GIGCAEVNKP GUYTRVTSFL DWIHEQMERD LKT

Seq ID NO: 109 DNA sequence  
 Nucleic Acid Accession #: NM\_000493.2  
 Coding sequence: 97..2139

10 1 11 21 31 41 51  
 CACCTTCTGC ACTGCTCATC TGGGCAGAGG AAGCTTCAGA AAGCTGCCAA GGCACCATCT 60  
 CCAGGAAGCTC CCAGCAGCGCA GAATCCATCT GAGAATATGC TGCCACAAAT ACCCTTTTGT 120  
 CTGCTAGTAT CCTTGAACCTT GGTTCATGGA GTGTTTTACG CTGAACGATA CCAATGCCCC 180  
 15 ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240  
 AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT 300  
 GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACCAGGAA AACCCAGGCTA CGGAAGTCTCT 360  
 GGACTCCAAG GAGAGCCAGG GTTGCCAGGA CCACCGGAC CATCAGCTGT AGGGAACCA 420  
 GGTGTGCCAG GACTCCACAG AAAACCAGGA GAGAGAGGAC CATATGGACC AAAAGGAGAT 480  
 20 GTTGGACAGC CTGGCTTACC AGGACCCCGG GGCCACACAG GACCACCTGG AATCCCTGGA 540  
 CCGGCTGGAAG TTCTGTGTCC AGGAAAACCT GGACACACAG GACCCACAGG AGCCCCAGGA 600  
 CCCAGGGGCT TTCTGAGAGA AAAGGGTGCA CCAGGAGTCC CTGGTATGAA TGGACAGAAA 660  
 GGGGAAATGG GATATGCTGC TCCTGCTGCT CCAGGTGAGA GGGGTCTTCC AGGCCCTCAG 720  
 GGTCCACAG GACCATCTGG CCCTCCTGGA GTGGGAAAA GAGGTGAAA TGGGGTTCCA 780  
 25 GGACAGCCAG GCATCAAAGG TGATAGAGGT TTCCGGGAG AAATGGGACC AATTGGCCCA 840  
 CCAGGTCCCC AAGGCCCTCC TGGGGAACGA GGGCCAGAAG GCATTGGAAG GCCAGGAGCT 900  
 GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAACAAAAG GTCTCCCTGG GGCTCCAGGA 960  
 ATAGCTGGGC CCCAGCGGCC TCCTGGCTTT GGGAAACCA GCTTGCCAGG CCTGAAGGGA 1020  
 GAAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA 1080  
 30 GGTCTTCTCG GGAAGCCAGG TCTGACTGGA CCCCTGGGGA ATATGGGACC CCAAGGACCA 1140  
 AAAGGCATCC CGGGTAGCCA TGGTCTCCCA GGCCCTAAAG GTGAGACAGG GCCAGCTGGG 1200  
 CCTGCAGGAT ACCTCGGGG TAAGGGTGAA AGGGGTTCCT CTGGGTGAGA TGGAAAAACA 1260  
 GGGTACCCAG GAAAACCAAG TCTCGATGGT CTAAGGGTA ACCCAGGGTT ACCAGTCCA 1320  
 AAAGGTGATC CTGGAGTTGG AGGACCTCCT GGTCTCCAG GCCCTGTGGG CCCAGCAGGA 1380  
 35 GCAGAGGGAA TGCCCGGACA CAATGGAGAG GCTGGCCCAA GAGGTGCCCC TGGAAATACCA 1440  
 GGTAAGTAGG GCCCTATTGG GCCACCAAGC ATTCCAGGAT TCCCTGGGTC TAAAGGGGAT 1500  
 CCAGGAAGTC CGGTCTCTCC TGGCCAGCT GGCATAGCAA CTAAGGGCCT CAATGGACCC 1560  
 ACCCGGCCAC CAGGGCCCTCC AGGTCCAAGA GGCACCTCTG GAGAGCCTGG TCTTCCAGGG 1620  
 40 CCCCTGGGC CTCAGGCCCC ACCAGGTCAA CGAGTCTGCG CTGAGGGTTT TATAAGGCA 1680  
 GGCCAAAGCG CCAGTCTTTC TGGGACCCCT CTGTGTTAGT CCAACCAAGG GGTAAACAGGA 1740  
 ATGCTGTAGT CTGCTTTTAC TGTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAATCCC 1800  
 ATACCAATTG ATAAATTTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC 1860  
 TTTACTTGTC AGATACCGAG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920  
 45 CATGTTTGGG TAGGCCTGTA TAAGAATGGC ACCCTGTAA TGTACACCTA TGATGAATAC 1980  
 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TGATCTCAT AGAAAAATGAC 2040  
 CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAAAATGGCC TATACTCTCT TGAGTATGTC 2100  
 CACTCTCTTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCAC AGAGCTAATC 2160  
 TAAATCTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220  
 50 AGGTAGGCTG AAAAGAAATG AATTTTTATT TTCTGAAAA CAGATTGTGAG CTATCAGACC 2280  
 AACAAACCTT CCCCTGAAA AGTGAGCAGC AAGCTAAAA CGTATGTGAA GCCTCTCTTG 2340  
 AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTTCT CCAATATTAA AAAATATCAC 2400  
 CAAAGAGATC CTGCTATGTT AAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAATAT 2460  
 TAAAAAATA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTTGATTGA GAAACTCGGC 2520  
 55 ATTTCTTTT TAAAAAGGCC TGTTCCTAAC TATGAATATG AGAATCTCTA GGAACATACC 2580  
 AGGAGGTATC ATATAACTTT GTAGAACTTA AATACTTGAA TATTCAAAT TAAAGACAC 2640  
 TGTATCCCTT AAAATATTTT TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTTCAT 2700  
 CAATATCTAT TCAATATATC AGGTGCATAT ATACTTGTTA AAGCTCTTAT AAAAAAAGC 2760  
 60 CCCAAATAT TGAAGTTTCT CTGAATGCA AGGTGCTTTC ATCAATGAAC CTTTCAAAA 2820  
 CTTTCTATG ATTGCAGAGA AGCTTTTAT ATACCCAGCA TAACCTGGAA ACAGGTATCT 2880  
 GACCTATTCT TATTAGTTA ACACAAGTGT GATTAAATTT ATTTCTTTAA TTCCTTATTG 2940  
 AATCTTATGT GATATGATTT TCTGGATTGA CAGAACATTA GCACATGTAC CTGTGCTC 3000  
 CCATTCAAGT GAAGTTATAA TTTCACTGA GGGTTTCAA ATTCGACTAG AAGTGGAGAT 3060  
 65 ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAC TTTTAAGCTG 3120  
 TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTACGAC ACAATAAAT 3180  
 AACATCAATA GATTTTAGG CTGAATTAAT TTGAAAGCAG CAATTTGCTG TTTCAACCA 3240  
 TTCTTCAAG GCTTTTCATT CGACACAATA AATAACATC AATAG

Seq ID NO: 110 Protein sequence  
 Protein Accession #: NP\_000484.2

70 1 11 21 31 41 51  
 MLPQIPFLLL VSLNLVHGVF YAERYQMPGT IKGPLPNTKT QFFIPYTIKS KGIIVRGEQG 60  
 75 TPGPFGPAGP RGHFGPSGPP GKPGYGSFGL QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120  
 GPYGPKGDVG PAGLPGPRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GFPGEKAPG 180  
 VPGMNGQKGB MGVGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPQG PGIKGDRGFP 240  
 GEMGPIGPPG PQGPFGPRGP EGIGKPGAGG AFGQPGIPGT KGLPGAPGIA GPPGPPGPGK 300  
 PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMGPQGPQG IPGSHGLPGP 360  
 80 KGETGPAGPA GYPGAKGERG SPGSDGKPGV PGKPLDGPK GNPGLPGPKG DPGVGGPPGL 420  
 PGVPGAGAK GMPGHNGEAG PRGAPGIPGT RGPFGPPGIP GPPGSKGDPG SPGPPGPAGI 480  
 ATKLNLPFTG PPGPPGPRGH SGEPLPGPP GPPGPPGQAV MPEGPIKAGQ RPSLSGTPLV 540  
 SANQVGTGMP VSAFTVILSK AYPAGTPIF FDKILYNRQQ HYDPRGTGFT CQIPGIYFYS 600  
 YHVHVKGTHV WGLYKGNTP VMYTYDEYTK GYLDQASGSA IIDLTENQV WLQLPNAESN 660  
 GLYSSEYVHS SPFGFLVAPM

Seq ID NO: 111 DNA sequence  
Nucleic Acid Accession #: NM\_000949  
Coding sequence: 285..2153

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACCTCTT 60  
CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCCACACA ATGGAGCTTC 120  
ATGTCCTCGT GCAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180  
TAAAGAACTC TCCTATTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCTTGAA 240  
GTGAACCTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300  
CATCTGCAAC CGTTTTCAC TGTCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT 360  
TACCTCTCTG AAAACCTGAG ATCTTTAAAT GTCTTCTCC CAATAAGGAA ACATTCACTT 420  
GCTGGTGGAG GCTCGGACA GATGGAGGAC TTCTACCAA TTATTCACTG ACTTACCACA 480  
GGGAAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCACTCCT 540  
GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCATGCCA 600  
CTAACAGGAT GGAAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660  
AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAAAA GCCAGAAGAC AGAAAAACCTT 720  
ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAAGTGGT TGGTTCAAGC 780  
TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTITGCTG 840  
GGCAGCAAAAC AGAGTTTAAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900  
TTGCTGCGAA ACCAGACCAT GGAATCTGGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960  
TACCTAGTGA CTTCAACCAT AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCTTTCTG 1020  
CTGTCTCTG TTTGATTATT GTCTGGGAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080  
GCATCTTTCC GCCAGTTCCT GGGCCAAAAA TAAAGGATT TGATGCTCAT CTGTGGGAGA 1140  
AGGGCAAGTC TGAAGAACTA CTGAGTGCCT TGGGATGCCA AGACTTTTCT CCCACTTCTG 1200  
ACTATGAGGA CTGTGGGATG GAGTATTAG AAGTAGATGA TAGTGAGGAG CAGCATCTAA 1260  
TGTCAGTCCA TTCAAAAGAA CACCCAGATC AAGGTATGAA ACCACATAC CTGGATCCTG 1320  
ACACTGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGCTGAA AAGTGTGAGG 1380  
AACCCAGGC CATCCCTCC ACATTCTATG ATCCTGAGGT CATTGAGAAG CCAGAGAATC 1440  
CTGAAACAAC CCACACCTGG GACCCCAAGT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500  
TTCATGCTGG TGGATCCAAA TGTTCACAT GGCCCTTACC ACAGCCAGC CAGCACAACC 1560  
CCAGATCTCT TTACACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG 1620  
CACCGGACCT CTCGTGTAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA 1680  
AGTCTAGAGA AGAGGGAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA 1740  
CTGACCAAGA TAAGCCCTGG CTGTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800  
CTTGAGGATTA TTGGAGATT CACAAGGTCA ACAAGATGG TGCAATTATCA TTGCTACCAA 1860  
AACAGGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920  
ATGCCAAGCT GTCCGGGCTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG 1980  
CTAAAAACGT GGCTTGCTTT GAAGAATCAG CCAAGAGGC CCCACCATCA CTGGAACAGA 2040  
ATCAAGCTGA GAAAGCCCTG GCCAATTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100  
TGGGTGGTGT GGATTACCTG GATCCCGCAT GTTTTACACA CTCCTTTCAC TGATAGCTTG 2160  
ACTAATGGA TGAATTGGTTA AATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA 2220  
AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGCTC CCAGCTCCTT TCATGCTCCA 2280  
TTTTTAACCA CTGCTCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCTT 2340  
AACTGTGATT TGATGATTTA CTTTGTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400  
AAAAGCACAC TGCCTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAGAAG 2460  
GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATGT TCAAAATGT TTACCATAGA 2520  
AAGATGACAA AAGAAAATTT TCCACATAGG AAAATGCCAT GAAAATGTCT TTTGAAAAAC 2580  
AACTGCATAA CCTTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAT ATAACCATTT 2640  
AAGAAAGAA TGCAATCCAG AACAAATGT TTACATAAGT TCCTATACCT TACTGACACA 2700  
TTGCTGATAT GCAAGTAAGA AAT

Seq ID NO: 112 Protein sequence  
Protein Accession #: NP\_000940

60  
65  
70  
75  
80

1 11 21 31 41 51  
MKENVASATV FTLLFLNTC LLNGQLPFGK PEIFKCRSEN KETFTCWWRP GTDGLPTNY 60  
SLTYHREGET LMHECPDYIT GGFNSCHFGK QYTSMWRTYI MMVNATNMQG SSFSELYVD 120  
VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWPTLLYEI RLKPEKAAEW 180  
EIHFAQQOTE FKILSLHPQG KYLVQVRCKP DHGYNASWSP ATFIQIPSDF TMNDITVWIS 240  
VAVLSAVIDL IIVWAVALKG YSMVTCIFPP VPGPKIKGPD AHLLEKKGSE ELLSALGQOD 300  
FPPTSDEYDL IVEYLEVDDG EDQHLMSVHS KEHPSQGMKP TYLDPDTSRG RGSCDPSLL 360  
SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPOCISME GKIPYFHAGG SKCSTWPLPQ 420  
PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQRVE 480  
SPHSETDQDT PWLLPQEKTP FGSAPKPLDYV EIHKVNKDDA LSLLPKQREN SGKPKKPGTP 540  
ENNKEYAKVS GVMDDNLLVL VPDPAKNVA CFEESEAKAP PSLEQNQAEK ALANFTATSS 600  
KRLQLGLGLD YLDPACPTHS FH

Seq ID NO: 113 DNA sequence  
Nucleic Acid Accession #: XM\_062811  
Coding sequence: 1..888

75  
80

1 11 21 31 41 51  
ATGTGGGGCG CTCGCCGCTC GTCCGTCTCC TCATCCTGGA AGCCCGCTTC GCTCCTGCAG 60  
CTGCTGCTGG CTGCGCTGCT GCGCGCGGGG GCGAGGGCCA GCGCGGAGTA CTGCCACGGC 120  
TGGCTGGAGC GCGAGGGGCT CTGCGGCATC GGCTTCCAGT GTCCCGAGCG CTTGACGGCG 180  
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCGGAG 240  
GCGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 300  
CGGGCGGACA AAGACGGGCC CGACGGCTCG GCAATGCCCA TCTACGTGCC GTTCTCTATT 360  
GTTGCTCCG TGTGTGTCG CTTATCATC TTGGGGTCCC TGGTGGCAGC CTGTGCTGCG 420

AGATGTCTCC GGCCTAAGCA GGATCCCCAG CAGAGCCGAG CCCAGGGGG TAACCGCTTG 480  
 ATGAGACCA TCCCCAGTAT CCCCAGTGCC AGCACCTCCC GGGGGTCGT CTCACGCCAG 540  
 TCCAGCAGAG CTGCCAGTTC CAGCTCCAGC GCCAATCTAG GGGCCCGGGC GCCCCCAACA 600  
 AGGTACAGA CCAACTGTGT CTGTCCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660  
 CCCACGAATT TCTCTGTGCT GAACTGTGAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720  
 CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780  
 GCTGTGCCAC CTTTTCATGGA CGGCCTGCAG CCTGGCTACA GGCAGATTCA GTCCCCCTTC 840  
 CCTCACACA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 114 Protein sequence  
 Protein Accession #: XP\_062811

1 11 21 31 41 51  
 MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60  
 GDATTCGCGS ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDFDGS AVPIYVFLI 120  
 VGSVFVAPII LGSILVAACC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180  
 SSTAASSSSS ANSGARAPPT RSQTNCLLPE GTMNNVYVNM PTNFSVLNQC QATQIVPHQG 240  
 QYLHPFVGVY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 115 DNA sequence  
 Nucleic Acid Accession #: NM\_013257  
 Coding sequence: 223..1512

1 11 21 31 41 51  
 GGTGTGCTCT TGAGGGGATTA AATGCAAGA GATCACACCA TGGACTACAA GAAAAGCTGC 60  
 CCAAGTGTAA GCATTCCCAG CTCOGATGAA CACAGAGAGA AAAAGAAGAG GTTTACTGTT 120  
 TATAAAGTTC TGGTTTCAGT GGGGAAGAAGT GAATGGTTTG TCTTCAGGAG ATATGCAGAG 180  
 TTTGATAAAG TTTATAACAC TTTAAAAAAA CAGTTTCTCT CTATGGCCCT GAAGATTCTT 240  
 GCCAAGAGAA TATTTGGTGA TATTTTGAT CCAGATTTTA TTAACAAAG ACGAGCAGGA 300  
 CTAACGAAT TCATTTCAGAA CCTAGTTAGG TATCCAGAAC TTTATAACCA TCCAGATGTC 360  
 AGAGCATTCC TTCAAATGGA CAGTCCAAAA CACCAGTCAG ATCCATCTGA AGATGAGGAT 420  
 GAAAGAAAGT CTCAAGAGCT AACTCTTACC TCACAGAAACA TCAACCTGGG ACCGCTCTGA 480  
 AATCCTCATG CCAAAACCAAC TGACTTTGAT TTTCTAAAAG TTATTGGAAA AGGCAGCTTT 540  
 GGCACAGGTTT TTTCTGCAA ACGGAAACTG GATGGAAAAT TTTATGCTGT CAAAGTGTTA 600  
 CAGAAAAAAA TAGTTCTCAA CAGAAAAGAG CAAAAACATA TTATGGCTGA ACGTAATGTG 660  
 CTCTGAAAAA ATGTGAAACA TCCGTTTTTG GTTGGATTGC ATTATTCCTT CCAAACTACT 720  
 GAAAAGCTTT ATTTTGTCTT GGATTTTGTT AATGGAGGGG AGCTTTTTTT CCACCTACAA 780  
 AGAGAACGGT CCTTTCTGCA GCACAGAGCT AGGTTTACG CTGCTGAAA TGTAGTAGTC 840  
 TTGGGTACT TACATTCCAT CAAATAGTA TACAGAGACT TGAACACAGA AAATATTCTT 900  
 TTGGATTGAG TAGGACATGT TGTCTTAACA GATTTTGGGC TTTGTAAGA AGGAATTGCT 960  
 ATTTCTGACA CCATACCCAG ATTTTGTGGG ACACCAGAGT ATCTTGCAAC TGAAGTAATT 1020  
 AGAAAAACAG CCTATGACAA TACTGTAGAT TGGTGGTGCC TTGGGGCTGT TCTGTATGAA 1080  
 ATGCTGTATG GATTGCTCTT TTTTATGTC CGAGATGTTG CTGAAATGTA TGACAAATATC 1140  
 CTTCAAAAC CCCTAAGTTT GAGGCCAGGA GTGAGTCTTA CAGCCTGTGC CATTCTGGAA 1200  
 GAATCCTAG AAAAAGACAG GCAAAATCGA CTTGGTGCCA AGGAAGACTT TCTTGAATT 1260  
 CAGAACTATC CTTTTGTGTA ATCACTCAGC TGGGCTGACC TTGTACAAA GAAGATTCCA 1320  
 CCACCATTTA ATCTTAATGT GGCTGGACCA GATGATATCA GAAACTTTGA CACAGCATTT 1380  
 ACAGAAGAAA TGTTCCTATA TTTCTGTGT GTATCTCTG ACTATTCTAT AGTGAATGCC 1440  
 AGTGATTGG AGGCAGATGA TGCAATCGTT GGTTCCTCT ATGCACCTCC TTCAGAAGAC 1500  
 TTATTTTGT GAGCAGTTTG CCATTGAGAA ACCATTGAGC AAAATAAGTC TATAGATGGG 1560  
 ACTGAAACTT CTATTGTGT GAATATATTC AAATATGTAT AACTAGTGCC TCATTTTAT 1620  
 ATGTAATGAT GAAAACTATG AAAAAATGTA TTTCTCTCTA TGTGCAAGAA AAATAGGGCA 1680  
 TTTCAAAGAG CTGTTTGTAT TAAAAATTAT ATTCTGTGTT AATAAGCTTA TTTTAAACA 1740  
 ATTTAAAGC TATTATCTT AGCATTAAAC TATTTTAA GAAACCTTTT TTGCTATTGA 1800  
 CTGTTTTTC CCTCTAAGTT TACATAACA TCTACCCAAG ATAGACTGTT TTTTAAAGT 1860  
 CAATTTTCACT TCAGCTAACA TATATTAATA CCTTTGTAAC TCTTTGCTAT GGCCTTTGTT 1920  
 ATCACACCAA AACTATGCAA TTGGTACATG GTTGTGTAAG AAGAAACCGT ATTTTCCAT 1980  
 GATAAATCAC TGTTTGAAAT ATTTGGTTCA TGGTATGATC GAAATGTAAA AGCATAATTA 2040  
 ACACATTGGC TGCTAGTTAA CAATTGGAAT AACTTTATTC TGCAGATCAT TTAAGAAGTA 2100  
 ACAGCCCGGG CGCGGTGGCT CACGCCGTGA ATCCAGCAC TTTGGGAGGC TGAGGCGGGC 2160  
 AGATCACCTG AGGTCAAGGAG TTGGAGACCA GCCTGACCAA CATGGACAAA CCCCCTCTCT 2220  
 ACTAAAAATA CAAAATGGC AGGGTGTGGT GGCACATGCC TATAATCCCA GCTACTTGGG 2280  
 AGGCTAAGGC AGGAGAATCG CTTGAACCG GAGGCGGAG GTTGCAATGA CCGAGATGCG 2340  
 CACCATGCA CTCCTGCTCT GGCACAAAGA GTGAACTCC ATCTCAAAA A

Seq ID NO: 116 Protein sequence  
 Protein Accession #: NP\_037389

1 11 21 31 41 51  
 MALKIPAKRI FGDNFDPDFI KQRRAGLNEF IQNLVRYPEL YNEPDVRAFL QMDSPEKHQSD 60  
 PSEDEDERSS QKLHSTSONI NLGPGSGNPHA KPTDFDFLKV IGKSGFGKVL LAKRRLDGKF 120  
 YAVKVLQKVI VLNRKEQKHI MAERNVLLKN VKHPFLVGLH YSFQTEKLY FVLDFVNGGE 180  
 LPFHILQERS FPEHRARFYA AEIASALGYL HSIKIVYRDL KPENILLDSV GHVVLTFDGL 240  
 CKEGIAISDT TTTFCGTPEY LAPEVIRKQF YDNTVDWVCL GAVLYEMLYG LPPFYCRDVA 300  
 EMYDNILHKL LSLRPGVSLT AWSILEELLE KDRQNLGAK EDFLEIQNH PFEELSADWL 360  
 VQKIPPPFFN PNVAGPDDIR NFDTAFTET VPYSVCVSSD YSIVNASVLE ADDAPVGFPSY 420  
 APPSEDLFL

Seq ID NO: 117 DNA sequence  
 Nucleic Acid Accession #: NM\_004004.1

Coding sequence: 1..681

1 11 21 31 41 51  
5 ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACACTC CACCAGCATT 60  
GGAAAGATCT GGCTCACCCT CCTCTTCATT TTTCGCATTA TGATCCTCGT TGTGGCTGCA 120  
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180  
AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACCA TCCGGCTATG GGCCTGTCAG 240  
CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300  
10 GAGAAGAAGA GGAAGTTTCA CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG 360  
ATCAAAACCC AGAAGGTCGG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420  
TTCTTCCGGG TCATCTTCGA AGCCGCTTTC ATGTACGTCT TCTATGTCTAT GTACGACGGC 480  
TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540  
TTTGTGTCCC GCGCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600  
15 ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTTCG TAATTAGATA TTGTTCTGGG 660  
AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 118 Protein sequence  
Protein Accession #: NP\_003995.1

20 1 11 21 31 41 51  
MDWGTLLQTL GGVNKHSTSI GKIWLTVLFI FRIMILVVA KEVWGDEQAD FVCNTLQPGC 60  
25 KVVYDHYFYP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEFKDIEE 120  
IKTQKRIEIG SLWWTYTSI FFRVIFEAAF MVFVVMYDG FSMQLRVKCN AWPCPNTVDC 180  
FVSRPTEKTV FTFVMIASVG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 119 DNA sequence  
Nucleic Acid Accession #: XM\_061091.1  
Coding sequence: 1..2481

1 11 21 31 41 51  
35 ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTGGC TTCTCCAAGA GCCGCCCGGG 60  
CACCGAGCGC TGGTGCGCGC TCTCCTTCGG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG 120  
CCCGGGTACC CGCCAGTGCC GGCTGCGGAT GACCGATTCA CGCTCCGAT GATTGGAGGT 180  
CAGATGTCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGT TTCTTTGCTA TGAATTTTAA 240  
40 GTTGGGAAGC CTCTTTTGA GGCAGAACAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300  
ATTTCACTAG CACAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTGTGTA 360  
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420  
GTCTGTGACG GTCTGACAT CAGCCCGGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480  
TCCACTCTCT ATCTGGAATT CCCCITGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540  
AGAATCAAGA GGAATGTTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600  
45 CTCTGTCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660  
GTCACTGATG GGAAGTCCCA GGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720  
GGTGTCACTG TGTGTGCTGT GGGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCACTG 780  
GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840  
GGCCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGTCTCA GCGCCAGGCC AGCTGGGAGC 900  
50 CCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCGC CTGTGACTCG 960  
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCTC 1020  
TGCCCGCTGG CCTTTGGAGG GAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080  
GTGACCTCC TCCTCTGCT GTGACAGCTCT GCGGGCACCA CTCTGGACGG CTCTCTGCGG 1140  
GCCAAAGTCT TCGTGAAGCG GTTGTGTCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA 1200  
55 GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCCCTGTGG GGAGTACCAG 1260  
GATGTGCTTG ACCTGTGCTG GAGCCTCGAT GGCATTCCCT TCCGTGTGGG CCCCACCTG 1320  
ACGGGCACTG CCTTGGCGCA GCGGGCAGAG CGTGGCTTGG GAGGCGCCAC CAGGACAGGC 1380  
CAGGACCGGC CAGTAGAGT GGTGGTTTGT CTCCTGAGT CACACTCCGA GGATGAGGTT 1440  
60 CGGGGCCAG CGCTCACGC AAGGGCGCGA GAGCTGTCTC TGCTGGGTGT AGGCAGTGAG 1500  
GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGGCCAA AGCATGTGAT GGTCTACTCG 1560  
GATCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG 1620  
CGGCCAGGCT GCGGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCTGCCTCA 1680  
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740  
GAGGTGAACC CTGACGTGAC ACAGTTCGGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800  
65 GCCTTCGGGC TGGACACCAA ACCCAACCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860  
CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGACATCTA TGACAAAGTG 1920  
ATGACCTTCC AGAGGGGTGC CCGGCTGGT GTCCCAAAG CTGTGGTGGT GCTCACAGGC 1980  
GGGAGAGGCG CAGAGGATGC AGCCGTTCTT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040  
70 GTCTTGTGCG TGGGCGTGGG GCCTGTCTTA AGTGGGGTTC TGCGGAGGCT TGCAGGTCCC 2100  
CGGATTTCCC TGATCCAGCT GGCAGCTTAC GCGACCTGTC GGTACCAACA GGACGTGCTC 2160  
ATTGATGGC TGTGTGGAGA AGCCAAGCAG CAGTCAACC TCTGCAACC CAGCCCGTGC 2220  
ATGAATGAG GCAGCTGCTT CTGCAAGAT GGGAGCTACC GCTGCAAGT TCGGATGGC 2280  
TGGAGGGGCC CCCACTGCGA GAACGCTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340  
75 GGATGGATTC TTGAGACGCC CTTGAGGCAC ATGGCTCCCG TGCAAGAGGG CAGCAGCGT 2400  
ACCCCTCCCA CCAACTACAG AGAAGGCCTG GGCAGTGAAA TGTGCTTAC CTCTGGAAT 2460  
GTCTGTGCCC CAGGTCTTGA G

Seq ID NO: 120 Protein sequence  
Protein Accession #: XP\_061091.1

80 1 11 21 31 41 51  
MPNTSGTTRI EIWLQEPFG HRLVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60  
QMHGKVDLW SLGLCYEFL VGRPPFEANE VHSVETIGK ISAASKMMC SAAVDIMFL 120

5 DGSNSVGKGS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQEVKA 180  
 RIKRMVFKGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240  
 GVTVFAGVVR FPRWEELHAL ASEPRGQHV L LAEQVEDATN GLFSTLSSA ICSSATPAGS 300  
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360  
 10 VDLLFLDSS AGTTLGDFLR AKVFKRFVR AVLSSEDSRAR VGVATYSREL LVAVPVGEYQ 420  
 DVDPDLVNSLD GIPFRGGPTL TGSALRQAAE RGFSGSATRTG QDRPRRVVVL LTESHSEDEV 480  
 AGPARHARAR ELLLLGVGSE AVRAELEETI GSPKHMVYS DPQDLFNQIP ELQKLCRSQ 540  
 RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSCALQF EVNPDVTQVG LVVYGSQVQT 600  
 AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660  
 GRGAEDAAPV AQKLRRNGIS VLVVGVGPVL SEGLRLLAGP RDSLIHVAAY ADLRYHQDVL 720  
 IEWLCEGAQK PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780  
 GWILETPLRH MAPVQEGSSR TPPSNYREGL GTEMVPTFWN VCAPGP

15 Seq ID NO: 121 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2424

20 1 11 21 31 41 51  
 ATGCCCCCTT TCCTGTGTCT GGAGGCCGCTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60  
 TCCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAGAAACCA TCGGGAAGAT TTCAGCTGCC 120  
 AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180  
 AGCGTCGGGA AAGGAGCTTT TGAAAGGTCC AAGCACTTTG CCATCAGAGT CTGTGACGGT 240  
 25 CTGGACATCA GCCCGAGAG GGTGAGAGTG GGAGCATTC AGTTCAGTTC CACTCCTCAT 300  
 CTGGAATTC CCTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360  
 ATGTTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAATACCT TCTGCACAGA 420  
 GGGTTCGCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480  
 AAGTCCCGAG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGCTACTGTG 540  
 TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600  
 30 AGAGGGCAGC ACGTGTCTGT GGCTGAGCAG GTGAGGATG CCACCAACGG CCTCTTCAGC 660  
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720  
 CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGAGTTGCT CTGCAATGC CCCATGCTGG 780  
 AGAGGATCGC GCGGAGCCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840  
 AGAGTGTTC TAAACCAACC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC 900  
 35 TCGCAGCCCT GCCAGAAATG AGGCACATGT GTTCCAGAA GACTGGAAGG CTACCAAGTGC 960  
 CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CTTGGAATGC 1020  
 AGGGTCGACC TCCTCTTCTT GCTGGACAGC TCTGCGGGCA CCACCTGGA CGGCTTCTGT 1080  
 CGGGCCAAAG TCTTGTGTA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140  
 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCTGT GGGGAGTAC 1200  
 40 CAGGATGTGC TAGCTGTGGT CTGGAGCCTC GATGGCATTG CCTTCCGTGG TGGCCCCACC 1260  
 CTGACGGGCA GTGCCCTGGC GCAGGCCGCA GAGCGTGCT TCGGAGCGCG CACCAGGACA 1320  
 GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACATC CGAGGATGAG 1380  
 GTTGGCGGCG GAGCGCTGCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440  
 GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCG CAAAGCATGT GATGGTCTAC 1500  
 45 TCGGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560  
 CAGCGGCCAG GTGCGCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620  
 TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680  
 TTTGAGGTGA ACCCTGAGCT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGACG 1740  
 ACTGCTCTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800  
 50 GCCCCTTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860  
 GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA 1920  
 GCGCGGAGAG GCGCAGAGGA TGCAGCGGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC 1980  
 TCTGTCTTGG TGTGGGCGGT GGGGCGCTGC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040  
 CCGCGGGATT CCTGATCCCA CGTGGCAGCT TACGCGGACC TGCGGTACCA CCAGGACGTG 2100  
 55 CTCAATGAGT GGTCTGTGGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160  
 TGCATGAATG AGGGCAGCTG CGTCTGCAG AATGGGAGCT ACCGCTGCAA GTGTGGGAT 2220  
 GGCTGGGAGG GCCCCCACTG CGAGAACCCT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280  
 CAGGGATGGA TTCTTGAGAC GCCCTGAGG CACATGGCTC CCGTGACAGA GGGCAGCAGC 2340  
 60 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400  
 AATGTCTGTG CCCAGGTCC TTAG

Seq ID NO: 122 Protein sequence  
 Protein Accession #: Eos sequence

65 1 11 21 31 41 51  
 MPPFLLEAV CVFLFSRVVP SLPLQEVHVS KETIGKISAA SKMMCSAAV DIMFLDGSN 60  
 SVGKGSFERS KHPAITVCDG LDISPERVRV GAPQFSSTPH LEFPLDSFST QQEVKARIKR 120  
 70 MVFKGGRTEI ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERVTV 180  
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCCPGPCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGITLDGFL 360  
 RAKVFKRFVR RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVDPDLVNSL DGIPFRGGPT 420  
 75 LTGSALRQAA ERGFGSATRT QDRPRRVVVL LTESHSEDE VAGPARHARA RELLLGVGS 480  
 EAVRAELEETI TGSFKHMVYV SDPQDLFNQI PELQKLCRSR QRPQCRTQAL DLVFMLDTS 540  
 SVGPENFAQM QSFVRSCALQ FEVNEPDVTOV GLVVYGSQVQ TAFGLDTPKT RAAMLRAISQ 600  
 APYLGGVGS G TALLHIYDK VMTVQRGARP GVPKAVVVLIT GGRGAEDAAP PAQKLRRNGI 660  
 SVLVVGVGPV LSEGLRLLAG PRDSLIHVA YADLRYHQDV LIEWLCEGAQ QPVNLCKPSP 720  
 80 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR WSSCSVCVS QGWILETPLR BMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFW NVCAFGP

Seq ID NO: 123 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 89..2356

1 11 21 31 41 51  
5 G C C C C T G G C C C G A G C C G C G C C G G G T C T G T A G T A G A G C G C C C G G G C A C C G A G C G C T G 60  
G T C G C G C G C T C T C C T T C C G T T A T A T C A A C A T G C C C C T T T C T G T T G C T G G A A G C C G T C T G 120  
T G T T T T C C T G T T T T C C A G A G T G C C C C C C C A T C T C C C T C T C C A G G A A G T C C A T G T A A G C A A 180  
A G A A A C A T C G G G A A G A T T T C A G C T G C C A G C A A A A T G A T G T G T G C T C G G C T G C A G T G G A 240  
C A T C A T G T T T C T G T T A G A T G G T C T A A C A G C G T C G G A A A G G A G C T T T G A A G G T C C A A 300  
G C A C T T T G C C A T C A C A G T C T G T A C G G T C T G G A C A T C A G C C C G A G A G G G T C A G A G T G G G 360  
10 A G C A T T C C A G T T C C A T T C C A C T C C T C A T C T G G A A T T C C C C T T G G A T T C A T T T C A A C C C A 420  
A C A G G A A G T G A A G G C A A G A A T C A A G A G G A T G T T T T C A A A G A G G G C A C G A G A C G G A 480  
A C T T G C T C T G A A A T A C C T T C T G C A C A G A G G G T T G C C T G G A G G C A G A A A T G C T T C T G T G C C 540  
C C A G A T C C T C A T C A T G T C A C T G A T G G G A A G T C C C A G G G G A T G T G G C A C T G C C A T C C A A 600  
G C A G C T G A A G A A A G G G G T G T A C T G T G T T G T G T G T G G G G T C A G G T T C C A G G T G G G A 660  
15 G G A G C T G C A T G T C C G G C C A G G A G C C T A G A G G C A G C A C G T G T G T G G C T G A G C A G G T 720  
G G A G A T G C C A C C A A C G G C C T C T T C A G C A C C C T C A G C A G C T G C C C A T C T G C C A G C G C 780  
C A G C C C A G A C T G C A G G G T G A G G C T C A C C C C T G T G A G C A C A G G A C G C T G G A G A T G G T C C G 840  
G G A G T T G C T G G C A A T G C C C C A T G C T G G A G A G A T G C G G G C G G A C C C T T G C G T G C T G G C 900  
T G C A C A C T G T C C C T T C A C G T G A A G A G A G T G T C C T A A C C A C C C T G C A C C T G C T A 960  
20 C A G G A C C A C C T G C C C A G G C C C T G T G A C T C G A G C C C T G C A G A A T G G A G C A C A T G T G T 1020  
T C C A G A A G G A C T G G A C G G C T A C C A G T G C C T C T G C C C G C T G G C C T T T G S A G G G A G C T A A 1080  
C T G T G C C C T G A A G C T G A G C C T G G A A T G C A G G G T C G A C C T C T C T T C C T G C T G G A C A G C T C 1140  
T G C G G C C A C C A C T C T G A C G C G C T C C C T G C G G C C A A A G T C T T C G T G A A G C G G T T T G T G C G 1200  
G G C C G T G C T G A G C A G G A C C T C T C G G G C C C G A G T G G G T G T G C C A C A T A C A C A G G G A G C T 1260  
25 C T G T G T G G G G T G C T G C G G C C A G G A G T A C C A G A T G T G C C T G A C C T G G T C T G A G C C T C G A 1320  
T G G C A T T C C C T T C C G T G G T G G C C C C A C C C T G A C G G C A G T G C C T T G C G C C A G G C G G C A G A 1380  
G C G T G C C T T C G G A G C G C C A C A G G A C A G G C C A G C C A C G T A G A G T G G T G G T T T T 1440  
G C T C A C T G A G T C A C A C T C C G A G A T G A G G T T G C G G G C C C A C G C G C T C A C G C A A G G G C G C G 1500  
A G A G C T G C T C T G C T G G G T G A G C A G T G A G G C C G T G C G G G C A G A G C T G G A G G A G A T C A C 1560  
30 A G G C A G C C C A T A G C A T C T A C T G G T C T A C T G G A T C C T C A G A T C T G T T C A A C C A A T C C C 1620  
T G A G C T G C A G G G A A G C T G T G C A G C C G C A C G C G C C A G G G T G C C G A C A C A A G C C C T G G A 1680  
C C T C G T C T T C A T G T T G G A C C C T G C C C T A G T A G G G C C C G A G A A T T T T G C T C A G A T G C A 1740  
G A G C T T T G T G A A A G C T G T G C C C T C C A G T T T G A G T G A A C C T G A C G T G A C A C A G G T C G G 1800  
C C T G G T G G T G T A T G G C A G C C A G G T C A G A C T G C C C T G C C G G C T G G A C C C A C C C G 1860  
35 G G C T G G C A T G T G C G G G C C A T T A G C A G G C C C C T A C C T A G G T G G G G T G G G T C A G C C G G 1920  
C A C C G C C C T G C T G C A C A T C T A T G A C A A A G T G A T G A C C G T C C A G A G G G G T G C C G C C T G G 1980  
T G T C C C A A A G C T G T G T G G T G C T C A C A G G C G G A G A G G A T G C A G C C G T T C C 2040  
T G C C C A A A G T G C A G A A C A A T G G C A T C T C T G T T G T C T G T G G G C G T G G G C C T G C C T 2100  
A A G T A G G G T C T G C G A G G C T T G C A G G T C C C C G G A T T C C T G A T C C A C G T G G C A G C T T A 2160  
40 G C C G A C C T G A G T A C C A C C A G G A C G T G C T C A T T G A G T G G C T G T G T G G A G A A G C C A A G C A 2220  
G C C A G T C A A C C T C T G C A A A C C A G C C C C T G C A T G A A T G A G G C A G C T G C G T C C T G C A G A A 2280  
T G G G A G C T A C C G T G C A A G T G T C G G A T G G C T G G A G G G C C C C A C T G C G A G A A C C G A T T 2340  
C T T G A G A C G C C C T G A G G C A C A T G G C T C C C G T G C A G A G G G C A G A C A G C C G T A C C C C T C C C 2400  
A G C A A C T A C A G A A G G C C T G G C A C T G A A A T G T G C C T A C C T C T G A A T G T C T G T G C C 2460  
45 C A G G T C C C T A G A A T G T C T G C T T C C C G C C G T G C C A G G A C C A C T A T T C T C A C T A G G G A G 2520  
G A G G A T G T C C C A A T G C A G C A T G C T G C T T A G A C A A A G A A G C A G C T G A T G T C A C C C A C 2580  
A A A C A T G T T G T T A A A A A G T T T G A T G T G T A A G T A A A T A C C A C T T T C T G T A C C T G C T G T 2640  
G C C T T G T T G A G C T T A T G T C A C C A C T T C C C T T G A G A T A A A C A A G A G G T C C T G A A 2700  
50 G A C T T A A A T T A G C G G C C T G A C G T T C C T T T G C A C A A A T C A A T G C T C G C C A G A A T G T T G T 2760  
T G A C A C A G T A A T G C C C A G C A G A G C C T T T A C T A G A C A T C C T T T G A C G G

Seq ID NO: 124 Protein sequence  
Protein Accession #: Eos sequence

55 1 11 21 31 41 51  
M P P F L L L E A V C V F L P S R V P P S L P L Q E V H V S K E T I G K I S A A S K M M W C S A A V D I M F L L D G S N 60  
S V G K S F E R S K H F A I T V C D G L D I S P E R V R V G A F Q F S S T P H L E F P L D S F S T Q E V K A R I K R 120  
M V F K G G R T E T E L A L K Y L L H R G L P G G R N A S V P Q I L I I V T D G K S Q G D V A L P S K Q L K E R G V T V 180  
60 F A V G V R F P R W E E L H A L A S E P R G Q H V L A E Q V E D A T N G L F S T L S S S A I C S S A T P D C R V E A H 240  
P C E H R T L E M V R E F A G N A P C W R S R R T L A V L A A H C P F Y S W K R V F L T H P A T C Y R T T C P G P C D 300  
S Q P Q N G G T C V P E G L D G Y Q C L C P L A F G G E A N C A L K L S L E C R V D L L F L L D S A G T T L D G F L 360  
R A K V F V K R F V R A V L S E D S R A R V G V A T Y S R E L L V A V P V G E Y Q D V P D L V W S L D G I P F R G G P T 420  
65 L T G S A L R Q A A E R G F G S A T R T G Q D R P R R V V V L L T E S H S E D E V A G P A R H A R A R E L L L L G V G S 480  
E A V R A E L E E I T G S P K H V M V Y S D P Q D L F N Q I P E L Q G K L C S R Q R P G C R T Q A L D L V F M L D T S A 540  
S V G P E N F A Q M Q S E V R S C A L Q F E V N P D V T Q V G L V V Y G S Q V Q T A R F L D T K P T R A A M L R A I S Q 600  
A P Y L G G V G S A G T A L L H I Y D K V M T V Q R G A R P G V P K A V V L T G G R G A E D A A V P A Q K L R N N G I 660  
S V L V V G V G P L S E G L R R L A G P R D S L I H V A A Y A D L R Y H Q D V L I E W L C G E A K Q P V N L C K P S P 720  
70 C M E G S C V L Q N G S Y R C K C R D G W E G P H C E N R F L R P

Seq ID NO: 125 DNA sequence  
Nucleic Acid Accession #: NM\_031942.1  
Coding sequence: 145..1260

75 1 11 21 31 41 51  
C C C G A G C C C C G C C C C T C C G G G C C C G G G T G C G C G G C C C A G C C T G C C A G C C G C G C T G C T G C 60  
T G C T C C T C C T G C T G T G G G A C G C T G A C C G C G C G C T G C T C G C T C C C C G C T C C A A G C G 120  
C C G A T C T G G G C A C C C C C A C C A G C A T G G A C G C T C G C G C G T G C C G C A G A A A G A T C T C A G A 180  
80 G T A A A G A A G A A C T T A A A G A A A T T C A G A T A T G T G A A G T T G A T T C C A T G G A A A C C T C G T C A 240  
T C C T C T G A T G A C A G T T G T G A C A G C T T T G C T T C T G A T A A T T T G C A A A C A C A G G C T G C A G 300  
T C A G T T C G G G A A G G C T G T A G A C C C G C A G C A G T G C A G G C A C T C T G G A C C T C T C A G G G T G 360  
G C G A T A A G A T T T C A G C G C G C G A G T A C C A G G G A C A A A A A A G C A G A G T C C C G C 420  
C A G C C C T C A G A G A A T T C T G T G A C T A T T C C A A C T C C A G A A G A T A A A G T G A A T G 480

AATTTTTTGG AGAAAAGGGC TTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACCTC 540  
 ATGTCGAAT TAGAAAGCTT CCCTGGCTCG TTCGTGGAA GACATCCCCT CCCAGGCTCC 600  
 GACTCACAAT CAAGGAGACC GCGAAGGCGT ACATTCCCGG GTGTGCTTC CAGGAGAAAC 660  
 CCTGAACGGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCTCGG GTCCCTTGAC 720  
 GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGGTGAG AAAGAGGAAG 780  
 ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCAGAA GCCGTCGCTC CAGATCATCC 840  
 GTGACCTTTC CGCATATAAT TCGCCCAAGT GAAGAAATTA CAGAGGAGGA GTTGAGAAC 900  
 GTCTGCAGCA ATTCTGAGA GAAGATATAT AACGTTTAC TGGGCTCTAC TTGTCATCAA 960  
 TGCCGTGAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGGCGTT 1020  
 CGAGGCCAGT TCTGTGGCCC CTGCCTTCGA AACGTTATG GTGAAGAGGT CAGGGATGCT 1080  
 CTGCTGGATC CGAAGTGGCA TTGCCCGCCT TGTGAGGAA TCTGCAACTG CAGTTTCTGC 1140  
 CGGACGCGAG ATGGACGGTG TGGGACTGGG GTCCTTGTGT ATTTAGCCAA ATATCATGGC 1200  
 TTTGGGAATG TGCATGCCTA CTGAAAAGC CTGAAACAGG AATTGAAAT GCAAGCATAA 1260  
 TATCTGAAA ATTGTCTGCC TGCCTTCTAC TTCTCAAATC TTTCTGTAA AAGTTTCCAA 1320  
 TTTTTCACCT GAAACCTGAG TTAATAATCT TGATGATCAG CCGTTTTCAT AAGAACTCC 1380  
 AATCAAGTTA ATCTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGGTA TATTGCTAGT 1440  
 TACACTTTC CCGCTTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCC 1500  
 TCTATTCCA ATGCTCCTCT CCAACGCTT AGTTTCTGAA TTTCTTTAA ATTACAGTTT 1560  
 TATGAAAGCA TATTTTATTT ACTTGGTGT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620  
 GAAACACAAT AATAGTATTA ACTAAGTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680  
 CTGTGTTACA CAAAAACGAG TATGATTTAG CACTCATACT AGTTGAAAT TTTAATAGAA 1740  
 TCAAGGCACA AAGCTCTTAA AACCATGTGG AAAAAATTAG TAATTATTGC AGATTGATG 1800  
 CTCTCAATCC CATGATTGTC GCTTATGTTA CAAGTTGTG TCACAGTTGA GACTTAATTT 1860  
 CTCTTAATTT CTCTGCCCG AAGGTAAGT GGTGCGTCCA GCTTACAGCA TCATAATTC 1920  
 AAGGTTGGTG GGCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980  
 ATGAGTAAGC TGATTTGAAT TTTCACTATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040  
 TATTTTCACT TCACATGTAA GGTATTGCAA ATAAATTCIT GGACAATTT GTATGGAAC 2100  
 TTGATATTAA AAAGTGTCT GTGTTTCTT GCAGTTTCTT GTAAATTTAT AAACAGGCA 2160  
 CAAGGTTCAA GTTTAGATT TAAGCACTTT TATAACAATG ATAAGTGCTT TTTTGGAGAT 2220  
 GTAACTTTA GCAGTTTGT AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280  
 CTGTGTCAGT ATTCCCGCTC CTCTTTCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340  
 AAGTGTTGT ATGTCCAATT TACTTGATA TGTAAACCAT TGCTGTGCCA TTCAATGTTT 2400  
 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTATCT GTAATGCTTT 2460  
 TATACAAAG TTTATTTTAA TAATAAATG TTTGTTCTAA AAAAAA

Seq ID NO: 126 Protein sequence  
 Protein Accession #: NP\_114148.1

1 11 21 31 41 51  
 MDARRVPQKD LRVKQNLKFP RYVKLISMET SSSDDSCDS FASDNFANTR LQSVREGCRT 60  
 RSQCRHSGLP RVAMKFPARS TRGATNKKAE SRQPSNSVT DSNSDSEDES GNMFLKRAL 120  
 NIKQNKAMLA KLMSELESFP GSFRGRELP GSDSQSRPR RRTFPGVASR RNPERRARPL 180  
 TRSRIRILGS LDALPMEEEE EEDKYNLVRK RKTVDGYMNE DDLPRSRSR SSVTLPHIIR 240  
 FVEEITEEEL ENVCSNSREK IYNRSLGSTC HQCRQKTI DT KTNCRNPDCW GVRGQFCGPC 300  
 LRNRYGEEVR DALLDPNWHC PPCRGICNCS FCRQRDRGCA TGVLVYLAKY HGFNVHAYL 360  
 KSLKQEFEMQ A

Seq ID NO: 127 DNA sequence  
 Nucleic Acid Accession #: AF305616.1  
 Coding sequence: 1..863

1 11 21 31 41 51  
 ATGCACCGCT TGATGGGGGT CAACAGCACC GCCGCGCGCG CCGCGGGGCA GCCCAATGTC 60  
 TCCTGCACGT GCAACTGCAA ACGCTCTTTG TTCCAGAGCA TGGAGATCAC GGAGCTGGAG 120  
 TTTGTTTACA TCATCATCAT CGTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCAOGTGC 180  
 CTGTGAGGCC ACTACAAGCT GTCTGCAOAG TCCTTCATCA GCCGGCACAG CCAGGGGGGG 240  
 AGGAGAGAAG ATGCCCTGTC CTCAGAAGGA TGCTGTGGC CCTCGGAGAG CACAGTGTCA 300  
 GGCAACGGAA TCCAGAGGCC GCAGGCTTAC GCCCGGCTC GGGCCACGGA CCGCTGGCC 360  
 GTGCCGCGCT TCGCCAGCGG GAGCGCTTC CACGCTTCC AGCCCACTA TCCGTACCTG 420  
 CAGCAOGAGA TCGACCTGCC ACCCACCATC TCGCTGTGAG ACGGGGAGGA GCCCCACCC 480  
 TACCAGGGCC CCGTCAACCT CCAGCTTGGG GACCCGAGC AGCAGCTGGA ACTGAACCGG 540  
 GAGTCGGTGC GCGCACCCCC AACAGAACCT ATCTTGACA GTGACCTGAT GGATAGTGCC 600  
 AGGCTGGGCG GCCCTGCCCC CCCAGCAGT AACTCGGGCA TCAGCGCCAC GTGCTACGGC 660  
 AGCGCGGGCG GCATGGAGGG GCGCGCGCCC ACCTACAGCG AGGTATCTCG CCACTACCCG 720  
 GGGTCTCTCT TCCAGCACCA GCAGAGCAGT GGGCGCGCT CCTGTGCTGA GGGGACCCGG 780  
 TCCACCAACA CACACATGCG GCCCTAGAG AGCGCAGCCA TCTGGAGCAA AGAGAAGGAT 840  
 AAACAGAAAG GACACCTCT CTAG

Seq ID NO: 128 Protein sequence  
 Protein Accession #: AAL09357.1

1 11 21 31 41 51  
 MRLMGVNST AAAAAGQPNV SCTCNCKRSL FQSMETILE FVQIIIVV MVVMVVITC 60  
 LLSHYKLSAR SFISRHSQGR RREDALSSSEG CLWPSESTVS GNGIPEPQV APPRPTDRLA 120  
 VPPFAQRERF HRFQPTYPL QHEIDLPTTI SLSDGEEPPP YQGPTLQLR DPEQQLLNLR 180  
 ESVRAPPRNT IPDSLDMSA RLGGPCPPSS NSGISATCYG SGRMBGPPP TYSEVIGHYP 240  
 GSSFQHQSS GPPSLLEGTR LHTHTIAPLE SAAIWSKEKD KQKGHPL

Seq ID NO: 129 DNA sequence  
 Nucleic Acid Accession #: NM\_004952.1

Coding sequence: 1..718

1 11 21 31 41 51  
5 ATGGCGGCGG CTCCGCTGCT GCTGCTGCTG CTGCTGCTG CCGTGCCGCT GCTGCCGCTG 60  
CTGGCCCAAG GGCCGCGAGG GGCCTGCGGA AACCGGCATG CCGTGTACTG GAACAGCTCC 120  
AACCAGCACC TCGCGCGAGA GGGCTACACC GTGCAGGTGA ACGTGAACGA CTATCTGGAT 180  
ATTACTGCC CGCACTACAA CAGCTCGGGG GTGGGCCCCG GGGCGGGACC GGGCCCCGGA 240  
GGCGGGGCGAG AGCATAAGT GCTGTACATG GTGAGCCGCA ACGGCTACCG CACCTGCAAC 300  
10 GCCAGCCAGG GCTTCAAGCG CTGGGAGTGC AACCGGCCGC ACGCCCCGCA CAGCCCCATC 360  
AAGTCTCGG AGAAGTTCCA GCGCTACAGC GCCTTCTCTC TGGGCTACGA GTTCCACGCC 420  
GGCCACGAGT ACTACTACAT CTCCACGCCC ACTCACAACC TGCACTGGAA GTGTCTGAGG 480  
ATGAAGGTGT TCGTCTGCTG CGCTCCACA TCGCACTCCG GGGAGAAGCC GGTCCCCACT 540  
15 CTCCCCCAGT TCACCATGGG CCCCAATGTG AAGATCAACG TGCTGGAAGA CTTTGAGGGA 600  
GAGAACCCTC AGGTGCCCAA GCTTGAGAAG AGCATCAGCG GGACCAGCCC CAAACGGGAA 660  
CACCTGCCCC TGGCCGTGGG CATCGCCTTC TTCTCATGA CGTCTTGGC CTCCTAG

Seq ID NO: 130 Protein sequence  
Protein Accession #: NP\_004943.1

20 1 11 21 31 41 51  
MAAAPLLLLL LLVPVPLPL LAQGPGGALG NRHAVYWNSS NOHLRREGYT VQNVNDYLD 60  
IYCPHYNSSG VGPGAGPGPG GGAEQVLYM VSRNGYRTCN ASQGFKRWEC NRPHAPHSPI 120  
25 KFSEKFORYS AFSLGYEFHA GHEYVYISTP THNLHWKCLR MKVFCVCCAT SHSGEKFVPT 180  
LPQFTMGPNV KINVLEDFEG ENPQVPKLEK SISGTSPPKRE HPLAVGIAF FLMTFLAS

Seq ID NO: 131 DNA sequence  
Nucleic Acid Accession #: NM\_012445.1  
Coding sequence: 276..1271

30 1 11 21 31 41 51  
GCACGAGGGA AGAGGGTGAT CGGACCCGGG GAAGGTGCTG GGGCAGGGCG AGTTGGGAAA 60  
35 GCGGCAGCCC CGCCGCGCCC CGCAGCCCCT TCTCCTCCTT TCTCCACAGT CCTATCTGCC 120  
TCTCGCTGGA GGCCAGGCCG TGCAGCATCG AAGACAGGAG GAACCTGGAGC CTCACTGGCC 180  
GGCCGCGGGG GCGCGCTCGG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCCGAGC 240  
GCTGCCGCGC GCGCTCCGCG TGCTCTCTGC GGTGTATGGA AAACCCGAGC CGGCGCGCGG 300  
40 CCTCGGGCAA GGCCTCTCTG GCTCTCTCTC TGGCCACTCT CGGCGCGCGC GGCCAGCCTC 360  
TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCCCGGCCAA ATACAGCATC ACCTTCACGG 420  
GCAAGTGGAG CCAGACGGCC TTCCCCAAGC AGTACCCCTT GTTCCGCCCC CCTTCGCGAGT 480  
GGTCTTCGCT GCTTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCACT 540  
ACGTCACTAA CCGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCTTGGGCG CTGATGAAGG 600  
45 AGATCGAGGC GCGCGGGGAG GCGCTGCAGA GCGTGCAAGC GGTGTTTTCG GCGCCGCGCG 660  
TCCCCAGCGG CACCGGGCAG ACGTCCGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720  
TCTCGTTTGT GGTGCGCATC GTGCCAGGCC CGGACTGGTT CGTGGGCGTG GACAGCCTGG 780  
ACCTGTGCGA CGGGGACCGT TGGCGGGAAC AGGCGGCGCT GGACCTGTAC CCCTACGAGC 840  
CGGGAGCGGA CAGCGGCTTC ACCTTCTCCT CCCCCAATT CGCCACCATC CCGCAGGACA 900  
50 CCGTGACCGA GATAAGCTCC TCTCTCCCA GCCACCGGCG CAACTCTTTC TACTACCGCG 960  
GGCTGAAGGC CTGCTCTCCC ATGCCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020  
GGGCTTTCAT CCTTCCCGCC CAGTCTCTCG CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080  
CCTCAGTTCC AGAAAGCGCG CTGGACTGCG AGGTCTCCCT GTGCTCGTCC TGGGACTGT 1140  
GCGGAGGCCA CTGTGGGAGG CTGGGACCA AGAGCAGGAC TCGCTACGTC CGGTCCAGC 1200  
55 CGCCCAACAA CCGGAGCCCC TGCCCCGAGC TCGAAGAAGA GGCTGAGTGC GTCCCTGATA 1260  
ACTGCGTCTA AGACCAAGAG CCGCAGCCCC CTGGGCCCCC CGGAGCCATG GGGTGTCCGG 1320  
GGCTCCTGTG CAGGCTCATG CTGCAGGCGG CCGAGGCACA GGGGGTTTGG CGCTGCTCCT 1380  
GACCGCGGTG AGCGCGCGCG GACCATCTCT GCCTGAAAGG GCGCTCTGTG GGCCGCGCAG 1440  
GGCATGCGGA AACAGCCTCC TCCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG 1500  
60 TCTGCTCTCA GCCTCCTCCT CCGCAGGAT AAAGTCATCC CCAAGGCTCC AGCTACTCTA 1560  
AATTATGGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCTTCTAT CGTCCAGGGG 1620  
CCTGGCTCCC ACGTGGTGGC AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680  
CTCTCCCGAG GCGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740  
65 GGAAGCGTCA GTGTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800  
TGCTCAC

Seq ID NO: 132 Protein sequence  
Protein Accession #: NP\_036577.1

70 1 11 21 31 41 51  
MENPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60  
PLFRPFAQWS SLLGAHSSD YSMWRKNQYV SNGLRDPFAER GEAWALMKEI EAAGALQSV 120  
HAVFSAPAVP SGTGQTSDEL EVQRHSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180  
75 ALDLYFYDAG TDSGFTSSP NFATIPQDTV TEITSSPSH PANFPYPRL KALPIARVT 240  
LVRLRQSPRA FIPPAVLPS RDNEIVDSAS VFETPLDCEV SLWSSWGLCG GHGCRGLTKS 300  
RTRYVRVQPA MNGSPCELE EEAECVPDNC V

Seq ID NO: 133 DNA sequence  
Nucleic Acid Accession #: NM\_019894  
Coding sequence: 1..1314

80 1 11 21 31 41 51  
ATGTTACAGG ATCTGACAGG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60



5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTT GCGGCGAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGACTGTCT CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCCACTGC AGGTGCTGGA CTGGGCCACA 360
GGGAAGTGGT TCTCTGCTG TTTGACAAC TTACAGAAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAACCCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAC AGCCAGGAGC TTGCATGCG GAACTCAAGT 540
GGGCCCTGTG TCTCAGGCTC CTTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGTCTGT GAGGGAGGCA TCCTGGACCC CCACTGGGTC 720
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCGCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTACG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGATCAT TGGATGGGCG TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACATG TGCAGGCTG AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GGTACACAGG GGAAGTCAAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG GTGGCTGGG CTATGGCTGC GGGGGCCGGA GCACCCGAG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
```

Seq ID NO: 134 Protein sequence

Protein Accession #: NP\_063947.1

1  
 11  
 21  
 31  
 41  
 51

```

MLQDPDSQPL LNSLDVKPLR KPRIPMETFR KVGPIPIIAL LSLASIIIVV VLIKVILDKY 60
YFLCQQLPHF IPRKQLCDGE LDCPLGEDEE HCVKSPFPEG AVAVRLSKDR STLQVILDSAT 120
GNWFACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNRS 180
GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSWPQV SIQYDQHVHC GGSILDPHV 240
LTAHCFRKH TDVFNWVRA GSKLGSFPS LAVAKIIIE FNPMPKND JALMKLQFPL 300
TFSGTVRIC LPFFDEELTP ATPLWIIGW FTQNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAGIPEGV DTCQGDSSGP LMTQSDQWHV VGIVSWGYGC GGPSTPGVYT 420
  
```

Seq ID NO: 135 DNA sequence

Nucleic Acid Accession #: NM\_003045

Coding sequence: 148..2037

1  
 11  
 21  
 31  
 41  
 51

```

CGATCCTGCC GGAGCCCCGC CGCCGCCGGC TTGGATTCTG AAACCTTCTT TGTATCCCTC 60
CTGAGACATC TTTGTGCAA GATCGAGGCT GTCTCTGGT GAGAAGGTGG TGAGGCTTCC 120
CGTATATTTC CAGCTCTGAA CAGCAACATG GGGTGCAAG TCCTGCTCAA CATTGGGCG 180
CAGATGCTGC GGGCGAAGT GGTGACTGT AGCCGGGAGG AGACGGCGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC 300
GTCTGGCTG GAGCTGTGGC CGGTGAGAAT GCAGGCCCTG CCATTGTCTAT CTCCTTCTC 360
ATGCTGCGC TGGCCTCAGT CCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420
CCCAAGACGG GCTCAGCTTA CTTCTACAGC TATGTCAACG TTGGAGAGCT CTGGGCCCTC 480
ATCACCGCT GGAACCTAAT CCTCTCTAC ATCATCGTA CTCAAGCGT AGCGAGGGCC 540
TGGAGCGCCA CCTTCGACGA CTGATAGGC AGACCATCG GGGAGTTCTC ACGGACACAC 600
ATGACTCTGA ACGCCCCCGG CGTCTGGCT GAAAACCCCG ACATATTCCG AGTGATCATA 660
ATTCTCATCT TGACAGGACT TTTAACTCTT GGTGTGAAAG AGTGGGCCAT GGTCAACAAA 720
ATATTCACTT GTATTAAAGT CTTGTCTCTG GGCCTCATAA TGGTGTGAGG ATTTGTGAAA 780
GGATCGGTTA AAAACTGGCA GCTCACGGAG GAGGATTTTG GGAACACATC AGGCCGTCTC 840
TGTTTGAACA ATGACACAAA AGAAGGGAAG CCGGTTGTG GTGGATTCAAT GCCCTTCGGG 900
TTCTCTGGTG TCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTGTGGG CTTTGACTGC 960
ATGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAG CCATCCCCGT GGGGATGTG 1020
GCGTCCCTCT TGATCTGCTT CATGCCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG 1080
ATGCCCTACT TCTGCCTGGA CAATAACAGC CCCCTGCCCG ACGCCTTTAA GCACGTGGGC 1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT CGGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCCT TGTTTCCCAT GCCTCGGTTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
TTTAAATTCT TAGCCACGCT CAATGATAGG ACCAAAACAC CAATAATCCG CACATTAGCC 1320
TCGGGTGCGG TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GSTGGACCTC 1380
ATGTCCATTG GCACTCTCCT GGCTTACTCG TTGGTGGCTG CCTGTGTGTT GGTCTTACGG 1440
TACCAGCCAG AGCAGCTTAA CTTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CCAGCAGAGT AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560
GCAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAAA ACATGGAGCC TTCCAAAATC 1620
TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTATAGCTG TTCTCATCAT CACTTCTGCG 1680
ATTGTGACCG TGCTTGAAGT GGAGGCTCTC ACCAAAGGGG CGCTGTGGGC AGTCTTCTG 1740
CTGCGAGGT CTGCCCTCCT CTGTGCGGTG GTACGCGGCG TCATCTGGAG CGAGCCGAG 1800
AGCAAGACCA AGCTCTCAT TAAGTTTCCC TTCTGCGCAG TGCTCCCAT CCTGAGCATC 1860
TTGTTGAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CTTGGGTCCG GTTTGCTGTG 1920
TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGACACAG CGAGGAGGCG 1980
TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCATG CAAGTGACGC 2040
ACAGCCCGCG CCCCCGAGG TGGCAGCAGC CCGGAGGGAC GCCCCGAGAG GACCCGAGG 2100
CACCCACCC TCCCCACCAG TGCAACAGAA ACCACCTGCG TCCACACCT CACTGCA
  
```

Seq ID NO: 136 Protein sequence

Protein Accession #: NM\_003045

1  
 11  
 21  
 31  
 41  
 51

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

MGCKVLLNIG QQMLRRKVV D CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60  
NAGPAIVISF LLAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNILLS 120  
YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPVL AENPDIFAVI IILILTGLLT 180  
LGVKESAMVN KIFTICINVLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKDG 240  
KPGVGGFMPF GFSGVLSGAA TCFYAFVGF D CIATTGEEVK NPQKAIPVGI VASLLICFIA 300  
YFGVSAALTL MPPYFCLDNN SPLPDAFKHV GWEGAKYAVA VGS LCALSAS LLSGMPFMPR 360  
VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAMVA FLFDLKDLDV LMSIGTLLAY 420  
SLVAACVLVL RYQPEQPNLV YQMASTSELD DPADQNELAS TNSQLGFLP EAEMFSLKTI 480  
LSPKNMEPSK ISGLVINIST SLIAVLIITF CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540  
VVTGVINRQP ESKTKLSFKV PFLPVLPILS IFVNVYLMQ LDQGTWVRFA VWMLIGFIIT 600  
FGYGLWHSSE ASLDADQART PDGNLDQCK

Seq ID NO: 137 DNA sequence

Nucleic Acid Accession #: NM\_032044.1

Coding sequence: 182..658

1 11 21 31 41 51  
AAGATATAAA AGCTCCAGAA AGCTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60  
GCCCTTAGAG TCTTGGTTCG CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA 120  
AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCAC TAGCTA CATCCTCAGG GTAGGAGGAA 180  
GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCTGGCCA AAACAGGAGT 240  
CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTACC ACAAGTCCAA 300  
TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCGAGCTCG AGTGTCTAGT 360  
TTACGSAAAC GGAGCCCACT TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC 420  
AGAGTACATA AGTGGCTATC AGAGAAGCCA GCGATATGG ATTGGCCTGC ACGACCCACA 480  
GAAGAGGAGC CAGTGGCAGT GGATTGATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG 540  
CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTAAAC 600  
TTGGAGCAGC AACGAATGCA ACAAGGCCA ACACCTCTCT TGCAAGTACC GACCATAGAG 660  
CAAGAATCAA GATTCTGCTA ACTCTGCTAC AGCCCGTCC TCTTCTCTTC TGCTAGCCTG 720  
GCTAAATCTG CTCATTATTT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780  
ACTACACTGG CTTTCTTAGG CTTAGAGACA GAAACTTTAG CATTGGCCCA CTAGTGGCTT 840  
CTAGCTCTAA ATGTTTGCCC CGCCATCCTT TTCCACAGTA TCCTTCTTCC CTCTCTCCCT 900  
GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960  
CTTTGGCCAT AAGAAGTAAA GATTTGAAAGA CAGAAGGAAG AAACCTAGGA GTAAGCTTCT 1020  
AGACCCCTTC AGCTTCTACA CCTTCTGCC CTCTCTCCAT TGCCTGCACC CCACCCAGC 1080  
CACTCAACTC CTGCTTGTGT TTCTCTTGGC CATAGGAAGG TTTACAGTA GAATCCTTGC 1140  
TAGGTTGATG TGGGCCATAC ATTCCTTTAA TAAACCAATG TGACATAAG AAAAAAAAAA

Seq ID NO: 138 Protein sequence

Protein Accession #: NP\_114433.1

1 11 21 31 41 51  
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWYFHKSN CYGYFRKLRLN WSDAELEQCS 60  
YGNAGHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG 120  
KSMGNGKHCA EMSNNNFLT WSSNECNKRO HFLCKYRP

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM\_051860.2

Coding sequence: 52..3042

1 11 21 31 41 51  
GCTCACCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60  
GTTAACCTCA GCACCGAGGT TGCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC 120  
GACCGGGGCA GAGCCTGCGG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180  
CCCAAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTGTGAGGAT 240  
AATGTACAGT CATGGAAACC TGGAGATACC CTGGTCAATG CCAGTACTGA TTACTCCATG 300  
TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAAA 360  
GTGCGAGGGA AACCAATGTA CTGCAATC GGGGAGGAGA TAGACGGGCT GGACATGCGG 420  
GCGGAGGTTG GGCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480  
TACCCCTACA GAAACCAATC CTGCAATTTT TTTGACTTGG ATACCTTTGG GGGCCACATC 540  
AAGTTTGCTC TGGGATTTAA GGCAGCACAC TTGGAGGGCA CGAGCTGAA GCATATGGGA 600  
CAGCAGCTGG TGGGTCACTA CCCGATTAC TTCCACCTGG CCGGTGATGT AGACGAAAGG 660  
GGAGGTTATG ACCCACCAC ATACATCAGG GACCTCTCCA TCATCATAC ATTCTCTGCT 720  
TGCGTACAG TCCATGGCTC CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780  
TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT 840  
CTTGGCCCTC TTGTCAAGTC TGGAAACCTC CTCCCTCGG ACGTGACAG CAAGATGTGC 900  
AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCCA AGCCAGGCA AGACTGCAAT 960  
GCTGTGTCCA CCTTCTGGAT GGCCAAATCC AACACAACCC TCATCAACTG TGCCGCTGCA 1020  
GGATCTGAGG AAATCTGATT TTGGTTTATT TTTCACCAAG TACCAAGGGG CCGCTCCGTT 1080  
GGAATGTACT CCCCAGGTTA TTCAGAGCAC ATTCCACTGG GAAAATTCTA TAACAACCGA 1140  
GCACATTCCA ACTACCGGGC TGGCATGATC ATAGACAACG GAGTCAAAAC CACGAGGGCC 1200  
TCTGCCAAGG ACAAGCGGCT GTTCTCTCTA ATCATCTCTG CCAGATACAG CCCTCACCAG 1260  
GACGCCGACC CGCTGAAGCC CCGGAGGCGG GCCATCATCA GACACTTCAT TGCTTACAAG 1320  
AACCAGGACC ACGGGGCTG GCTGCGCGG GGGGATGTGT GGCTGACAG CTGCGGGTTT 1380  
GCTGACAAAG GCATGGGCTT GACCTGGGCC AGTGGTGGAA CCTTCCCGTA TGACGACGGC 1440  
TCCAAGCAAG AGATAAGAA CAGCTTGTGT GTTGGGAGGA GTGGCAACGT GGGGACGGAA 1500  
ATGATGGACA ATAGGATCTG GGGCCCTGGC GGCTTGGACC ATAGCGGAAG GACCTCCCT 1560  
ATAGGCCAAT ATTTTCCAT TAGAGGAATT CAGTTATATG ATGGCCCCAT CAACATCCAA 1620  
AATGCACTT TCCGAAGTT TGTGGCCCTG GAGGGCGGCG ACACCAAGGC CCTGGCCCTC 1680  
CGCCTGAATA ATGCTTGGCA GAGCTGCCCC CATAACAAGC TGACCGGCAT TGCTTTGAG 1740  
GAOGTTCCGA TTACTTCCAG AGTGTCTTTC GGAGAGCCTG GGCCCTGGTT CAACCACTG 1800

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65

GACATGGATG GGGATAAGAC ATCTGTGTTT CATGACGTG ACGGCTCCGT GTCOGAGTAC 1860  
 CCTGGCTCCT ACCTCACGAA GAATGACAA TGGCTGGTCC GGCACCCAGA CTGCATCAAT 1920  
 GTTCCCGACT GGAGAGGGGC CATTGTCAGT GGGTGCTATG CACAGATGTA CATTCAAGCC 1980  
 TACAAGACCA GTAACTCTGC AATGAAGATC ATCAAGAATG ACTTCCCCAG CCACCTCTCT 2040  
 TACCTGGAGG GGGCGCTCAC CAGGAGCACC CATTACCAGC AATACCAACC GGTGTGCACC 2100  
 CTGCAGAAGG GCTACACCAT CCACTGGGAC CAGACGGCCC CCGCCGAATC GGCATCTGG 2160  
 CTCATCAAT TCAACAAGG CGACTGGATC CGAGTGGGTC TCTGTACCC GCGAGGCACC 2220  
 ACATTCTCCA TCTCTCGGA TGTTCACAA TGGCTGCTGA AGCAAAGTC CAAGACGGGC 2280  
 GTCTTCGTGA GGACCTTGCA GATGGACAAA GTGGAGCAGA GCTACCTCGG CAGGAGCCAC 2340  
 TACTACTGGG ACGGAGACTC AGGGCTGTTG TTCTGAAAG TGAAGACTCA GAACGAGAGA 2400  
 GAGAAGTTTG CTTTCTGCTC CATGAAAGGC TGTGAGAGGA TAAAGATTAA AGCTCTGATT 2460  
 CCAAAGAAGC CAGGCGTCAG TGAATGCACA GCCACAGCTT ACCCAAGTT CACCGAGAGG 2520  
 GCTGTGCTAG ACCTGCGGAT GCCCAAGAAG CTCTTTGGTT CTCAGCTGAA AACAAAGGAC 2580  
 CATTTCTTGG AGTGAAGAT GGAGAGTTCC AAGCAGCACT TCTTCCACCT CTGGAAACGAC 2640  
 TTGCTTACA TTGAAGTGA TGGGAAGAAG TACCCAGTT CGGAGGATGG CATCCAGGTG 2700  
 GTGGTGAATT ACGGGAACCA AGGGCGCGTG GTGAGCCACA CGAGCTTCAG GAATCCATT 2760  
 CTGCAAGGCA TACCATGGCA GCTTTTCAAC TATGTGGCGA CCATCCCTGA CAATTCATA 2820  
 GTGCTTATGG CATCAAAGGG AAGATACGTC TCCAGAGGCC CATGGACCGA AGTCTGGAA 2880  
 AAGCTTGGGG CAGACAGGGG TCTCAAGTTG AAGAGACAAA TGGCATTCTG TGGCTTCAA 2940  
 GGCAGCTTCC GGGCCTCTG GTGACACTG GACACTGAGG ATCACAAGC CAAATCTTC 3000  
 CAAGTTGTGC CCATCCCTGT GGTGAAGAAG AAGAAGTTGT GAGGACAGCT GCCGCCGGT 3060  
 GCCACCTCGT GGTAGACTAT GACGGTGACT CTTGGCAGCA GACCAGTGGG GGATGGCTGG 3120  
 GTCCCCAGC CCTGCGCAGC AGCTGCTGG GAAGGCGGTG TTTCAGCCCT GATGGGCCAA 3180  
 GGGAGGCTA TCAGAGACCC TGGTGTCTCC ACCTGCCCTT ACTCAAGTGT CTAGCTGGAG 3240  
 CCCTGGGGC GGTGCTGGCC AATGCTGAA ACATTCACT TCCTGCAGCC TCTGGGTGC 3300  
 TTCTCTCTA TCTGTGCTC TTCACTGGG GTTTGGGGAC CATATCAGGA GACCTGGGT 3360  
 GTGCTGACG CAAAGATCCA CTTTGGCAGG AGCCCTGACC CAGCTAGGAG GTAGTCTGGA 3420  
 GGGCTGTGTA TTCAAGATC CCATGGTCT TCAGCAGACA AGTGAAGGTG GTAAATGTAG 3480  
 GAGAAAGAGC CTTGGCCCTA AGGAAATCTT TACTCTGTGA AGCAAGAGCC AACCTCAGC 3540  
 GATTAGGAGC TGGGCTAGAA CTGGCTATCC TTGGGGAAGA GGCAGGCCCT GCCTCTGGCC 3600  
 GTGTCCACCT TTCAAGAGAC TTTGAGTGGC AGGTTTGGAC TTGACTAGA TGACTCTCAA 3660  
 AGGCCCTTTT AGTCTGAGA TTCCAGAAAT CTGCTGCATT TCACATGGTA CCTGGAACCC 3720  
 AACAGTTTAT GGATATCCAT TGATATCCAT GATGCTGGT GCCCCAGCCG ACACGGGATG 3780  
 GAGAGGTGAG AACTAATGCC TAGCTTGAGG GGTCTGCAGT CCAGTAGGGC AGGCAGTCAG 3840  
 GTCCATGTGC AACTCAATGC CAGGTGGAGA AATCAGAGAG AGGTAAATG GAGGCCAGTG 3900  
 CCATTTTACA GGGGAGGCTC AGGAAGGCTT CTGCTTACA GGAATGAAGG CTGGGGGCAT 3960  
 TTTGCTGGG GGAGATGAGG CAGCCTCTGG AATGGCTCAG GGATTCAGCC CTCCCTGCCG 4020  
 CTGCTGTCT AAGCTGTGTA CTACGGGGTC GCCCTTTGCT CAGCTCTCTC TGGCCCACTC 4080  
 ATGATGAGGA AGTGTGTGTA GAGGGGAGCA ATGGGCTTTG CTGCTTATGA GCACAGAGGA 4140  
 ATTCAGTCCC CAGGCGAGCC TGCCCTGAC TCCAGAGGG TGAAGTCCAC AGAAGTGAGC 4200  
 TCCTGCTTA GGGCCTCAT TGTCTTCTAT CCAGGGAATC GAGCACAGGG GGCCTCCAGG 4260  
 AGACCTTGA TGTGCTCGTA CTCCCTCGGC CTGGGATTTT AGAGCTGGA ATATAGAAA 4320  
 TATCTAGCCC AAAGCCTTCA TTTTAAACAGA TGGGGAAGT GAGCCCCAA GATGGGAAAG 4380  
 AACACACAG CTAAGGGAGG GCCTGGGGAG CCCCACCTTA GCCCTTGTCT CCACACCACA 4440  
 TTGCTCAAC AACCGGGCC AGAGTGCCCA GGCACCTCTG AGGTAGCTTC TGGAAATGGG 4500  
 GACAAGTCCC CTCGAAGGAA AGGAATGAC TAGAGTAGAA TGACAGCTAG CAGATCTCTT 4560  
 CCTCTCTGT CCCAGCGCAC ACAAACCCGC CCTCCCTTTG GTGTGGGCG TCCCTGTGGC 4620  
 CTTCACTTGT TTCACTACT GTACGCCCAG CTTGGGTGCA CAGTAGCTGC AACTCCCCAT 4680  
 TGGTCTTACC TGGCTCTCT GTCTCTGAG CTCTACAGGT GAGGCCAGC AGAGGGAGTA 4740  
 GGGCTCGCA TGTTTCTGGT GAGCCAAATT GGCTGATCTT GGGTGTCTGA ACAGCTATTG 4800  
 GGTCCACCCC AGTCCCTTTC AGCTGCTGCT TAATGCCCTG CTCTCTCCCT GGCCACCTT 4860  
 ATAGAGAGCC CAAGAGSCTC CTGTAAGAGG GAGAACTCTA TCTGTGGTTT ATAATCTTGC 4920  
 ACGAGGACCC AGAGTCTCCC TGGGTCTTGT GATGAACCTAC ATTTATCCCC TTCTCTGCC 4980  
 CAACCAACAA CTCTTCTCT CAAAGAGGGC CTGCTGGCT CCTCCACCC AACTGCACCC 5040  
 ATGAGACTCG GTCCAAAGT CCATTCGCCA GGTGGGAGCC AACTGTCAAG GAGGTCTTTC 5100  
 CCACCAACAA TCTTTCAGCT GCTGGGAGGT GACCATAGGG CTCTGCTTTT AAAGATATGG 5160  
 CTGCTTCAA GGCCAGAGTC ACAGGAAGGA CTTCTTCCAG GGAGATTAGT GGTGATGGAG 5220  
 AGGAGAGTTA AAATGACCTC ATGTCTTCTT TGTCCAGGT TTTGTTGAGT TTTCACTCTT 5280  
 CTAATGCAAG GGTCTCACAC TGTGAACACC TTAGGATGTG ATCATTCTCA GGTGGCCAGG 5340  
 AATGTTGAAT GTCTTTGGCT CAGTTCAATT AAAAAAGATA TCTATTGAA AGTTCTCAGA 5400  
 GTGTGATACA TGTTCACAG TACAGGATCT GTACATAAAA GTTCTTTCC TAAACCATTC 5460  
 ACCAAGAGCC AATATCTAGG CATTTTCTTG GTAGCACAAA TTTTCTTATT GCTTAGAAAA 5520  
 TTGCTCTCTT TGTATTCTT GTTTGTAAGA CTTAAGTGAG TTAGGTCTTT AAGGAAGCA 5580  
 ACGCTCTCTT GAAATGCTTG TCTTTTCTT GTTGGCGAAA TAGCTGTGCC TTTTTOGGGA 5640  
 GTTAGATGTA TAGAGTGTGT GTATGTAAC ATTCTTGTG GGCATCACA TGAACAAAGA 5700  
 TATATTTTCT ATTTATTAT TATATGTGCA CTTCAAGAAG TCACTGTGAG AGAAATAAAG 5760  
 AATTGTCTTA AATGTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA

70 Seq ID NO: 140 Protein sequence  
 Protein Accession #: XP\_051860.2

75  
80

1 11 21 31 41 51  
 MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLTVTI DTNVNSTILN 60  
 LEDNVQSWKP GDTLVIASTD YSMYQAEFQ VLPSCRSCAPN QVKVAGKPMY LHIGEEIDGV 120  
 DMRAEVGLLS RNIIIVGEME DKCYPYRNHI CNFFDFDTFG GHIFKALGFK AARLEGTELK 180  
 HMQQQLVGQY PIHFHLAGDV DERGGYDPPT YIRDLISHT PSRCVTVHGS NGLLIKDVVG 240  
 YNSLGHCFPT EDGPEERNTP DHCLGLLVKS GTLLPSDRDS KMKRMITGDS YPGYIPKPRQ 300  
 DCNAVSTFW ANFNINLINC AAAGSEETGF WPIFHVPTG PSVGMYSFGY SEHIPGLKPY 360  
 NNRAHSNYRA GMIIIDNGVKT TEASAKDKRP FLSIIISARYS PHQDADFLKP REPAIRRHPI 420  
 AYKQDHGAW LRGGDVWLDL CRFADNIGL TLASGGTFPY DDGSQKEIKN SLFVGESGNV 480  
 GTEMMDNRW GPGLDHSR TLPIGNFPI RGIQLYDGP NIQNTFRKF VALEGRHTSA 540  
 LAFLNNAWQ SCFHNNTGI AFEDVPITSR VFFGEPGPHF NQLMDGDKT SVPHVDVGSV 600

SEYFSGSYLTK NDNMLVRHPD CINVPDWRGA ICSGCTAQM Y IQAYKTSNLR MKIIKNDFPS 660  
 HPLYLEGALT RSTHYQYQYP VVTLQKGYTI HWDQTAPAEI AIWLINFNKG DWIRVGLCYP 720  
 RGTTFSILSD VHNRLKQTS KTGVPVFTLQ MDRVQSYSPG RSHYYWDEDS GLLFLKLAQ 780  
 NEREKFAFCS MKGCEKIKK ALIPKNAGVS DCTATYPKF TERAVVDVPM PKLLFGSQLK 840  
 TKDHFLEVKM ESSKQHFHFL WNDPAYIEVD GKYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900  
 NSILQGIPIW LFMYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLGADRG LKLEQMAFV 960  
 GPKGSFRPIW VTLDTEDHKA KIPQVVPFV VKKKKL

Seq ID NO: 141 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 261..2861

1 11 21 31 41 51  
 15 GAGCTAGCGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG 60  
 CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGCTCT GAACCCAGAT TTCCAGACT 120  
 AGCTACCACT CCCTPTGCCC ACGCCCCGGG AGCTCGCGGC GCTTGGCGGT CAGCGACCAG 180  
 ACGTCCGGGG CGCTGCGCT CCTGGCCCGC GAGGCGTGAC ACTGTCTGG CTACAGACCC 240  
 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GSACTTCCTC TTCAGGCCA 300  
 20 TGCTGACCAT CAGCTGCTC ACTCTGACCT GCTTCCCTGG GGCACATCC ACAGTGGCTG 360  
 CTGGGTGCCC TGACCAAGAG CCGTGTGTC AACCTGGAA CCCTGGCCAT GACCAAGACC 420  
 ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTCTGCC ACGTCTATT 480  
 CCATCCACAT CTGAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT 540  
 25 TCGCAACCGG GCACATCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTCCCTCT 600  
 GCCCTTTCCA GGGCAATTTT ACCATCATTT TGTATGGAAG GGTGATGAA GGTATTTCAGC 660  
 CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGTGTA AGGAGGCGCT CTGAGTTGC 720  
 ATGGACAGAA AAGCTCTTCC TGGACATTTT TGAACAAGAC CCTTACCCA GGTGGCATGG 780  
 CAGAAAGGAG CTATTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA 840  
 30 TCGACCCCAA CTACAGGACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAGA 900  
 AAGAGAGTGA ACGTCTGGTC CAGTATTTGA ACGCGTGGC CGATGGCAGG ATCTCTTCTG 960  
 TTGCACTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020  
 AATGGGAGG CAACACCTTC CTGCACTTGG GATTTAGACA CCTTGGAGT TTTCTAACTG 1080  
 TGAAGGAGAA TCCATCATCT TCAGTGAAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140  
 35 CTGCTGCTGC CGGGTATTTC AAATTGTTCC AGACAGAGCA TGGCAATAT TTCATGTTT 1200  
 CTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCCAT CATGATAAAG 1260  
 TATCTCAGAC TAAAGTGGG GAGAAATTT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA 1320  
 TATGCAATCG TCCCATTTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGACCG 1380  
 AGGTTGTCTA CAAAAAAGGC CAGGATTATA GGTTCCTG CTACGACCGG GGCAGAGCCT 1440  
 40 CCGGAGCTCA CGTGTACGG TTCTCTGTG GGAAGCCTGT GAGGCCCAA CTCACAGTCA 1500  
 CCATTGACAC CAATGTGAAC AGCACCATT C TGAACCTGGA GGATAATGTA CAGTCATGGA 1560  
 AACCTGGAGA TACCTGGTTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAGAGT 1620  
 TCCAGTGCTC TCCTGCGAGA TCTTGCGCC CCAACCAAGT CAAAGTGCCA GGGAAACCAA 1680  
 TGTACTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC 1740  
 45 TGAGCGGAGA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800  
 ACATCTGCAA TTCTTTGAC TTGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT 1860  
 TTAAGGCAGC ACACCTGGAG GGCACGGAGC TGAAGCATAT GGCACAGCAG CTGGTGGGTC 1920  
 AGTACCGAT TCCTTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC 1980  
 CCACATACAT CAGGACCTTC TCCATCCATC ATACATTCTC TCGCTGCTC ACAGTCCATG 2040  
 50 GCTCCATAGG CTGTGTGATC AAGGAGTTG TGGGCTATAA CTCTTGGGC CACTGCTTCT 2100  
 TCACGGAAGA TGGGCGGAG GAACGCAACA CTTTGAACA CTGCTTGGC CTCTCTGTCA 2160  
 AGTCTGGAAC CCTCTCCCTC TCGGACGGTG ACAGCAAGAT GTGCAAGATG ATCAGAGAGG 2220  
 ACTCTTACCC AGGCTACATC CCCAAGCCCA GGCAAGACTC CAATGCTGTG TCCACCTTCT 2280  
 GGATGGCCAA TCCCAACAA AACCTCATCA ACTGTGCGGC TGCAGGATCT GAGGAAACTG 2340  
 GATTTTGTGT TATTTTTCAC CAGTACCAA CGGGCCCTC GGTGGGAATG TACTCCCGAC 2400  
 55 GTTATTGAGA GCACATTCCA CTGGGAAAT TCTATAACAA CCGAGCACAT TCCAACTACC 2460  
 GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCAACGA GGCCTCTGCC AAGGACAAGC 2520  
 GGCCTGTCT CTCAATCATC TCTGCCAGAT ACAGCCTCA CCAGGACGCG GACCOGCTGA 2580  
 AGCCCGGAGC GCGGCGCATC ATCAGACACT TCATTGCTTA CAAGAACCAG GAACCAAGGG 2640  
 60 CCGGCTGCG CGGCGGGAT GTGTGGCTGG ACAGCTGCCA TTTCAGAGG GAGGCTCAGG 2700  
 AAGGCTTCT CTCTACAGGA ATGAAGGCTG GGGCATTTT GCTGGGGGGA GATGAGGCG 2760  
 CCTCTGGAAT GGTCTAGGGA TTCAGCCCTC CCGGCGCTG CCGTCTGAAG CTGGTGACTA 2820  
 CGGGGTGCG CTGTCTCAC GTCTCTCTGG CCCACTCATG ATGGAGAAAT GTGGTCAGAG 2880  
 GGGAGCAATG GGTCTTGTCT CTTATGAGCA CAGAGGAAT CAGTCCCGAG GCAGCCCTGC 2940  
 65 CTCTGACTCC AAGAGGGTGA AGTCCACAGA AGTGAGCTCC TGCCTTAGGG CCTCATTTGC 3000  
 TCTTCACTCA GGAACCTGAG CACAGGGGCG CTCCAGGAGA CCCTAGATGT GCTGTACTC 3060  
 CCTCGGCTG GATTTTCA GCTGGAAATA TAGAAAATAT CTAGCCCAA GCCTTCATTT 3120  
 TAACAGATGG GGAAGTGAG CCCCAAGAT GGGAAAGAAC CACACAGCTA AGGGAGGGCC 3180  
 TGGGAGAGCC CACCTAGCC CTGTCTGCA CACCAATTG CCTCAACAC CGGCCCCAGA 3240  
 70 GTGCCAGGC ACTCTGAGG TAGCTTCTGG AATGGGGAC AAGTCCCTC GAAGGAAAGG 3300  
 AATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCTGCTCCC AGCGCACACA 3360  
 AACCGCCCT CCCTTGGTG TTGGCGGTCC CTGTGGCCTT CACTTTGTTC ACTACCTGTC 3420  
 AGCCAGCCT GGGTGACAGC TAGCTGCAAC TCCCAATTGG TGCTACCTGG CTCTCCTGTC 3480  
 TCTGCACTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTGCCATGT TTCTGGTGAG 3540  
 75 CCAATTGGC TGAATTTGGG TGTCTGAACA GCTATTGGGT CCACCCAGT CCGTTTCAGC 3600  
 TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGCCCAA AGAGCTCCTG 3660  
 TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGCAAG AGGCACCAGA GTCTCCCTCG 3720  
 GTCTTGATG GAACATATT TATCCCTTTT CCGGCCCAA CCACAACTC TTTCTTCAA 3780  
 AGAGGCGCTG CCGGCTCCC TCCACCCAA TGCACCCATG AGACTCGGT CAGAGTCCA 3840  
 80 TTCCCTTGGC GGGAGCCAA TGTCAAGGAG GTCTTTCCCA CCAACATCT TTCAGTGTCT 3900  
 GGGAGGTGAC CATAGGGCTC TGTCTTAAA GATATGGCTG CTTCAAAGGC CAGAGTCACA 3960  
 GGAAGGACTT CTTCAGGGA GATTAGTGGT GATGGAGAGG AGAGTTAAAA TGACCTCATG 4020  
 TCCTCTTGT TCACGGTTTT GTTGAGTTTT CACTCTTCTA ATGCAAGGGT CTCACACTGT 4080  
 GAACCACTTA GATGTGATC ACTTTCAGGT GGCCAGGAAT GTTGAATGTC TTTGGCTCAG 4140  
 TCAATTTAAA AAAGATATCT ATTTGAAAGT TCTCAGAGT GTACATATGT TTCACAGTAC 4200

5  
10  
AGGATCTGTA CATAAAAGTT TCTTCTCTAA ACCATTACC AAGAGCCAAT ATCTAGGCAT 4260  
TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAATTG TCCTCCTTGT TATTCTGTGT 4320  
TGTAAGACTT AAGTAGATTA GGTCTTAAAG GAAAGCAACG CTCCTCTGAA ATGCTTGTCT 4380  
TTTTTCTGTT GCCGAAATAG CTGGTCCCTT TCCGGAGTT AGATGTATAG AGTGTGTGTA 4440  
TGTAACATT TCTGTAGGC ATCACCATGA ACAAAGATAT ATTTTCTATT TATTATTAT 4500  
ATGTGCACCT CAAGAAGTCA CTGTACAGAGA AATAAGAAAT TGTCTTAAAT GTCATGTATG 4560  
GAGATGTCTT TTGCATTGCT TGGAAAGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620  
TTGGAATAAT TTTGCTGTGA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680  
AAAAAAAAA AAAAAAATAA AA

Seq ID NO: 142 Protein sequence  
Protein Accession #: Eos sequence

15  
20  
25  
30  
1 11 21 31 41 51  
MGAAGRQDFL FKAMLTISWL TLTCTPGATS TVAAGCPDQS PELQFWNPGH DQDHHVHIGQ 60  
GKTLILLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFGQNF 120  
TILLYGRADE GIQPDYPYGL KYIGVGKGA LELHQKLLS WTLNKLTHP GMAEGGYFF 180  
ERSHGHRGVI VHVDPKSGT VIHSDRFDY RSKKESERLV QYLAIVPDGR ILSVAVNDEG 240  
SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAARVF 300  
KLFQTEHGY FNVLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360  
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVPRK LTVTIDTNVN 420  
STILNLEDIV QSWKPGDTLV IASTDYSMYQ AEEOVLPCR SCAPNQVQVA GKPMVLHIGE 480  
BIDGVDMRAE VGLLSRNIV MGEMEDKCP YRNHICNFFD FDTFGSHIKP ALGFKAAHLE 540  
GTELKHMGGQ LVGQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600  
KDVVGYNISG HCFPTEDGPE ERNTEFDHCLG LLVKSGLTLP SDRDSKMKCM ITEDSYPGYI 660  
PKPRQDCNAV STFMANPNPN NLINCAAAGS EETGFWFIPH HVPTGPSVGM YSPGYSEHIP 720  
LGKFFYNRAH SNYRAGMI ID NGVKTTEASA XDKRPFLLSI SARYSPHODA DPLKPREPAI 780  
IRHFIAYKNQ DHGAWLRGGD VMLDSCHFRG EAQEGFLLTG MKAGGILLGG DEAAAGMAQG 840  
FSPPCRCCLK LVTTGSPFAH VSLARS

Seq ID NO: 143 NM DNA sequence  
Nucleic Acid Accession #: NM\_006017  
Coding sequence: 38..2635

35  
40  
45  
50  
55  
60  
65  
70  
75  
80  
1 11 21 31 41 51  
CCAAGTCTTA CCTCATGTTT GGAGGATCTT GCTAGCTATG GCCCTCGTAC TCGGCTCCCT 60  
GTTGCTGCTG GGGCTGTGCG GGAACCTCCTT TTCAGGAGGG CAGCCTTCAT CCACAGATGC 120  
TCCTAAGSCT TGGAATTATG AATTGCCCTGC AACAAATTAT GAGACCCAAG ACTCCCATAA 180  
AGCTGGACCC ATTGGCATTCT TCTTTGAACT AGTGCAATATC TTTCTCTATG TGGTACAGCC 240  
GCGTGATTTC CCAGAAGATA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAAT 300  
TGATTATGAC AAGCCAGAAA CTGTAATCTT AGGTCTAAAG ATTGTCTACT ATGAAGCAGG 360  
GATTATTCTA TGCCTGTGCTC TGGGGCTGCT GTTTATTATT CTGATGCCTC TGGTGGGTA 420  
TTTCTTTTGT ATGTGTCTGT GCTGTAACAA ATGTGGTGA GAAATGCACC AGCGACAGAA 480  
GGAAATGGG CCCTTCTCTGA GGAATGCTT TGCAATCTCC CTGTTGGTGA TTTGTATAAT 540  
AATAAGCATT GGCATCTTCT ATGGTTTGTG GGCAATCAC CAGGTAAGAA CCGGATCAA 600  
AAGGAGTCGG AAATGCGCAG ATAGCAATTT CAAGGACTTG CGAACTCTCT TGAATGAAAC 660  
TCCAGAGCAA ATCAAAATATA TATTGGCCCA GTACAACT ACCAAGGACA AGCGCTTAC 720  
AGATCTGAAC AGTATCAATT CAGTGCTAGG AGGCGGAATT CTGACCGAC TGAGACCCAA 780  
CATCATCCCT GTTCTTGATG AGATTAAATC CATGGCAACA GCGATCAAGG AGACCAAAGA 840  
GGCGTTGGAG AACATGAACA GCACCTTGAA GAGCTTGAC CAACAAAGTA CACAGCTTAG 900  
CAGCAGTCTG ACCAGCGTGA AAATAGCCT GCGGTCTATCT CTCAATGACC CTCTGTGCTT 960  
GGTGCATCCA TCAAGTGAAG CCTGCAACAG CATCAGATTG TCTCTAAGCC AGCTGAATAG 1020  
CAACCTGAA CTGAGGCAGC TTCCACCCGT GGATGCAGAA CTGACAACG TTAATAACGT 1080  
TCTTAGGACA GATTTGATG GCTGGTCCA ACAGGGCTAT CAATCCCTTA ATGATATACC 1140  
TGACAGAGTA CAAGCCCAAA CCACGACTGT CAGTACAGGT ATCAAAAGGG TCTTGAATTC 1200  
CATTGGTTCA GATATCGACA ATGTAATCTA GCGTCTCTCT ATTCAAGGTA TACTCTCAGC 1260  
ATTCTCTGTT TATGTTAATA ACACGAAAG TTACATCCAC AGAAATTATC CTACATTGGA 1320  
AGAGTATGAT TCATCTGCTT GCGTGGGTGG CTTGGTCTATC TGCTCTCTGC TGACCTCAT 1380  
CGTGATTTT TACTACCTGG GCTTACTGTG TGGCGTGTGC GGCTATGACA GGCATGCCAC 1440  
CCCGACCAAC CGAGGCTGTG TCTCCACAC CGGAGCGCTC TTCCTCATGG TTGGAGTTGG 1500  
ATTAAGTTTC CTCTTTTGTCT GGATATTGAT GATCATGTG GTTCTTACCT TTGCTTTGG 1560  
TGCAATGTTG GAAAACTGA TCTGTGAACC TTACAGAGC AAGGAATTAT TCCGGGTTT 1620  
GGATACACCC TACTTACTAA ATGAAGACTG GGAATACTAT CTCTCTGGGA AGCTATTTAA 1680  
TAAATCAAAA ATGAAGCTCA CTTTGAACA AGTTTACAGT GACTGCAAAA AAAATAGAGG 1740  
CACTTACGGC ACTCTTCAAC TGCAGAACAG CTTCAATATC AGTGAACATC TCAACATTAA 1800  
TGAGCATACT GGAAGCATAA GCAGTGAATT GGAAGTCTG AAGGTAAATC TTAATATCTT 1860  
TCTGTGGGTG GCAGCAGGAA GAAAAACCT TCAGGATTTT GCTGCTGTG GAATACAGAG 1920  
AATGAATTAT GACAGTACT TGGCTCAGC TGGTAAATCC CCGCAGGAG TGAATCTTTT 1980  
ATCATTTGCA TATGATCTAG AAGCAAAAGC AAACAGTTTG CCCCAGGAA ATTTGAGGAA 2040  
CTCCCTGAAA AGAGATGCAC AAACTATTAA AACAACTCAC CAGCAACGAG TCCTTCCTAT 2100  
AGAACAATCA CTGAGCACTC TATACCAAGG CGTCAAGATA CTTCAACGCA CAGGGAATGG 2160  
ATTGTGGAG TATGTAATCA GGATTCTAGC TTTCTGATG TTTGCTCAGA ACTTCATCAC 2220  
AAACAATACT TCCTCTGTTA TTATTAGGA AACTAAGAAG TATGGAGAA CAATAATAGG 2280  
ATATTTTGAA CATTATCTGC AGTGGATGGA GTTCTCTATC AGTGAGAAAG TGGCATCTGT 2340  
CAACCTGTG GCCACCGCTC TAGATACTGC TGTGTATGTC TTTCTGTGTA GCTACATTAT 2400  
CGACCCCTTG AATTGTTTTT GGTGTGGCAT AGGAAAGCT ACTGTATTTT TACTTCCGGC 2460  
TCTAATTTT GCGGTAAAC TGGCTAAGTA CTATGCTGGA ATGGAATTCGG AGGACGTGTA 2520  
CGATGATGTT GAACTATAC CCATGAAAAA TATGGAATAA GGTAAATAAT GTTATCATAA 2580  
AGATCATGTA TATGGTATTC ACAATCTGT TATGACAAGC CCATCACAAC ATTGATAGCT 2640  
GATGTTGAAA CTGTTGAGC ATCAGGATAC TCAAAGTGGG AAGGATCACA GATTTTGGT 2700  
AGTTTCTGGG TCTACAGGA CTTTCCAAAT CCAGGAGCAA CGCCAGTGGC AACGTAGTGA 2760  
CTCAGGCGGG CACCAAGGCA ACGGCACCAT TGGTCTCTGG GTAGTGCTTT AAGAATGAAC 2820

5  
10  
15

ACAATCACGT TATAGTCCAT GGTCCATCAC TATTCAAGGA TGACTCCCTC CCTTCCTGTC 2880  
TATTTTGT TTTTACTTTT TTACTGAG TTTCTATTTA GACACTACAA CATATGGGGT 2940  
GTTTGTCCCC ATGGATGCA TTTCTATCAA AACTCTATCA AATGTGATGG CTAGATTCTA 3000  
ACATATTGCC ATGTGTGGAG TGTGCTGAAC ACACACCAGT TTACAGGAAA GATGCATTTT 3060  
GTGTACAGTA AACGGTGTAT ATACCTTTTG TTACCACAGA GTTTTTTAAA CAAATGAGTA 3120  
TTATAGGACT TTCTTCTAAA TGAGCTAAAT AAGTCCACAT TGACTTCTTG GTGCTGTGTA 3180  
AAATAATCCA TTTTCACTAA AAGTGTGTGA AACCTACAGC ATATTCTTCA CGCAGAGATT 3240  
TTCATCTATT ATACTTTATC AAAGATTGGC CATGTTCCAC TTGGAATGG CATGCAAAAG 3300  
CCATCATAGA GAAACCTGCG TAACTCCATC TGACAAATTC AAAAGAGAGA GAGAGATCTT 3360  
GAGAGAGAAA TCCTGTTTCG TCAGAAAGTG AGTTGTTTAA ACAGATGCCA ATTACGGTGT 3420  
ACAGTTTAAC AGAGTTTTCT GTTGCAATTAG GATAAACATT AATTGGAGTG CAGCTAACAT 3480  
GAGTATCATC AGACTAGTAT CAAGTGTCT AAAATGAAAT ATGAGAAGAT CCTGTCACAA 3540  
TTCTTAGATC TGGTGTCCAG CATGGATGAA ACCTTTGAGT TTGCTCCCTA AATTGTCATG 3600  
AAAGCACAAG GTAAATATTC ATTTGCTTCA GGAGTTTTCAT GTTGGATCTG TCATTATCAA 3660  
AAGTGATCAG CAATGAAGAA CTGGTCGGAC AAAATTTAAC GTTGATGTAA TGGAAATCCA 3720  
GATGTAGGCA TTCCCCCAG GTCTTTTCAT GTGCAGATTG CAGTCTGAT TCATTTGAAT 3780  
AAAAGGAAC TTGG

20 Seq ID NO: 144 NP Protein sequence  
Protein Accession #: NP\_006008.1

1 11 21 31 41 51  
MALVLGSLLL LGLCNSFSFG QPSSSTDAPK AMNYELPATN YETQDSHKAG FIGILFELVH 60  
IFLVVVGPRD PFEDTLRKFL QKAYESKIDY DKPETVILGL KIVVYEAGII LCCVLGLLFI 120  
ILMPLVGYYF CMCRCCNCKG GEMHQKQKEN GPFLRKCFAL SLIVICIIIS IGFYGFVAN 180  
HQVTRTRKRS RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFTDL NSINSVLGGG 240  
ILDRLRPNI FVLDEIKSMA TAIKETKEAL ENMNSTLKS L HQQSTQLSSS LTSVKTSLRS 300  
SLNDPLCLVH PSSETCNSIR LSLSQLNSNP ELRQLPPVDA ELDNVNVLRL TDLDGLVQQG 360  
YQSLNDIPDR VQRQTTTVA GIKRVLNSIG SDIDNVTQRL PIQDILSAFS VYVNNTESYI 420  
HRNLPTLEEY DSYWVLGLV ICSLLTLIVI FYILGLLQGV CGYDRHATPT TRGCVSNTGG 480  
VFLMVGVLGS FLFCWILMII VVLTFVFGAN VEKLICEPYT SKELPRVLDL PYLLNEDWEY 540  
YLSGKLFNKS KMKLTFEQVY SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES 600  
LKVNLNIFLL GAAGRKLNQD FAACGIDRMN YDSYLAQTGK SPAGVNLLSF AYDLEAKANS 660  
LPPGNLRNSL KRDAQTIKTI HQQRLPIEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL 720  
DFAQNFITNN TSSVIIIEBK KYGRITIGYF EHYLQWIEFS ISEKVASCKP VATALDITVD 780  
VFLCSYIIDP LNLFNFGIGK ATVPLLPALI FAVKLAKYR RMDSEVDYDD VETIPMKNME 840  
NGNNGYHDXH VYGIHNPVMT SPSQH

40 Seq ID NO: 145 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 38..2605

45 1 11 21 31 41 51  
CCAAGTTCTA CCTCATGTTT GGAGGATCTT GCTAGCTATG GCCCTGCTAC TCGGCTCCCT 60  
GTTGCTGCTG GGGCTGTGGG GGAACCTCCT TTCAGGAGGG CAGCCTTCAT CCACAGATGC 120  
TCCTAAGGCT TGGAAATTAT AATTGCCTGC AACCAATTAT GAGACCCAAG ACTCCCATAA 180  
AGCTGGACCC ATTTGGCATT CTTTGAACCT AGTGATATAT TTTCTCTATG TGGTACAGCC 240  
CGGTGATTTT CCAGAAAGTA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAT 300  
TGATTATGAC ATTTGCTACT ATGAAGCAGG GATTATTTCTA TGCTGTGTCC TGGGGCTGCT 360  
GTTTATTATT CTGATGCCCT TGGTGGGTTA TTTCTTTTGT ATGTGTGCTT GCTGTAAACA 420  
ATGTGGTGGA GAAATGCACC AGCGACAGAA GGAAAATGGG CCTTCTCTGA GGAAATGCTT 480  
TGCAATCTCC CTGTTGGTGA TTTGTATAAT AATAAGCATT GGCATCTTCT ATGTTTGTGT 540  
GGCAAAATCAC CAGGTAAGAA CCGGATCAA AAGGAGTCGG AAACCTGGCAG ATAGCAATTT 600  
CAGGACTTGG CGAATCTCTT TGAATGAAC TCCAGAGCAA ATCAAAATTA TATTGGCCCA 660  
GTACAACTAT ACCAAGGACA AGGCGTTTCA AGATCTGAAC AGTATCAATT CAGTGCTAGG 720  
AGCGGGAATT CTTGACCGAC TGAGACCCAA CATCATCCCT GTTCTTGATG AGATTAAATG 780  
CATGGCAACA GCGATCAAGG AGACCAAGAA GCGGTGGAG AACATGAACA GCACCTTGAA 840  
GAGCTTGAC CAACAAAGTA CACAGCTTAG CAGCAGTCTG ACCAGCGTGA AAACCTAGCCT 900  
GCGGTCTATC CTCAATGACC CTCTGTGCTT GGTGATCCA TCAAGTGAA CCTGCAACAG 960  
CATCAGATGG TCTCTAAGCC AGCTGAATAG CAACCTGAA CTGAGGCAGC TTCCACCCGT 1020  
GGATGCAGAA CTTGACAACG TTAATAACGT TCTTAGGACA GATTTGGATG GCCTGGTCCA 1080  
ACAGGGCTAT CAATCCCTTA ATGATATAAC TGACAGAGTA CAACGCCAAA CCACGACTGT 1140  
CGTAGCAGGT ATCAAAAGGG TCTTGAATTC CATTTGGTTCA GATATCGATA ATGTAACTCA 1200  
CGGTCTTCTT ATTCAGGATA TACTCTCAGC ATTCTCTGTT TATGTTAATA ACACCTGAAAG 1260  
TTACATCCAC AGAAATTTAC CTACATTGGA AGAGTATGAT TCATACTGGT GGCTGGGTGG 1320  
CCTGGTCTAT TGCTCTCTGC TGACCCCTCAT CGTGATTTT TACTACTCTG GCTTACTGTG 1380  
TGGCGTGTGC GGCTATGACA GGCATGCCAC CCGGACCACC CGAGGCTGTG TCTCCAACAC 1440  
CGGAGGCGTG TTCTCTATGG TTGGAGTTGG ATTAAGTTTC CTCTTTTGCT GGATATTGAT 1500  
GATCATTGTG GTTCTTACCT TTGTCTTTGG TGCAAAATGTG GAAAACTGA TCTGTGAACC 1560  
TTACAGAGAC AAGGAATTAT TCCGGGTTTT GGATACACCC TACTTACTAA ATGAAGACTG 1620  
GGAATACTAT CTCTCTGGGA AGCTATTATA TAAATCAAAA ATGAAGCTCA CTTTGAACA 1680  
AGTTTACAGT GACTGCAAAA AAAATAGAGG CACTTACGGC ACTCTTCACC TGCAAGACAG 1740  
CTTCAATATC AGTGAACATC TCAACATTAA TGAGCACTACT GGAAGCATAA GCAGTGAATT 1800  
GGAAAGTCTG AAGGTAATCT TTAATATCTT TCTGTTGGGT GCAGCAGGAA GAAAAACCT 1860  
TCAGGATTCT TGTCTTGTG GAATAGACAG AATGAATTAT GACAGTACT TGGCTCAGAG 1920  
TGGTAAATCC CCGCAGGAG TGAATCTTTT ATCATTTGCA TATGATCTAG AAGCAAAAGC 1980  
AAACAGTTTG CCGCAGGAA ATTTGAGGAA CTCCCTGAAA AGAGATGCAC AAACATTATA 2040  
AACAAATCAC CAGCAACGAG TCCTTCTTAT AGAACAATCA CTGAGCACT TATACCAAGG 2100  
CGTCAAGATA CTTCAACGCA CAGGGAATGG ATTTGTTGGG AGAGTAACCTA GGATTCTAGC 2160  
TTCTCTGGAT TCTCTGAGC ACTTCATCAC AAACAATACT TCCTCTGTGA TTATTGAGGA 2220  
AACTAAGAAG TATGGAGAA CAATAATAGG ATATTTTGAA CATTATCTGC AGTGGATCGA 2280  
GTTCTCTATC AGTGAGAAAG TGGCATCGTG CAAACCTGTG GCCACCGCTC TAGATACTGC 2340

TGTGTGATGTC TTTCTGTGTA GCTACATTAT CGACCCCTTG AATTGTGTTT GGTTTGCCAT 2400  
 AGGAAAAGCT ACTGTATTTT TACTTCCGGC TCTAATTTT GCGGTAAAC TGGCTAAGTA 2460  
 CTATCGTCGA ATGGATTCCG AGGACGTGTA CGATGATGTT GAAACTATAC CCATGAAAAA 2520  
 TATGGAATAA GGTAAATAAG GTTATCATAA AGATCATGTA TATGGTATTC ACAATCTCTGT 2580  
 TATGACAAGC CCATCACAAC ATTGATAGCT GATGTTGAAA CTGCTTGAGC ATCAGGATAC 2640  
 TCAAAGTGGG AAGGATCACA GATTTTCTGGT AGTTTCTGGG TCTACAAGGA CTTTCCAAAT 2700  
 CCAGGAGCAA CGCCAGTGGC AACGTAGTGA CTCAGGCGGG CACCAAGGCA ACGGCACCAT 2760  
 TGGTCTCTGG GTAGTGCITT AAGAATGAAC ACAATCAOGT TATAGTCCAT GGTCCATCAC 2820  
 TATTCAAGGA TGACTCCCTC CTTCTCTGTC TATTTTGTG TTTTACTTTT TTACACTGAG 2880  
 TTTCTATTTA GACACTACAA CATATGGGGT GTTGTGTCCC ATTGGATGCA TTTCTATCAA 2940  
 AACTCTATCA AATGTGATGG CTAGATTCTA ACATATTGCC ATGTGTGGAG TGTGCTGAAC 3000  
 ACACACCATG TTACAGGAAA GATGCATTTT GTGTACAGTA AACGGTGTAT ATACCTTTTG 3060  
 TTACCACAGA GTTTTTTAAA CAAATGAGTA TTATAGGACT TTCTTCTAAA TGAGCTAAAT 3120  
 AAGTCACCAT TGACTTCTTG GTGCTGTGTA AAATAATCCA TTTTCACTAA AAGTGTGTGA 3180  
 AACCTACAGC ATATTCTTCA CGCAGAGATT TTCATCTATT ATACTTTATC AAAGATTGGC 3240  
 CATGTTCCAC TTGGAATGGG CATGCAAAAG CCATCATAGA GAAACCTCGG TAACTCCATC 3300  
 TGACAAATTC AAAAGAGAGA GAGAGATCTT GAGAGAGAAA TGCTGTTCGT TCAAAAGTGG 3360  
 AGTGTGTTTA ACAGATGCCA ATTACGGTGT ACAGTTTAAAC AGAGTTTCTT GTTGCAATTAG 3420  
 GATAAACATT AATTGGAGTG CAGCTAACAT GAGTATCATC AGACTAGTAT CAAGTGTCTT 3480  
 AAAATGAAAT ATGAGAAGAT CCGTGCACAA TTCTTAGATC TGGTGTCCAG CATGGATGAA 3540  
 ACCTTTGAGT TTGGTCCCTA AATTGTCATG AAAGCACAAG GTAAATATTC ATTTGCTTCA 3600  
 GGAGTTTATC GTTGGATCTG TCATTATCAA AAGTGATCAG CAATGAAGAA CTGGTCGGAC 3660  
 AAAATTTAAC GTTGATGTAA TGGAAITCCA GATGTAGGCA TTCCCCCAG GTCTTTTCAT 3720  
 GTGCAGATTG CAGTTCTGAT TCATTGAAT AAAAAGGAAC TTGG

Seq ID NO: 146 Protein sequence

Protein Accession #:

1 11 21 31 41 51  
 MALVLGSLLL LGLCGNSPSG QPSSTDAK AMNYELPATN YETQDSHKAG PIGILFELVH 60  
 IFLYVVQPRD FPEDTLRKFL QKAYESKIDY DIVVYEAGII LCCVLGLLFI ILMLPLVGYFF 120  
 CMCRCKNKG GEMHQKQEN GPFLRKCFAI SLLVICIIS IGIFYGEVAN HQVRTRIKRS 180  
 RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFTDL NSINSVLGGG ILDRLRPNII 240  
 PVLDEIKSMA TAIKETKEAL ENMNSTLKSL HQSTQLSSS LTSVKTSLSR SLNDPLCLVH 300  
 PSSETCNSIR LSLSQLNSNP ELRLPPVDA ELDNVNVLRL TDLDGLVQQG YQSLNDIPDR 360  
 VQRQTITVVA GIKRVLSNSIG SDIDNVTRL PQIDILSAFS VYVNTESYI HRNLPTLEEY 420  
 DSYWMLGLIV ICSLLTLIVI FYVLGLLCGV CGYDRHATPT TRGCVSNTGG VFLMVGVLGS 480  
 LFLCNILMII VVLTFFVGAN VEKLICEPYT SKELFRVLDY PYLLNEDWEY YLSGKLPNKS 540  
 KMKLTFEQVY SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES LKVNLIIFLL 600  
 GAAGRNLQD FAACGIDRNM YDSYLAQTGK SPAGVNLISF AYDLEAKANS LPPGNLRNSL 660  
 KRDAQTIKTI HQQRVLPIEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL DFAQNFITNN 720  
 TSSVIEETK KYGRITIGYF EHYLQWIEFS ISEKVASCCK VATALDTAVD VFLCSYIIDP 780  
 LNLFWFGIGK ATVFLPALI FAVKLAKYR RMDSEDVYDD VETIPMNME NGNNGYHKDH 840  
 VYGIHNPVMT SPSQH

Seq ID NO: 147 DNA sequence

Nucleic Acid Accession #: BC012089.1

Coding sequence: 236..2806

1 11 21 31 41 51  
 ATGCTCTCAG CTCCTCCGCC GCGGGATGGT GCCTTGAGTG AATGACCCCC TTGGAGAACA 60  
 TTCTTCGCA TCCCTCGCCT CAAGCCAGCC TCAGACAGAA AACTGAAGAT TCAGCAGATC 120  
 CAGTGCTTCC TGCTCTCTCT CTGCCAGGA ACAAGCTTGC CTTCCCAAG GCTTCCAGAA 180  
 GCTCTGAGGC AGGAGGCACC AAGTTCTACC TCATGTTTGG AGGATCTTGC TAGCTATGGC 240  
 CCTGTAATC GGCTCCCTGT TGCTGCTGGG GCTGTGCGGG AACTCCTTTT CAGGAGGGCA 300  
 GCCTTCATCC ACAGATGCTC CTAAGGCTTG GAATTATGAA TTGCTGCAG CAAATTATGA 360  
 GACCCAAGAC TCCATAAAG CTGGACCCAT TGGCATTCTC TTTGAAGTAG TGCATATCTT 420  
 TCTCTATGTC GTACAGCCGC GTGATTTCCT AGAAGATACT TTGAGAAAAT TCTTACAGAA 480  
 GGCATATGAA TCCAAAATTG ATTATGACAA GATTGTCTAC TATGAAGCAG GGATTATTCT 540  
 ATGCTGTGTC CTGGGGCTGC TGTTTATTAT TCTGATGCCT CTGGTGGGGT ATTTCTTTTG 600  
 TATGTGTCTG TGCTGTAACA AATGTGGTGG AGAATATGAC CAGCGACAGA AGGAAAATGG 660  
 GCCCTTCCCT AGGAAATGCT TTGCAATCTC CCGTGTGGTG ATTTGTATTA TAATAAGCAT 720  
 TGGCATCTTC TATGGTTTGG TGGCAATCA CCAGGTAAGA ACCCGGATCA AAAGGAGTCG 780  
 GAAACTGGCA GATAGCAATT TCAAGGACTT GCGAAGCTCT TTGAATGAAA CTCCAGAGCA 840  
 AATCAATAT ATATTGGCCC AGTACAACAC TACCAAGGAC AAGGCGTTCA CAGATCTGAA 900  
 CAGTATCAAT TCAGTGCTAG GAGGCGGAAT TCTTGACCGA CTGAGACCCA ACATCATCCC 960  
 TGTCTTGAT GAGATTAAAT CCATGGCAAC AGCGATCAAG GAGACCAAAG AGGCGTTGGA 1020  
 GAACATGAAC AGCACCTTGA AGAGCTTGCA CCAACAAAGT ACACAGCTTA GCAGCAGTCT 1080  
 GACCAGCGTG AAAACTAGCC TGCGGTCTAT TCTCAATGAC CCTCTGTGCT TGGTGCATCC 1140  
 ATCAAGTGA ACCTGCAACA GCATCAGATT GTCTCTAAGC CAGCTGAATA GCAACCCCTGA 1200  
 ACTGAGGCGG CTTCCACCGG TGGATGCAGA ACTTGACAAC GTTAATAACG TTCTTAGGAC 1260  
 AGATTGGAT GGCCTGTGTC AACAGGGCTA TCAATCCCTT AATGATATAC CTGACAGAGT 1320  
 ACAACGCCAA ACCACGACTG TCGTAGCAGG TATCAAAAGG GTCTTGAATT CCATTGGTTC 1380  
 AGATATGAC AATGTAATCT AGCGTCTTCC TATTGAGGAT ATACTCTCAG CATTCTCTGT 1440  
 TTATGTTAAT AACACTGAAG GTTACATCCA CAGAAATTTA CCTACATTGG AAGAGTATGA 1500  
 TTCATCTCGG TGGCTGGGTG GCCTGCTCAT CTGCTCTCTG CTGACCTCA TCGTGTATTT 1560  
 TTACTACCTG TACTACTCTG GTGGCGTGTG CGGCTATGAC AGGCATGCCA CCCCAGCCAC 1620  
 CCGAGGCTGT GTCTCCAACA CCGGAGGCGT CTTCTCTATG GTTGGAGTTG GATTAAAGTT 1680  
 CCTCTTTTGC TGGATATTGA TGATCATTGT GGTCTTACC TTTGTCTTTG GTGCAAAATG 1740  
 GGAAAAAGT ATCTGTGAGC CTTACACGAG CAAGGAATTA TTCCGGGTTT TGGATACACC 1800  
 CTACTTACTA AATGAAGACT GGAATACTA TCTCTCTGGG AAGCTATTTA ATAAATCAAA 1860  
 AATGAAGCTC ACTTTTGAAC AAGTTTACAG TGACTGCAAA AAAAATAGAG GCACTTACGG 1920

5 CACTCTTCAC CTGCAGAAC GCTTCAATAT CAGTGAACAT CTCAACATTA ATGAGCATAC 1980  
 TGGAAAGCATA AGCAGTGAAT TGGAAAGTCT GAAGGTAAAT CTTAATATCT TTCTGTTGGG 2040  
 TGCAGCAGGA AGAAAAAACC TTCAGGATTT TGCTGCTTGT GGAATAGACA GAATGAATTA 2100  
 TGACAGCTAC TTGGCTCAGA CTGGTAAATC CCCCAGGAGA GTGAATCTTT TATCATTTGC 2160  
 10 ATATGATCTA GAAGCAAAAG CAAACAGTTT GCCCCAGGA AATTTGAGGA ACTCCCTGAA 2220  
 AAGAGATGCA CAACTATTA AAACAATTCA CCAGCAACGA GTCCCTTCTTA TAGAACATC 2280  
 ACTGAGCACT CTATACCAAA GCGTCAAGAT ACTTCAACGC ACAGGGAATG GATTGTTGGA 2340  
 GAGAGTAACT AGGATTTCTAG CTTCTCTGGA TTTTGTCTAG AACTTCATCA CAAACAATAC 2400  
 TTCCTCTGTT ATTATTGAGG AAACCTAGAA GTATGGGAGA ACAATAATAG GATATTTTGA 2460  
 ACATTATCTT CAGTGACGTG AGTTCTCTAT CAGTGAGAAA GTGGCATCGT GCAAACTGAT 2520  
 GGCCACCGCT CTAGATACGT CTGTTGATGT CTTTCTGTGT AGCTACATTA TCGACCCCTT 2580  
 GAATTTGTTT TGGTTTGGA TAGGAAAAGC TACTGTATTT TTACTTCCGG CTCTAATTTT 2640  
 TGCGGTAAAT CTGGCTAAGT ACTATCGTGG AATGGATTGG GAGGACGTGT ACAGATGATG 2700  
 15 TGAAACTATA CCCATGAAAA ATATGAAAAA TGGTAATAAT GGTATACATA AAGATCATGT 2760  
 ATATGGTATT CAAATCCCTG TTATGACAAAG CCCATCACAA CATTGATAGC TGATGTTGAA 2820  
 ACTGCTTGAG CATCAGGATA CTCAAAGTGG AAAGGATCAC AGATTTTGGG TAGTTTCTGG 2880  
 GTCTACAAGG ACTTTCACAA TCCAGGAGCA ACGCCAGTGG CAACGTAGTG ACTCAGGCGG 2940  
 GCACCAAGGC AACGCGACCA TTGGTCTCTG GGTAGTGCTT TAAGAATGAA CACAATCAGG 3000  
 20 TTATAGTCCA TGGTCCATCA CTATTCAGG ATGACTCCCT CCCTTCCGT CTATTTTGT 3060  
 TTTTACTTT TTACACTGTA GTTTCTATT AGACACTACA ACATATGGGG TGTTTGTTC 3120  
 CATTGGATGC ATTTCTATCA AAACCTATC AAATGTGATG GCTAGATTCT AACATATTGC 3180  
 CATGTGTGGA GTGTGCTGAA CACACACCAG TTTACAGGAA AGATGCATTT TGTGTACAGT 3240  
 AAACGGTGA TATACCTTTT GTTACCACAG AGTTTTTTAA ACAAATGAGT ATTATAGGAC 3300  
 25 TTTCTTCTAA ATGAGCTAAA TAAGTACCA TTGACTTCTT GGTGCTGTG AAAATAATCC 3360  
 ATTTTCACTA AAAGTGTGTG AAACCTACAG CATATCTTC ACGCAGAGAT TTTCTATCT 3420  
 TATACCTTAT CAAAGATTGG CCATGTTCCA CTTGGAAATG GCATGCAAAA GCCATCATAG 3480  
 AGAAACCTGC GTAACCTCAT CTGACAAATT CAAAAGAGAG AGAGAGATCT TGAGAGAGAA 3540  
 ATGCTGTGTA TTCAAAAGTG GAGTTGTTTT AACAGATGCC AATTACGGTG TACAGTTTAA 3600  
 30 CAGAGTTTTT TGTGCAATTA GGATAAATCAT TAATTGGAGT GCAGCTAACA TGAGTATCAT 3660  
 CAGACTAGTA TCAAGTGTTC TAAAAAGAAA TATGAGAAGA TCCTGTCAACA ATTCTAGAT 3720  
 CTGGTGTCCA GCATGGATGA AACCTTTGAG TTTGGTCCCT AAATTGTCAT GAAAGCACAA 3780  
 GGTAAATATT CATTTGCTTC AGGAGTTTCA TGTGGATCT GTCAATTATCA AAAGTATCA 3840  
 GCAATGAAGA ACTGGTCCGA CAAAATTTAA CGTTGATGTA ATGGAATTCC AGATGTAGGC 3900  
 35 ATTCCCCCA GGTCTTTTCA TGTGCAGATT GCAGTTCTGA TTCATTGAA TAAAAAGGAA 3960  
 CTGGAAAAA AAAAAAAA AAA

Seq ID NO: 148 Protein sequence  
 Protein Accession #: AAH12089.1

40 1 11 21 31 41 51  
 MALVLGSLLL LGLCGNSPFG QPSSSTDAPK AWNYELPATN YETQDSRKAG PIGILFELVH 60  
 IFLYVVQPRD FPDITLRKFL QKAYESKIDY DKIVYYEAGI ILCCVLGLLF IILMLPVGYF 120  
 45 FCMCRCCNKC GGMHQKQKKE NGPFLRKCFA ISLVICIII SIGIFYGFVA NHQVTRIKR 180  
 SRKLADSNFK DLRLTLNETP EQIKYILAQY NTKDKAFID LNSINSLVGG GILDLRLPNI 240  
 IPVLDEIKSM ATAIKETKEA LENMNSTLKS LHQSTQLSS SLTSVKTSRLR SSLNDPLCLV 300  
 HPSSSETCNSI RLSLSQLNSN PELRQLPPVD ABLDNVNNVL RTDLGLVQQ GYQSLNDIPD 360  
 RVQRQTITVV AGIKRVLNSI GSDIDNVTOR LPIQDILSAF SVYVNMTESY IHRNLPTLEE 420  
 50 YDSYWNLGLL VICSLTLIV IFYYLGLLGG VCGYDRHATP TTRGCVSNTG GVPLMVGVL 480  
 SFLEFCHILMI IIVLTTFVFGA NVEKLICEPY TSKELPFRLD TPYLLNEDWE YLISGKLENF 540  
 SKMKLTFEQV YSCKKNRGT YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNLIIFL 600  
 LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLLS FAYDLEKAN SLPPGNLRNS 660  
 LKRDAGTIKT IHQKRVLPLE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFACNFITN 720  
 55 NTSSVILIBET KKGRTIIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID 780  
 PLNLFWFGIG KATVFLPAL IFAVKLAKYY RRMDSDEVVD DVETIPMKNM ENGNNGYHRD 840  
 HVGIEHPVM TSPSQH

Seq ID NO: 149 DNA sequence  
 Nucleic Acid Accession #: NM\_033049.1  
 Coding sequence: 28..1566

60 1 11 21 31 41 51  
 CCACGGTCC GAGCAAGAAC AGCTAAAATG AAAGCCATCA TTCACTCTAC TCTTCTGCT 60  
 CTCCTTTCTG TAAACACAGC CACCAACCAA GGCAACTCAG CTGATGCTGT AACCAACACA 120  
 65 GAAACTGCGA CTAGTGGTCC TACAGTAGCT GCAGCTGATA CCACTGAAAC TAATTTCCCT 180  
 GAACTGCTA GCACCACAGC AAATACACCT TCTTCCCAA CAGCTACTTC ACCTGCTCCC 240  
 CCATAATTA GTACACATAG TTCCTCCACA ATTCTACAC CTGCTCCCCC CATAATTAGT 300  
 70 ACACATAGTT CTTCCACAA CTCTATACCT ACTGCTGCAG ACAGTGAGTC AACCACAAAT 360  
 GTAAATTCAT TAGTACCTC TGACATAATC ACCGCTTCAT CTCCAAATGA TGGATTAAATC 420  
 ACAAATGGTC CTTCTGAAC ACAAGTAAC AATGAAATGT CCCCCACCA AGAAGACAAT 480  
 CAATCATCAG GGCCTCCAC TGGCACCGCT TTATTGGAGA CAGCACCTCT AAACAGCACA 540  
 GGTCCCGACA ATCCTTGCCA AGATGATCCC TGTGCAGATA ATTGTTATG TGTTAAGCTG 600  
 75 CATAATACAA GTTTTGCCT GTGTTAGAA GGGTATTACT ACAACTCTTC TACATGTAAG 660  
 AAAGGAAAGG TATTCCCTGG GAAGATTTC GTGACAGTAT CAGAAACATT TGACCCAGAA 720  
 GAGAAACATT CCAATGGCTA TCAAGACTTG CATAGTGAAA TTACTAGCTT GTTTAAAGAT 780  
 GTATTGGCA CATCTGTTA TGGACAGACT GTAATTCCTA CTGTAAGCAC ATCTCTGTCA 840  
 CCAAGATCTG AAATGCGTGC TGATGACAAG TTTGTTAATG TAACAAATAGT AACAAATTTG 900  
 80 GCAGAAACCA CAAGTGACAA TGAGAAGACT GTGACTGAGA AAATTAATAA AGCAATTAGA 960  
 AGTAGCTCAA GCACTTTCT AAACATGAT TTGACCCCTC GGTGTGATTA TTATGGCTGT 1020  
 AACCAAGCTG CCGATGACTG CTTCAATGGT TTAGCATGCG ATTGCAATC TGACCTGCAA 1080  
 AGGCCTAAC CACAGAGCCC TTTCTGCGTT GCTTCCAGTC TCAAGTGTCC TGATGCTGCG 1140  
 AACGCACAGC ACAAGCAATG CTTAATAAAG AAGAGTGGTG GGGCCCTGTA GTGTGCGTGC 1200  
 GTGCCCGGCT ACCAGGAAGA TGCTAATGGG AACTGCCAAA AGTGTGCATT TGCTACAGT 1260



5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

GGACTCGACT GTAAGGACAA ATTTGAGCTG ATCCTCACTA TTGTGGGCAC CATCGCTGGC 1320  
 ATTGTGATTC TCAGCATGAT AATTGCATTG ATTGTGACAG CAAGATCAAA TAACAAAACG 1380  
 AAGCATATTG AAGAAGAGAA CTGTATTGAC GAAGACTTTC AAAATCTAAA ACTGCGGTG 1440  
 ACAGGCTTCA CCAATCTTGG AGCAGAAGGG AGCGTCTTTC CTAAGGTGAG GATAACGGCC 1500  
 TCCAGAGACA GCCAGATGCA AAATCCCTAT TCAAGACACA GCAGCATGCC CGGCCCTGAC 1560  
 TATTAGAAATC ATAAGAAATGT GGAACCCGCC ATGGCCCCCA ACCAATGTAC AAGCTATTAT 1620  
 TTAGAGTGTG TAGAAAGACT GATGGAGAAG TGAGCACCAG TAAAGATCTG GCCTCCGGGG 1680  
 TTTTCTTCC ATCTGACATC TGCCAGCCTC TCTGAATGGA AGTTGTGAAT GTTTGCAACG 1740  
 AATCCAGCTC ACTTGCTAAA TAAGAATCTA TGACATTAAT TGTAGTAGAT GCTATTAGCG 1800  
 CTGTGACAG AGGTGGTTTT CTTCATCAG TACAAGTAC TGAGACAATG GTTAGGGTTG 1860  
 TTTTCTTAAT TCTTTTCTGT GTAGGGCAAC AAGAACCATT TCCAATCTAG AGGAAAGCTC 1920  
 CCCAGCATGT CTGTCTCTGT GGCAACATT GCTCTTGAGT TAAGTGACCT AATTCCTG 1980  
 GGAGACATAC GCATCAACTG TGGAGGTCCG AGGGGATGAG AAGGGATACC CACCACCTTT 2040  
 CAAGGTCAC AAGCTCACTC TCTGACAAGT CAGAATAGGG ACACCTGCTT TATCCCTCCA 2100  
 ATGGAGAGAT AGGTGGCAAC TTGGAACAGC CCAGAGCTTG CAACCTAGCC TCACCCAAGA 2160  
 AGACTGGAAA GAGACATATC TCTCAGCTTT TTCAAGAGGC GTGCCTGGGA ATCCAGGAAC 2220  
 TTTTGTAGTG TAATTAGAA GCCTGGACTA AAAATGTCCA CTATGGGGTG CACTCTACAG 2280  
 TTTTGTAAAT GCTAGGAGGC AGAAGGGGCA GAGAGTAAAA AACATGACCT GGTAGAAGGA 2340  
 AGAGAGGCCA AGGAAACTGG GTGGGGAGGA TCAATTAGAG AGGAGGCACC TGGGATCCAC 2400  
 CTCTTCTCTT AGGTCCCTCT CTCCATCAGC AAAGGAGCAC TTCTCTAATC ATGCCCTCCC 2460  
 GAGAGCTGGC TGGGAGAAAG TTTAAAAACA AAAAATCCAG GAGTAAGAGC CTTAGGTGAG 2520  
 TTGAAATGT GAGACAAACT GTCTGGCAAA GGGTGGGAGA GGGAGCTTGT GCTCAGGAGT 2580  
 CCAGCCGTCC AGCCTCGGGG TGTAGGTTC TGAGGTGTGC CATTTGGGCC TCAGCCTTCT 2640  
 CTGGTGACAG AGGCTCAGCT GTGGCCACCA ACACACACCC ACACACACAC AACACACAC 2700  
 ACAATGGGG GCAACCAACAT CCAGTACAG CTTTTACAAA TGTATTAGT GTCCTTTTTT 2760  
 ATTTCTAATG CCTGTCTCTC TTAAGAGTTA TTTTATTGT TATTATTAT TGTCTTGAC 2820  
 TGTAAATGT GAATGTAAT GCAATAAAGT GCCTTTGTGA GATGGTGAAG AAAAAA 2880  
 AAAAAA

Seq ID NO: 150 Protein sequence  
 Protein Accession #: NP\_149038.1

1 11 21 31 41 51  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

MKAIHLTL ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60  
 PSFPTATSPA PPIIETHSSS TIPTAPPPII STHSSSTIPI PTAADSEST NVNSLATSDI 120  
 ITASSPNDGL ITMVPSETQS NNEMSPPTED NQSSGPPTGT ALLETSTLNS TGPSPNQDD 180  
 PCADNSLCVK LHNTSFCLCL EGYIYNSSSTC KKGKVPFGKI SVTVSETFDP EEKHSMAQD 240  
 LHSEITSLFK DVFGTSVYGV TVILTVSTSL SPRSEMRADD KFNVTIVTI LAETTSNDEK 300  
 TVTEKINKAI RSSSSNFLNY DLTLRCDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360  
 VASSLKCPDA CNAQHKQLLI KXSGGAPECA CVPGYQEDAN GNCQKCAFY SGLDCKDKFK 420  
 LLLTIVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480  
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY

Seq ID NO: 151 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 87..914

1 11 21 31 41 51  
 50  
 55  
 60  
 65  
 70  
 75  
 80

AGTACGCGGG GCCGCGTTTT GCCTCCGAG CAGCTCTGGG CTCTTCTCAG CTGCGCGAGC 60  
 AGCTGCTCCA ATGCCCGGGA GTGGCCATGG GCGCCCGCA CTGGTGGGAC CAGCTGCAGG 120  
 CTGGTAGCTC GGAGGTGGAC TGGTGGGAGG ACAACTACAC CATCGTGCTT GCTATCGCCG 180  
 AGTTCTACAA CAGGATCAGC AATGTCTTAT TTTTCAATTT ACCGCCCCATC TGCATGTGCT 240  
 TGTTTCTGCA GTATGCAACA TGCTTCAACA GTGGCATCTA CTTAATCTGG ACTCTTTTGG 300  
 TTGATGTGGG AATTGGATCC GTCTACTTCC ATGCAACCCCT TAGTTTCTGT GGTGAGATGC 360  
 TTGATGAATC TGCAGTCTTT TGGGTCTGTA TGTGTGCTTT GGCCATGTGG TTCCCGAGAA 420  
 GGTATCTACC AAAGATCTTT CGGAATGACC GGGGTAGGTT CAAGGTGGTG GTCACTGTCC 480  
 TGTCTGCGGT TACGAGTGC CTGGCATTGG TCAAGCCTGC CATCAACAAC ATCTCTCTGA 540  
 TGACCCCTGG AGTTCCTTGC ACTGCATGCG TCATGCGAGA GCTAAAGAGG TGTGACAACA 600  
 TGGCTGTGTT TAAGCTGGGC CTCTTCTCGG GCCTCTGGTG GACCTCGGCC CTGTTCTGCT 660  
 GGATCAGTGA CCGAGCTTTC TGGAGCTGCG TGTATCTCTT CAACTTCCCC TACCTGCACT 720  
 GCATGTGGCA CATCTCATC TGCTTGTCTG CCTACCTGGG CTGTGTATGC TTTGCTTACT 780  
 TTGATGCTGC CTGAGGATT CCTGAGCAAG GCCCTGTCTT CAAGTTCTGG CCCAATGAGA 840  
 AATGGGCTTT CATTTGTGTC CCTATGTGT CCTCTCTGTG TGCCAACAAG AAATCATCAG 900  
 TCAAGATCAC GTGATGGCAA GATGGTGGCT GGCTTCTCTG CTTATCGCCC CTCATGCAGT 960  
 GGGCTTCTTT TGCTAGGAAG ACAGCCAAGG GAGTTGGAAT AGTTGGGGTG TGGGCTATCT 1020  
 TTTCAAAAT CTATTTGCTG GGGCTCTTAA TTTCTTATG GTTCTTTGTA TGTAGGGATT 1080  
 TAAACITTTG CATATGGTAC AAATATTCCC TGCCCCCTG CAGTTTCCCA TTTGTCTTTC 1140  
 AGTATGTTAA TATTTTGTG CCATACCTGT TTTAACTTT CATGTGTGCA CATCTGTTAA 1200  
 TCTTTCTTCT AGGATTCTGT GATTTTGTGT AATTTTAAAA AAGGTCCCTT CCTCTCTCTC 1260  
 AATGTGCTGT TGGAGCACTT GGATTCCACT GTACAAGGGG AAAAGTGTCT ATTCTTTTCC 1320  
 CAAGATGGA AAATGGAGGG CTTAGGGACA CTAGATGCAT CTTTCTCAGC ATCACTTCCA 1380  
 GATGCACTGA CTGTGTTGGC TGGTCTCTTA ATGGCCATGG CAGAGCAGTC CTTTGGGGGA 1440  
 TCCAGCCCTG TACAATGCAT CTCTTCTGTG AGAAGCTGG CCTGCTCCAG ACCCCACCAT 1500  
 TCCAGGCGC CCTTGGAGTG GACTCTACTG ATGACAGACA GACCTCTGAG GAGACAAAGC 1560  
 CCTCTGACTT TGTGATGGA GATGCCAGAG ATTTTCTTCT GGGGTAATGT TCCTTAAACA 1620  
 AAACCAACA GATGAACAC ACACAGGACT TGTGGCTAAA AAGGCTAGTT TTTCACTTGC 1680  
 ATTTCTCAAC TAACCAAGT TTTACATGCA TCTGTGAATC CTTTACTAC TACCTCTGTG 1740  
 GAGAGATGGA GAGACTTCAG ATAAACGTGA AGCTAATGAG TAAACCCCTC TCTGCCAAAA 1800  
 CCTACTCTCC ACTTTAGGCC CTCTCTGAAG ATGAGCAACA TTTTAAATA CTGAGCAACA 1860  
 TTTTAAATA CTGACATCAC TTCCTCTTCC CCCTCCACCC CCAGCTCAGC AGCCTCAAA 1920  
 CTACAGAGAA GAAGAATTAT GGCATGAACA TCCCAACAGA CCCACCATCT TTAAGACTTG 1980  
 ACCTCTGTA GTTTACAAA GGGCTCTCTA CAATTGTGGT GGGGTTCTGT GTTCAAAATT 2040

TGGAGCAAAC ATGAAGTTTT TGGAAACGTT TTCTCATTTG AAGCCTCCAG TATGCTGTAC 2100  
 TATTCTGGAA ATTACCTTCA AGAGTCTCAC TTCTGTGTTT TGTGTGGGCA 2160  
 TCAITGTTCTT CACGCTTGCA GTAGAAGGTG CTTTCTCGGT TTCCAGAGT ATCCAACGGC 2220  
 TCACCTTTCT CAAGTGTGG CAGTAGCTAT GCACTCACGG GCTGGTTTGG GTGCTGGTG 2280  
 5 CAGCAGCCCA AATCTGTTGC CTTCTGAATT TTTCTCACCT AATGTGACAC TGGCTACAAT 2340  
 GAATCTTCTC TTCATCGGGC TGAATGAAAG ATTCAAGAAC CATCTTCAAG GTGCTAGGTG 2400  
 GGAATTATCA ACCTCAGGGA TACTCATTTT AACTCAGGCG TGTCCTGCTT TGTAAACATC 2460  
 CATTGTTGGG AGAGGGCAGG ACAGGTGTGT TCTTCTGTGG GCAGGAGTCA TGTCATGTTC 2520  
 10 CTACATATGT AAGAGTTGGG AAGGTGACGA TTTTGTACAC ATCCAGGAAC TCTTACTCTA 2580  
 GTTAGAATTT GTACCAGATC CAAGGTGAAA ACCCCAATAA GCAACTGAAT TTAGAGTTTA 2640  
 AAAATGAATG ACTTTATGCT ACATCTGTGG TTATCAAATT ATATAGGTTG TTGAGAAGCA 2700  
 GAACGCTGTT TGTAGTAAGA AATCTTTGTG GAACCCCACT GTGTGAAGTA AATTGTATGT 2760  
 TATTAATTTT ATTTAAGTTT AAATTTATGG CATTACTTA ATAATATATG AGGTGGTGAA 2820  
 15 AATGCAAAAT AACAAATGG TAATTTCCAA GGTAGAAAAA TTAGGTGTGT AATGAATGTA 2880  
 TATGTTGGTT TATTATAGTT TTATATATAT ATAGAGAGAG TGTTTTGTTT TTGAGTCAGG 2940  
 GTCTTGCTCT ATTACCCAGG CTGGAGTGCA GTGGTGCACT CATGACTCAC TGTAGCCTCT 3000  
 GTCTCCAGG CTCAAGTGAT CCTCTCACT CAGCCTCCCC AGGAGCTGGG AGTACTGGTG 3060  
 CGTGCTCCA TTCCAGCTCA ATTTTGTAT TTTTTCATAG AGATGGGGTT TCACCATTTT 3120  
 20 GCCCAGGCTG GTCTCAAACT TCTGGGCTCA AGAGATTGCG CCGCTCGGC CTCOCOAAGT 3180  
 GCTGGGAATA GGCATGAGCC GTCACGCTG GCCTAAAAAA TATTTTAAAT ATGATCTTTG 3240  
 AATTAAATAT TCGTAGAATT TCTAATGTAT CTCCTTGAGA CCTAGGAGGT TGTGGAACA 3300  
 GAACGCTGTT TAAGTCCCTT GGGTTTCAAG TCTAGAATTT TTTAAAGGCA AATATCAGCT 3360  
 CATTCTATT TTAAAGTTG CTTATCAGGC ATGGATTCTG GTCTCATCTA CTTTATGGTA 3420  
 25 TAAATGCTCC AAGGTAGGGG GTTTGGTATA TATTTTAAGC CCGCTTTT TTTTTTTTTT 3480  
 TTTTTTTTTT TTTTAAATGT GAGAAGCAGA ATGTGCTTCT AGAACTGGT TTTAAAGAGA 3540  
 TGAGCTGAGA AAGAAATGTG GAATGGAGTA TATTTGAGGA GGACAAAACA TAACCTCACT 3600  
 TTTGAACAGA AATCACTCTA GCCTGCCAGC ATGGGATGTA AACCAAGAGA GTAGAAATAT 3660  
 ACCCATCTTA TTTAAGTTG GGTTTATGGC ATCGCTCATA TATGTAAAAG CACTACAAAC 3720  
 30 TCTTAAAGA AATTTGGGAA ACTACAGAGA AGTCAAGAAA AAAAAAAGT AACCCATATT 3780  
 TCTATTGCC AGGTATAATC CTTGTTAATA TTTGGTTTG GTCTCCTCTT TTTTCCCC 3840  
 AATATAGTTG TAATAAATG ATGTCTTCA GAGTTGACAT TTATCCTGTA GCTTGAATGG 3900  
 CATGTAAATG CCACTGTGAT ATTTTTCAT GAAGTGTAGG TTTGGAATAC ACTAGAGTTA 3960  
 GCTATATGCT TGAATGCTGA TCACTGGATT CTGAGACTGA CTACTGAGTC TACCTTTTA 4020  
 35 ATCAAGCCTA ACATGAATG GCTCCAAAAA GTAATGAATG TAATGTACT TTTTGTATG 4080  
 CCTCTGCACT TGGCTTGGTG AGTCATATA AATAGCTGTT AATATGTGA CTTTACAGAT 4140  
 TTTGATATGT TCAGATTGTA AAAAATGAAT AGTTTATTTT ATTAATTGAT GGGCAGTCAA 4200  
 GAATCTCCCT CC

Seq ID NO: 152 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 45 MGAPFWWDQL QAGSSEVDWC EDNYTIVPAI AEFYNTISNV LFFILPPICM CLFRQYATCF 60  
 NSGIYLIWTL LVVVIGISVY FHATLSPLGQ MDELAVLKV LMCALAMWFP RRYLPKIFRN 120  
 DRGRFKVVVS VLSAVTTCLA FVKPAINNIS LMTLGVPTA LLIAELKRCD NMRVFKLGLF 180  
 SGLMWTLALF CNISDRAFCE LLSSPNFPYL HCMWHILICL AAYLGCVCF A YFDAASEIPE 240  
 QGFVIRKFWPN EKWAFIGVPY VSLLCANKKK SVKIT

Seq ID NO: 153 DNA sequence  
 Nucleic Acid Accession #: NM\_001432.1  
 Coding sequence: 167..676

1 11 21 31 41 51  
 55 TCACTTGCCCT GATATTTCOA GTGTCAGAGG GACACAGCCA ACGTGGGGTC CTTCTAGGC 60  
 TGACAGCCGC TCTCCAGCCA CTGCCGCGAG CCCGTCTGCT CCCGCCCTGC CCGTGCACCTC 120  
 TCCGAGCCCG CCTCCGCGCA AGCCCCAGCG CCCGCTCCCA TCGCCGATGA CCGCGGGGAG 180  
 GAGGATGGAG ATGCTCTGTG CCGGCGGGT CCCTGCGCTG CTGCTCTGCC TGGGTTTCCA 240  
 60 TCTTCTACAG GCAGTCTCTA GTACAACCTG GATTCCATCA TGTATCCAG GAGAGTCCAG 300  
 TGATAACTGC ACAGCTTTAG TTCAGACAGA AGACAATCCA CGTGTGGCTC AAGTGTCAAT 360  
 AACAAAGTGT AGCTCTGACA TGAATGCTA TGTTTGCTAT GGACAGTGCA TCTATCTGGT 420  
 GGACATGAGT CAAAACACT GCAAGTGTGA AGTGGGTTAT ACTGGTGTCC GATGTGAACA 480  
 CTTCTTTTAA ACCGTCCACC AACCTTTAAG CAAAGAGTAT GTGGCTTTGA CCGTGATTCT 540  
 65 TATTATTTTG TTTCTTATCA CAGTGTGCG TTCCACATAT TATTTCTGCA GATGGTACAG 600  
 AAATCGAAAA AGTAAAGAAC CAAAGAAGGA ATATGAGAGA GTTACCTCAG GGGATCCAGA 660  
 GTTGCAGCAA GTCTGAATGG CGCCATCAAA CTTATGGGCA GGGATAACAG TGTGCCCTGGT 720  
 TAATATTAAT ATTCCATTTT ATTAATAATA TTTATGTTGG GTCAAGTGT AGGTCAATAA 780  
 70 CACTGTATTT TAATGTACTT GAAAAATGTT TTTATTTTGG TTTTATTTT GACAGACTAT 840  
 TTGCTAATGT ATAATGTGCA GAAAAATTTT AATATCAAAA GAAATTTGAT ATTTTATATC 900  
 AAGTAATTTT CTGAGCTAAA TGCTTCATTG AAAGCTTCAA AGTTTATATG CCTGGTGAC 960  
 AGTGCTTAGA AGTAAGCAAT TCCCAGGTCA TAGCTCAGA ATTGTTAGCA AATGACAGAT 1020  
 TCTGTAAAGC CTATATATAT AGTCAAATCG ATTTAGTAAG TATGTTTTT ATGTTCTCA 1080  
 75 AATCAGTGAT AATTGGTTTG ACTGTACCAT GGTTTGATAT GTAGTTGGCA CCATGGTATC 1140  
 ATATATTAAG ACAAATATGC AATTAGAATT TGGGAGAAGC AATATAGGT CCTGTGTTAA 1200  
 ACACACACCA TTTGAAACAA GCTAACCCCTG GGGAGTCTAT GGTCTCTCA CTCAGGTCTC 1260  
 AGCTATAATT CTGTTATATG AGGGGCGAGT GACAGTTCCC TATGCCAACT CACGACTCCT 1320  
 ACAGGTACTA GTCACATATC TACCAGATTG TGCCTATGTA AATGAATTG AAAAAAAT 1380  
 80 TTTCTGTAAC TTTTATTTAA GTAGTGGGCA TTTATAGCT TCACAAATGT CCTTTTTTGT 1440  
 ATATTACAAC ATTTATGTGA GGTAAATTAT GCTCAACAGA CAATTAGAAA AAAGTCCACA 1500  
 CTGAAGCCT AAATTTGTGC TTTTAAAGAA TATTTTGA CTATTTCTTT TTATAGGGGC 1560  
 TTTGCTGAAT TCTAACATTA AATCACAGCC CAAATTTTGA TGGACTAATT ATTAATTTAA 1620  
 AATATATGAA GACAAATAT CTACATGTTG TCTTAAGATG GAAATACAGT TATTTCTCT 1680  
 TTTATTCAG GAAGTTTAA CTTTAAATACA GCTCAGTAAA TGCTCTCTCT TAGAATGTAA 1740

AGTTATGTAT TTAAGTTGT ATCTTGACAC AGGAAATGGG AAAAACTTA AAAATTAATA 1800  
 TGGTGTATTT TTCCAAATGA AAAATCTCAA TTGAAAGCTT TTAATATGTA GAAACTTAAA 1860  
 CACACCTTCC TGTGGAGGCT GAGATGAAAA CTAGGGCTCA TTTTCTGAC ATTTGTTTAT 1920  
 TTTTGGGAAG AGACAAAGAT TTCTTCTGCA CTCTGAGCCC ATAGGTCTCA GAGAGTTAAT 1980  
 5 AGGAGTATTT TTGGGCTATT GCATAAGGAG CCACTGCTGC CACCCTTTT GGATTTTATG 2040  
 GGAGGCTCCT TCATCGAATG CTAAACCTTT GAGTAGAGTC TCCTGGATC ACATACCGAG 2100  
 TCAGGGAGGA TCTGTCTCTC CTCTACGTTT ATCTGGCAT GTGCTAGGGT AAACGAAGGC 2160  
 ATAATAAGCC ATGGCTGACC TCTGGAGCAC CAGGTGCCAG GACTTGTCTC CATGTGTATC 2220  
 CATGCATTAT ATACCCCTGGT GCAATCACAC GACTGTCATC TAAAGTCTCG GCCTGGGCC 2280  
 10 TTACTATTAG GAAATATAAC AGACAAAAAC AAGTAAATAT ATATGGTCTT ATACATATTG 2340  
 TATATATATT CATATACAAA CATGTATGTA TACATGACCT TAATGGATCA TAGAATTGCA 2400  
 GTCATTTGGT GCTCTGCTAA CCATTATAT AAAACTTAAA AACAGAGAA AAGAAAAATC 2460  
 AATTAGATCT AAACAGTTAT TTCTGTTTCC TATTTAATAT AGCTGAAGTC AAAATATGTA 2520  
 AGAACACATT TTAATACTC TACTTACAGT TGGCCCTCTG TGGTTAGTTC CACATCTGTG 2580  
 15 GATTCAACCA AGCAAGGACG GAAAATGCTT AAAAAATAAT ACAACAACAA CAAAAAATAC 2640  
 ATTATAACAA CTATTACTT TTTTTTTTTT CTTTTTGAGA TGGAGTCTCG CTCTGTTGCC 2700  
 CAGGTGAGT TGCAGTGGCA CGATCTGGC TCACTGCAAC CTCACCTCC GGGTTCAAGA 2760  
 GATCTCTCTG CCTCAGCCTC CTGAGCAGCT GGGACTACAG GCGCATGCCA CCATGCCCAG 2820  
 20 CTAATTTTTG TATTTTATG AGAGGGGGGG TTTCACCATG TTGGCCAGGA TGGTCTCAAT 2880  
 CTCCTAACCT GCTGATCCAC CCTCCACAGC GCTGGGATTA CAGGCGTGAG 2940  
 CCACCGCAGC TAGCATTTAC ATTAGGTATT ACAAGTAATG TAAAGATGAT TTAAGTATAC 3000  
 AGGAGGATGT GAATAGGTTA TATGCAAGCA CTATGCCCTT TTATATAAGT GACTTGAACA 3060  
 TCTGTGCCCG ATTTTAGTAT GTGCAAGGGG GCGATCTGGG AATCAGTCCC CTGTGGATAC 3120  
 CAAGGTACAA CTGTATTAT TAAACGCTAC TAGATGTGAG GAGAGTCTGA ATATTTTCAG 3180  
 25 TGATCTTGGC TGTTCCTAAA AAATCTATTG ACTTTTCAAT AAATCAGCTG CAATCCATT 3240  
 ATTTTATTAA CAAAGATTT ATTGTAAGCC TCTCAATCTT GGTTTTTCAG TTGATCTTAA 3300  
 GCATGTCAAT TCATAAAAAA AAGTCATTTT TGTATTTTTC ATCTTTAAGA ATGCTTAAAA 3360  
 AAGCTAATCC CTAATAAGT TAGATCTTTG TAAATGCATA TTAATAATAA AAGTATGACC 3420  
 CACATTTACT TTTATGGGTG AAAATAAGAC AAAAAATAA GTTTTAGTGA GGTATGGTCT 3480  
 30 GAGTAAACAT AAAAACTGAT TTGCTCTCAG CTGATGTGTC CTGTACACAG TGGGAAGATT 3540  
 TTAGTTTACA CTAGTCTTAA CTCGCCCATT TTACAGATT CTCACTATAT ATATTTCTAG 3600  
 AAGGGGCTGT CATATTCAA TGTATTGAGA ACCAAGCAAA CCACAAATGC ATAAATGCAT 3660  
 AATTTATGTT CTCAACCAA GGCCACATAA TAACCCAGTT AACTTACTCT TTAACCAGGA 3720  
 ATATTAAGTT CTATAACTAG TACTCAAGGT TTAACCTTAA AATTAAGATT TCCTTAACCT 3780  
 35 TAACCTTAAA ATTGATATTA TATTAACAT ACATAATACA ATGTAACCTC ACTGTTCTCC 3840  
 TGAATATTTT TTGCTCTAAT CTCTCTGCCG AAGTCAAGT TGATGGGAGA ATTGGTATAC 3900  
 TGGTATGAGT AGTCTCTAAG TCAGATTTT ATTTATGAGT CTTTGAGACT AAATCAATC 3960  
 ACCACCAGGT ATCAAATCAA CTTTATGCA GCAATATAT GATTCTAGTG TCTGACTTTT 4020  
 GTTAAATCCA GTAATGCAAT TTTTAAAAAC CTGTATCTGA CCCACTTTGT AATTTTGTCT 4080  
 40 CCAATATCCA TTCTGTAGAC TTTTGAAAAA AAGTTTITTA ATTGATGCC CAATATATT 4140  
 TGACCGTTAA AAAATCTCTG TTCAATAGGG AGAAGGGGGA GTAATGACTT GTACAAACAG 4200  
 TATTTCTGGT GTATATTTTA ATGTTTTTAA AAGAGTAAT TTCATTAAAA TATCTGTTAT 4260  
 TCAAATTGTA TGATGTTAAA TGTAAATATA TGTATTTTCT TTTTATTTTG CACTCTGTAA 4320  
 TTGCACTTTT TAAGTTTGAA GAGCCATTTT GGTAAACGGT TTTTATTAAG GATGCTATGG 4380  
 45 AACATAAAGT TGTATTGCAAT GCAATTAAAA GTAACCTATT TGACTATGAA TATTATCGGA 4440  
 TTAAGTAATT GTATCAATTT GTTTGTGTTT AATATCAGCT TGTATAATTG TGTACCTTAA 4500  
 GATATTGAAG GAGAAAATAG ATAATTACA AGATATTATT AATTTTATT TATTTTCTTT 4560  
 GGAATTGAA AAAAATTGAA ATAAATAAAA ATGCATTGAA CATCTTGCAT TCAAAATCTT 4620  
 CACTGAC

Seq ID NO: 154 Protein sequence  
 Protein Accession #: NP\_001423.1

1 11 21 31 41 51  
 | | | | |  
 MTAGRRMEML CAGRVFALLL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60  
 AQVSIITKSS DMNGYCLHQQ CILVDMSON YCRCEVGYTG VRCEHPFLTV HQPLSKEYVA 120  
 LTVILILFL ITVVGSTYYF CRWYRNKSK EPKKEYERVV SGDPPELPQV

Seq ID NO: 155 DNA sequence  
 Nucleic Acid Accession #: NM\_013282.2  
 Coding sequence: 85..2466

1 11 21 31 41 51  
 | | | | |  
 CGACTCCTTA GAGCATGGCA TGGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTGTCT 60  
 GTCCCTCCCC TCAGGCGCGA CACCATGTGG ATCCAGGTTT GGACCATGGA CGGGAGGCGAG 120  
 ACCACACCGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAGATC 180  
 70 CAGGAGCTGT TCCACGTGGA GCCAGGCGCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG 240  
 GAGGACGGCC ATACCTCTTT CGACTACGAG GTCCGCTGTA ATGACACCAT CCAGCTCCTG 300  
 CTCGCGCCAG GCCTCGTGCT CCCCAACAGC ACCAAGGAGC GGGACTCCGA GCTCTCGAC 360  
 ACCGACTCCG GCTGCTGCTT GGGCCAGAGT GAGTCAGACA AGTCTCTCAC CCAAGGCGAG 420  
 GCGGCGCGCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG 480  
 GGGCTGTACA AGGTCAATGA GTACGTGATG GCTCGGGACA CGAACATGGG GCGTGTGTTT 540  
 75 GAGGCGCAGG TGGTCAGGGT GACGCGGAAG GCCCCTCCCG GGGACGAGCC CTGAGCTCC 600  
 ACCTCAGAGC CGGCGCTGGA GGAGGAGCTC ATTACCAAGC TGAATACGTA CGACTACCCG 660  
 GAGAAGCGAG TGGTCCAGAT GAACTCCAGG GACGTCCGAG CGCGCGCCCG CACCATCATC 720  
 AAGTGCAGG ACCTGAGAGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC 780  
 AAGGAGCGGG GCTTCTGTTA CGAGCGGGAG ATCTCCAGGA AGGCGGAGAC CAGGACGGCG 840  
 80 CGGGAATCTT ATGCCAACGT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC 900  
 TCTGTGGAGC AAGTCTTCAA GATTGAGCGG CGGGGTGAAG GGGACCCCAT GGTGACAAAC 960  
 CCATGAGAC GGAAGAGCGG GCCGTCTGTC AAGCACTGCA AGGACGAGCT GAACAGACTC 1020  
 TGCGGGTCT GCGCCTGCCA CCTGTGCGGG GCGCGGCGAG ACCCGACAA GCAGCTCATG 1080  
 TCGATGAGT GCGACATGGC CTTCCACATC TACTGCCTGG ACCCGCCCTT CAGCAGTGTT 1140

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45

```

    CCCAGCGAGG ACGAGTGGTA CTGCCCTGAG TGCCCGAATG ATGCCAGCGA GGTGGTACTG 1200
    GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGCCCTCGGC CACATCGTCC 1260
    TCACAGCGGG ACTGGGCAA GGGCATGGCC TGTGTGGGCC GCACCAAGSA ATGTACCATC 1320
    GTCCCGTCCA ACCACTACGG ACCATCCCG GGGATCCCGG TGGGACCAT GTGGCGGTTC 1380
    CGAGTCCAGG TCAGCGAGTC GGGTGTCCAT CGGCCCAAG TGGCTGGCAT ACACGCCCGG 1440
    AGCAACGACG GAGGTACTCT CCTAGTCTTG GCGGGGGGCT ATGAGGATGA CGTGGACCAT 1500
    GGGAAATTTT TCACATACAC GGGTAGTGGT GGTCGAGATC TTTCCGGCAA CAAGAGGACC 1560
    GCGGAACAGT CTTGTGATCA GAAACTCACC AACACCAACA GGGCGCTGGC TCTCAACTGC 1620
    TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAGG ACTGGCGGTC GGGGAAGCCG 1680
    GTCAGGGTGG TCAGCAATGT CAAGGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC 1740
    AACCGCTACG ATGGCATCTA CAAGGTGTGT AAATACTGGC CCGAGAAGGG GAAGTCCGGG 1800
    TTTCTCGTGT GCGCTACCTT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG 1860
    GAGGGGAAGG ACCGGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG 1920
    GAAGCCCTGG CCAACCGAGA GCGAGAGAAG GAGAACAGCA AGAGGGAGGA GGAGGAGCAG 1980
    CAGGAGGGGG TCTGCGCTG CCCCAGGACG GGCAAGGGCA AGTGGAAAGG GAAGTCCGGC 2040
    GGAGGTGGCC CGAGCAGGAC CCGGTCCCGG CGCCGGACAT CCAAGAAAC CAAGGTGGAG 2100
    CCTACAGTGT TCACGGCCCA GCAGAGCAGC CTCATCAGAG AGGACAAGAG CAACGCCAAG 2160
    CTGTGGAATG AGGTCTGGC GTCACTCAAG GACCGGCCGG CGAGCGGCGAG CCGTGTCCAG 2220
    TTGTTCTCTG GTAAAGTGGG GAGAGCGTTC CAGTGTATCT GCTGTACAGA GCTGGTGTTC 2280
    CGGCCCATCA CGCGCTGTG CCAGCACAAC GTGTGCAAGG ACTGCCTGGA CAGATCCTTT 2340
    CCGGCACAGG TGTTCAGCTG CCTGCTGTC CGCTACGACC TGGGCGCAG CTATGCCATG 2400
    CAGGTGAACC AGCCTCTGCA GACCGTCTCT AACCAGTCTT TCCCGGCTA CGGCAATGGC 2460
    CGGTGATCTC CAAGCACTTC TCGACAGGCG TTTTGTGAA AACGTGTCCG AGGGCTCGTT 2520
    CATCGGCACT GATTTTGTTC TTAGTGGGCT TAACCTAAAC AGGTAGTGT TTCTCGTTC 2580
    CCTAAAGAGG TTTGCTCTTC TTTTATTTT TTTTATTTT TCAAATCTAT ACATTTTCAG 2640
    GAATTTATGT ATTCGGCTTA AAGTTGGAC TTCTCAGTAT TGTGTTTAGT TCTTTGAAAA 2700
    CATAAAGGCC TGCATTTCT CGACAAAAA ACACAAGATT TTTTAAAGAT GGAATCAGAA 2760
    ACTAGTGGT GTGAGGCTG TTGATGTTTC TGGTGTCAAG TTCTCAGAAG TTGCTGCCAC 2820
    CAACTCTTTA AGAAGCGCAG AGGATCAGTC CTCTCTAGG GTTCTGGGCC CCAAGGTGCA 2880
    AGCAAGAGTC TTCTGACAG CATTTTGTCA TCTAAAGTCC AGTGACATGG TTCCCGTGG 2940
    TGGCCCGTGG CAGCCCGTGG CATGGCGTGG CTCAGCTGTC TGTGTAAGT GTTGCAAGGA 3000
    AAAGAGGAAA CATCTCGGGC CTAGTTCAA CTTTGCCTC AAAGCCATCC CCCACGAGC 3060
    TGCTTAGCGT CTGAGATCCG CGTGAAGAGT CCTCTGCCCA CGAGAGCAGG GAGTTGGGGC 3120
    CAGCGAGAAA TGGCCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGACTGACGC 3180
    TGTCCGACGA AGCGCGCCAC GGACGACGCG CAGCACACGA AGTCACGTGC AAGTGCTTT 3240
    GATTCGTCTC TTCTTCTAA AGACGACAGT CTTTGTGTT AGCACTGAAT TATTGAAAAT 3300
    GTCAACGCTA TCTTAGAAGC TGCGGTATC CAGTCTCTCC TGACACCGGA TGGGTGCTGT 3360
    GGAACCGTTT GAGCCTTATA GATCATTAC ATTCAATTTT TTTAACTCAG CAAGTGAGAA 3420
    CTTACAAGAG GGTTTTTTTT TAATTTTTTT TTCTCTTAAT GAACACATT TCTAAATGAA 3480
    TTTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACGTTAGGGT TTGGTTGTTT 3540
    TTGTTTTTGT ATTTTTTTTC TTTTGAAGG GTTTGTAAT TTTTCTAAT TTACCAAAGT 3600
    TTGACGCTA TACCTCAATA AAACAGGAT ATTTAAATC ACATACCTGC AGACAAACTG 3660
    GAGCAATGTT ATTTTTAAAG GGTTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT 3720
    AGGAAGAGAT GAGACAATTT TGTGTAGGCT TTTTCTAAG TCCAGTACTT TGTCCAGATT 3780
    TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAA AAAAAAAA
  
```

Seq ID NO: 156 Protein sequence  
 Protein Accession #: NP\_037414.2

50  
 55  
 60  
 65

```

    1 11 21 31 41 51
    MWIQVRTMDG RQHTVDLSL RLTKVELRR KIQLPHVEP GLQLPYRGK QMEDGHTLFD 60
    YEVRLNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSESDKSSTH GEAAAEYDSR 120
    PADENMDDET ELGLYKNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE 180
    DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMNLNPNP NPKERGFWDY 240
    AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPGEPSPMV DNPMMRKSXP 300
    SKXKCKDDVN RLCRVCAHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSDEMYC 360
    PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTEKC TIVPSNHYGP 420
    IPGIPVGTMW RFRVQVSESG VHRPHVAGIH GRSNDGAYSL VLAGGYEDDV DHGNFPTYTG 480
    SGGRLSGNK RTAEQSCDQK LNTNRLALAL NCFAPINDQE GAELKDWRSQ KPVVRVNRVK 540
    GGNKSKYAPA EGNRYDGIYK VVKYNPEKKG SGFLVWRYLL RRDDDEPGPW TKEGDKRIKK 600
    LGLTMQYPEG YLEALANRER EKENSKREEE EQQEGGFASP RTGKGKWKRK SAGGGPSRAG 660
    SPRRTSKTKK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE 720
    TFQCICQDEL VFRPITTVQC HNVCKDCLDR SFRAQVFSQP ACRYDLGRSY AMQVNPQLQT
  
```

Seq ID NO: 157 DNA sequence  
 Nucleic Acid Accession #: NM\_000756.1  
 Coding sequence: 186..776

70  
 75  
 80

```

    1 11 21 31 41 51
    AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA 60
    GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC 120
    TCTCTGCGAG GAGGCGCGAG CACCGGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGGCC 180
    CTAACATGCG GCTGCGGCTG CTTGTGTCCG CGGGAGTCCCT GCTGGTGGCT CTCCTGCCCT 240
    CGCCGCCATG CAGGCGGCTC CTGAGCCGCG GGCCGGTCCC GGGAGCTCGG CAGGCGCCGC 300
    AGCAACCTCA GCCCTTGGAT TTCTTCCAGC CGCGCGCGCA GTCCGAGCAG CCCAGCAGC 360
    CGCAGGCTCG GCGGTCTCTG CTCCGCTATG GAGAGGAGTA CTCTCTCGCG CTGGGGAACC 420
    TCAACAGAGC CCGGCGGCTC CCCCTTTGCG CGGCTCTCTC GCTCTCTGCC GGAGGCGAGC 480
    CGAGCCGCCC TCGCGCGGAA CAGGCGACCG CCAACTTTTT CGCGTGTGTT CTGACGACG 540
    TGCTGCTGCG TCGGCGCTCG CTCGACAGCC CCGCGGCTCT CGCGGAGCGC GCGCTAGGA 600
    ATGCGCTCGG CGGCGACGAG GAGGACCGCG AGAGAGAAAG GGGTCCGAG GAGCCTCCCA 660
    TCTCCCTGGA TCTCACCTTC CACCTCTCTC GGAAGTCTTT GGAATGCGCC AGGCGCGAGC 720
    AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAAGC 780
  
```

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

GTGCGTTTGG CCAAAAAGAA TCTGCATTGA GCACAAAAAA AATTTAAAAA AATACAGTAT 840  
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900  
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAGTGTGA TTCACGTGCA 960  
GCAGCAACAC AATGTTATTC GTTTTGTCTA OGTTTAGITT CCGTTTCCAG GTGTTTATAG 1020  
TGGTGTTTGA AAGAGAATGT AGACCTGTGA GAAAACGTTT TGTTTGAAAA AGCAGACAGA 1080  
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAGAGA ATGCCATTCT CTTGGGTGGG 1140  
TAAGACTAAA TCTGTAAAGCT CTTTGAAACA ACTTTCTCTT GTAAACGTTT CAGTAATAAA 1200  
ACATCTTTCC AGTCTTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260  
TAATAAAGT TGCAAAGGT

Seq ID NO: 158 Protein sequence  
Protein Accession #: NP\_000747.1

1 11 21 31 41 51  
MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ 60  
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLAGGSGS RPSPEQATAN FFRVLLQQLL 120  
LPRRLDSPA ALAERGARNA LGGHQEAPEP ERRSEEPPI SLDLTFHLLRE VLEMARAEQL 180  
AQQAHSNRKL MEIIGK

Seq ID NO: 159 DNA sequence  
Nucleic Acid Accession #: NM\_001200.1  
Coding sequence: 325..1514

1 11 21 31 41 51  
GGGGAATTCT TGAACCTTGA GGGAGAATAA CTTGCGCACC CCACCTTGCG CCGGTGCCTT 60  
TGCCCCAGCG GAGCCTGCTT CGCCATCTCC GAGCCCCACC GCGCTTCCAC TCCTCGGCCT 120  
TGCCCGACAC TGAGACGCTG TTCCAGCGT GAAAAGAGAG ACTGCGCGCG CGGCACCCCG 180  
GAGAAGGAGG AGGCAAAAGAA AAGGAACGGA CATTGCGTCC TTGCGCCAGG TCCTTTGACC 240  
AGAGTTTTTC CATGTGGACG CTCTTTCAAT GGACGTGTCC CCGCGTGCTT CTAGACCGGA 300  
CTGCGGTCTC TTAAGGTTCG ACCATGGTGG CCGGACCCCG CTGTCTTCTA CGGTGTCTGC 360  
TTCCCGAGGT CTTCTGGGCG GCGCGGCGTG GCGTCTGTCC GGAGCTGGGC CGCAGGAAGT 420  
TCGCGGCGCG GTGCTGGGCG CGCCCTCAT CCGACCCCTC TGACGAGTTC CTGAGCGAGT 480  
TCGAGTTGCG GCTGCTCAGC ATGTTCCGCC TGAACAGAG ACCCACCCCG AGCAGGAGCG 540  
CCGTGGTGCC CCCCTACATG CTAGACCTGT ATGCGAGGCA CTCAGGTGAG CCGGGCTCAC 600  
CGCCCGGAG CCACCGGTG GAGAGGCGAG CCAGCCGAGC CAACACTGTG CGCAGCTTCC 660  
ACCATGAAGA ATCTTTGAAA GAACCTACAG AAACAGGTGG GAAACAACCC CGGAGATTCT 720  
TCTTAAATTT AAGTTCTATC CCCACGGAGG AGTTTATCAC CTCAGCAGAG CTTGAGGTTT 780  
TCCGAGAACG GATGCAAGAT GCTTTAGGAA ACAATAGCAG TTTCCTCAC CGAATTAATA 840  
TTTATGAAT CATAAAACCT GCAACAGCCA ACTCGAAATT CCGCGTGACC AGACTTTTG 900  
ACACGAGTT GSTGAATCAG AATGCAAGCA GGTGGGAAAG TTTTGTATGC ACCCCGCTG 960  
TGATGCGGTG GACTGCACAG GGACACGCCA ACCATGGATT CGTGGTGGAA GTGGCCCACT 1020  
TGGAGGAGAA ACAAGGTGTC TCCAAGAGAC ATGTTAGGAT AAGCAGTCTT TTGACCAAG 1080  
ATGAACACAG CTGGTCACAG ATAAGGCCAT TGCTAGTAAC TTTTGGCCAT GATGGAAAG 1140  
GGCATCTCTT CCACAAAGA GAAAACGTC AAGCCAAACA CAAACAGCGG AAACGCTTGA 1200  
AGTCCAGCTT TAAGAGACAC CCTTTGTACG TGGACTTCAG TGACGTGGGG TGGAAATGACT 1260  
GGATTGTGGC TCCCGCGGGG TATCACGCGT TTTACTGCCA CGGAGAAATG CTTTTCCTC 1320  
TGGCTGATCA TCTGAATCTC ACTAATCATG CCATGTTTCA GACGTGTGTC AACTCTGTTA 1380  
ACTCTAAGAT TCCTAAGGCA TGCTGTGTCC CGACAGAACT CAGTGTCTATC TCGATGCTGT 1440  
ACCTTGACGA GAATGAAAG GTTGTATTAA AGAACTATCA GGACATGGTT GTGGAGGGTT 1500  
GTGGGTGTCG TAGTACAGC AAAATTAAAT ACATAAATAT ATATATA

Seq ID NO: 160 Protein sequence  
Protein Accession #: NP\_001191.1

1 11 21 31 41 51  
MVAGTRCLLA LLLPQVLLGG AAGLVPELGR RKFAAASSGR PSSQPSDEV LSEFELRLLSM 60  
FGLKQRPPTS RDAVVPFVYL DLYRRHSGQP GSPAPDHRLE RAASRANTVR SFHHEESLEE 120  
LEETSGKTR RFFNLSIP TEEFITSSEL QVFEQMQDA LGNNSFFHR INIYEIIPKA 180  
TANSKFPVTR LLD

Seq ID NO: 161 DNA sequence  
Nucleic Acid Accession #: NM\_001999.2  
Coding sequence: 1..8736

1 11 21 31 41 51  
ATGGGGAGAA GACGGAGGCT GTGTCTCCAG CTCTACTTCC TGTGGCTGGG CTGTGTGGTG 60  
CTCTGGGCGC AGGSCACGCG CGGCCAGCCT CAGCCTCTCC GCGCCAGGCC GCGCCGGCCC 120  
CAGCCGCGCG GCGCAACAGT TCGGTCCGCT ACAGCAGGCT CTGAAGGCGG GTTCTAGCG 180  
CCCGAGTATC GCGAGGAGGG TGCCGCGAGT GCCAGCCGCG TCCGCGGGGG AGGACAGCAG 240  
GACGTGCTCC GAGGGGCCAA CGTGTGCGGC TCCAGATTCC ACTCCTACTG CTGCCCTGGA 300  
TGGAGAGCGC TCCCTGGAGG AAACCAAGTC ATGTCCCGA TTTGTAGAAA TAGTTGTGGA 360  
GATGGATTTT GTTCCCGTCC TAACATGTGT ACTTGTTCGA GTGGGCAAT ATCATCAACC 420  
TGTGGATCAA AATCAATTCA GCAGTGCAGT GTGAGATGCA TGAATGGTGG GACCTGTGCA 480  
GATGACCACT GCCAGTGCCA GAAAGGATAT ATTGGAACCT ATTGTGGACA ACCTGTCTGT 540  
GAAATGGAT GTCAAGATGG TGGACGTTGC ATGCCCCAAC CGTGTGCTTG TGTATTATGG 600  
TTCACTGGTC CACAGTGTGA AAGAGATTAC AGGACAGGCC CGTGTTCAC TCAGGTCAAC 660  
AACCAGATGT GCCAAGGCGA GCTGACAGGC ATTGTCTGCA CGAAGACTCT GTGCTGTGCC 720  
ACCACTGGAC GGGCGTGGGG CCATCCCTGT GAGATGTGTC CAGCCAGGCC TCAGCCCTGC 780  
CGAGGGGGTT TCATCCCCAA CATCCGCACT GGAGCTTGCC AAGATGTTGA TGAATGCCAG 840  
GCTATCCAG GGATATGCCA AGGAGGAAAC TGTATCAATA CAGTGGGCTC TTTTGAATGC 900

	AGATGCCCTG	CTGGTCACAA	ACAGAGTGAA	ACTACTCAGA	AATGTGAAGA	CATTGATGAG	960
	TGCAGCATCA	TTCTCTGGAT	ATGTGAAACT	GGTGAATGTT	CCAACACCGT	GGGAAGCTAT	1020
	TTTTGTGTTT	GTCCACGTGG	ATATGTAACC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080
5	AGAACAGGCA	TGTGTTTCTC	GGGCCTGGTG	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG	1140
	AGAAATGACG	AAATGTCAGT	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCATT	1200
	CCTGAAGCCT	GTCCTGTGAG	AGGTTCTGAG	GAATATCGCA	GACTTTGCAT	GGATGGACTT	1260
	CCAATGGGAG	GAATTCACAG	GAGTGTCTGG	TCCAGACCTG	GAGGCACCTG	GGGAAATGGC	1320
	TTTGCCCCAA	GTGGCAATGG	CAATGGCTAT	GGCCACGGAG	GGACAGGCTT	CATCCCCATC	1380
	CCTGGAGGCA	ATGGCTTTTC	TCCTGGCGTT	GGGGAGAGCG	GTGTGGGGGC	CGGGGGACAG	1440
10	GGACCTATCA	TCACCTGGAG	AACAATTCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT	1500
	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACCTGCT	CAAGCTACCG	ATGTGAATGC	1560
	AACATGGGTT	ATAAGCAGGA	TGCAAAATGA	GATTGTATAG	ATGTTGATGA	ATGCACATCA	1620
	AATCCCTGCA	CTAATGGAGA	TTGTGTTAAT	ACACCTGGTT	CCTATTATTG	TAAATGTCAT	1680
	GCTGGATTCC	AGAGGACTCC	TACCAAGCAA	GCATGCATTG	ATATTGATGA	GTGCATCCAG	1740
15	AATGGGTTTC	TTTGTAAAAA	CGGTGATGTC	GTGAACTCAG	ATGGAAGTTT	CCAATGCATT	1800
	TGCAATGCCG	GCTTTGAATT	AATACAGAT	GGAAAAAAT	GTGTTGATCA	TGATGAATGT	1860
	ACAACTACCA	ACATGTGTTT	GAATGGAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTGCAAA	CAGGATTGTT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA	1980
20	TGCGACACCC	CAGGAATCTG	CATGAATGGG	CACCTGCATC	ACAGTGAAGG	GTCCCTCCGC	2040
	TGTGACTGTC	TCCCTAGGCT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCCGGT	2160
	GCAGTGACCA	AGTCCGAATG	CTGCTGTGCC	AATCCAGACT	ATGTTTGTGG	AGAACCCTGC	2220
	CAGCCATGCC	CTGCAAAAAA	TTCAAGCTGAA	TTCCACGGCC	TTTGTAGTAG	TGGAGTAGGT	2280
25	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
	GGGATTGTTC	AAACTTACCT	TGGTAGTTAC	CGTTGTAATT	GCAACAGTGG	CTATGAACCA	2400
	GATGCCTCTG	GAAGAAACTG	TATTGACATT	GATGAATGTT	TAGTAAACAG	ACTGCTTTGT	2460
	GATAACGGAT	TGTGCCGAAA	CACGCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGSTAT	2520
	GTGTTTCAGG	CTGAGACAGA	GACCTGTGAA	GATATAAATG	AATGTGAAGG	CAACCCATGT	2580
30	GTCAATGGGG	CCTGCAGAAA	CAACCTTGGA	TCTTTCAATT	GTGAATGTTT	GCCCGGCAGC	2640
	AAACTCAGCT	CCACAGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
	ATCCAGGACA	GCCGCTGTGA	GGTGAATATT	AATGGAGCCA	CTCTGAAATC	TGAATGCTGT	2760
	GCCACCCCTG	GAGCGCGCTG	GGGAGGCCCC	TGTGAGCGGT	GTGAACCTAGA	TACAGCTTGC	2820
	CCAAGAGGGC	TTGCCAGGAT	TAAAGGTGTT	ACGTGTGAAG	ATGTTAATGA	GTGTGAGGTG	2880
35	TTCCCTGGCG	TTTGTCCAAA	TGGACGCTGT	GTCAACAGTA	AGGGATCTTT	TCATTGCGAG	2940
	TGCCCTGAAG	GCCTTACGTT	GGATGGGACT	GGCCGTGTAT	GTTTGGATAT	TGCGATGGAG	3000
	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACG	CCGTTCTCTG	AAAGTTCCGC	3060
	ATGGATGCTT	GCTGCTGTGC	TGTGCGGGCG	GCTTGGGCGA	CCGAGTGTGA	GGAGTGGCCC	3120
	AAACCTGGCA	CAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	TGCTAACCGA	3180
40	GGGGATGTTT	TTACTGGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
	GGGATGTGTA	CTTATGGGAA	GTGCAGAAAT	ACAATCGGAA	GCTTCAAATG	CCGTTGCAAT	3300
	AGTGGCTTTG	CTCTAGACAT	GGAGGAAGA	AATGCAACGG	ACATCGACGA	GTGCAGGATT	3360
	TCTCCTGACC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGCAG	3420
	TGCTTGGAG	GCTATGAAAG	TGGCTTCATG	ATGATGAAGA	ACTGCATGGA	CATTGACGGA	3480
45	TGTGAACGTA	ACCTCTCTCT	TTGTAGGGGT	GGCACCTGTG	TGAACACTGA	GGGCAGCTTT	3540
	CAGTGTACT	GCCCACTGGG	ACACGAGCTG	TCACCATCCC	GTGAGGACTG	TGTGGATATT	3600
	AATGAATGCT	CCCTGAGTGA	CAATCTCTGC	AGAAATGGAA	AATGTGTGAA	CATGATTGGA	3660
	ACCTATCAGT	GCTCTTGCAA	TCCTGGATAT	CAGGCTACGC	CAGACCGCCA	GGGCTGTACA	3720
	GATATTGATG	AATGTATGAT	AATGAACGGA	GGCTGTGACA	CCCACTGCAC	AAATTGAGAG	3780
50	GGAGGCTACG	AATGACAGCT	CAGTGAGGGT	TATGCCCTGA	TGCCAGATGG	GAGATCGTGT	3840
	CGAGACATG	CTGATGTGAA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC	3900
	ATTCTGGAG	AGTATGCTGT	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA	3960
	ACATGCATTG	ATGTCAATGA	ATGTGACCTA	AATTCAAATA	TCTGCATGTT	TGGGAATGT	4020
	GAGAACACAA	AGGGATCCTT	CATTTGCCAC	TGTCAGCTGG	GTTACTCAGT	GAAGAAGGGG	4080
55	ACACACAGAT	GTACAGATGT	GGATGAGTGT	GAAATTGGTG	CTCAATAACT	CGACATGCAT	4140
	GCCTCATGTC	TGAATATCCC	AGGAAGCTTC	AAGTGTAGCT	GCAGAGAAGG	CTGGATTGGA	4200
	AACGGCATCA	AGTGTATTGA	TCTGGAGCAA	TGTTCTAATG	GAACCCACCA	GTGTAGCATC	4260
	AATGCTCAGT	GTGTAAATAC	CCCCGGCTCA	TACCGCTGTG	CCTGCTCCGA	AGGTTTCACT	4320
	GGTGATGGCT	TTACCTGCTT	AGATGTTGAT	GAGTGTGAG	AAAACATAAA	CCTCTGTGAG	4380
60	AAOCSGACGT	GCCTTAATGT	CCCCGGTGCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCACT	4440
	CCAGCCTCAG	ACAGCAGATC	CTGCCAAGAT	ATTGATGAAT	GCTCCTTCCA	AAACATTGTT	4500
	GTCTCTGGAA	CATGTAATAA	CCTGCTGGA	ATGTTTCATT	GCATCTGCGA	TGATGGTTAT	4560
	GAATTGGACA	GAACAGGAGG	GAACGTGACA	GATATTGATG	AGTGTGACGA	TCCTATAAAC	4620
	TGTGTCAATG	GCCTATGTGT	CAACACGCTT	GGTGTCTATG	AGTGTAACTG	CCCACCCGAT	4680
65	TTTCAGTTGA	ACCCAACTGG	TGTGGGTTGT	GTGTGACAA	GTGTGGGCAA	CTGCTACCTG	4740
	AAGTTTGGAC	CTGAGGAGGA	TGGGAGTCTG	TCTTGCAACA	COGAGATCGG	GGTGGGCGTC	4800
	AGTGCCTCTT	CATGCTGCTG	CTCTCTGGGA	AAGGCTGGG	GAACCCCTG	TGAGACATGC	4860
	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCCCG	GAGGTGAAGG	CTTCAGACCT	4920
	AACCCCATCA	CAATCAITTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
70	CAGGGTGGAA	ACTGCATCAA	CACITTTGGG	AGCTTCCAGT	GTGAGTGCCC	ACAAGGCTAC	5040
	TACCTCAGCG	AGGATAACCG	CATCTGTGAG	GATATTGATG	AGTGTTTTGC	ACATCCTGGT	5100
	GTGTGTGGGC	CTGGGACCTG	CTATAACACC	CTGGGAAATT	ACACCTGCAT	TTGCCCAOCT	5160
	GAGTACATGC	AGGTCAATGG	AGGCCACAAC	TGCATGGACA	TGAGAAAAAG	CTTTTGCTAC	5220
	CGAAGCTATA	ATGGAAACCA	TTGTGAGAA	GAGTTGCTTT	TCAATGTGAC	AAAAAGGATG	5280
75	TGCTGTGCGA	CATATAATGT	GGGCAAGCT	GGGAACAAAC	CTTGTGAACC	ATGCCCAACT	5340
	CCAGGAACAG	CTGACTTTAA	AACCATATGT	GGAAATATTC	CTGGAATTCAT	CTTTGACATT	5400
	CACACAGGAA	AAGCTGTGGA	CATTGATGAA	TGTAAAGAGA	TTCCAGGCAT	TTGTGCAAA	5460
	GGTGTGTGCA	TTAACCAGAT	TGGCAGTTTC	CGCTGTGAAT	GOCCTACAGG	ATTGAGTTAC	5520
	AATGACCTGC	TGTTGGTTTG	TGAAGATATA	GATGAGTGCA	GCAATGGTGA	TAACTCTTGC	5580
80	CAGCGGAATG	CAGACTGCAT	CAATAGTCTT	GGTAGTTACC	GCTGTGAATG	TGCCGCGGGT	5640
	TTCAAACTTT	CACCAATGAG	GGCCTGTGTA	GATCGCAATG	AATGTTTAGA	AATTCTCAAT	5700
	GTGTGACGTC	ATGGCTGTGT	TGTTGATCTG	CAAGGAAGTT	ACCAGTGCAAT	CTGCCACAAT	5760
	GGCTTTAAGG	CTTCTCAGGA	CCAGACCATG	TGCATGGATG	TTGATGAGTG	CGAGCGGCAC	5820
	CCATGTGGAA	ATGGAACTTG	TAAAAACACC	GTTGGATCCT	ATAACTGTCT	GTGCTACCCA	5880
	GGGTTTGAAC	TCACCTATAA	TAAATGATGC	CTGGACATAG	ATGAGTGACG	TTCTTTT	5940

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70

```

GGTCAGSTGT GCAGAAATGG ACGTTGTTTT AATGAAATGG GTTCTTTCAA GTGCTATGT 6000
AACGAAGGTT ATGAACCTTAC CCCAGATGGC AAAAAGCTGTA TAGACACTAA TGAGTGTGTC 6060
GCCCTTCCCG GCTCTTGCTC TCCTGGTACC TGTGAGAAAT TGGAGGGATC CTTGAGATGC 6120
ATCTGTCCCC CAGGGTATGA AGTAAAGAGC GAGAACTGCA TTGATATAAA TGAATGTGAT 6180
GAAGATCCCA ACATTGTCT TTTGGTTCC TGTACTAATA CTCCAGGGGG CTTCCAGTGC 6240
CTCTGCCCCC CTGGCTTGT ACTATCTGAT AATGGAOSGA GATGCTTTGA TACTGCCAG 6300
AGCTTCTGCT TCACAAATTT TGAAGATGGA AAGTGTCTG TACCCAAAGC TTTCAACACC 6360
ACAAAAGCAA AATGCTGCTG TAGTAAGATG CCAGGAGAGG GCTGGGGGGA CCCCTGTGAG 6420
CTGTGCCCCA AAGACGATGA AGTTGCATTT CAGGATTTGT GTCCATATGG CCATGGAAC 6480
GTCCCTAGTC TTCTATGATC ACGTGAAGAT GTCAATGAGT GTCTTGAGAG CCCAGGCATT 6540
TGTTCAAATG GTCAATGATC CAACACCGAC GGATCTTTTC GCTGTGAATG TCCAATGGGC 6600
TACAACCTTG ACTACACTGG AGTACGCTGT GTGGATAGTG ATGAGTGTTC AATCGGCAAT 6660
COGTGTGGAA ATGGTACATG CACCAATGTT ATTGGGAGTT TTGAATGCAA TTGCAATGAA 6720
GGCTTTGAGC CAGGGCCCAT GATGAATTTT GAAGATATCA ACGAATGTGC CCAGAACCCA 6780
CTGCTGTGTG TTTACGCTG CATGAACACT TTTGGGTCT ATGAATGCAC GTGCCCGATT 6840
GGCTATGCCC TCAGGGAAGA TCAAAAGATG TGCAAGATC TGGATGAATG TGCTGAAGGG 6900
TTACACGAGT GTGAATCTAG GGGCATGATG TGTAAAGATC TAATCGGCAC CTTGATGTGC 6960
ATCTGCCCTC CTGGAATGGC CCGAAGGCCC GATGGAGAAG GCTGTGTAGA TGAAGATGAA 7020
TGACGAGCCA AGCCAGGAAT CTGTGAAATG GGACGTTGTG TTAACATTAT TGAAGGCTAT 7080
AGATGTGAGT TCAATGAAGC ATTCCAGTCA AGTCTTTCAG GCACTGAATG CCTTGACAT 7140
CGACAGGGTC TCTGCTTTGC AGAGGTACTG CAGACAAATG GTCAATGGC ATCCAGTAGT 7200
CGCAATCTCG TCACTAAGTC AGAATGCTGC TGTGATGCTG GCGAGGCTG GGGCCACCAG 7260
TGCGAGCTTT GCCACITTC TGGAACTGCC CAGTACAAAA AGATATGTCC TCATGGCCCA 7320
GGATATACAA CTGATGGAAG AGATATTGAT GAATGTAAAG TAATGCCAAA CCTCTGCACC 7380
AATGTGAGT GCATCAATAC CATGGGCTCA TTCCGATGCT TCTGCAAGT TGGCTACACC 7440
ACAGACATCA GTGGAACCTC TTGTATAGAC CTTGATGAAT GCTCCAGTC CCGGAAACCA 7500
TGCAACTACA TCTGCAAGAA CACTGAGGGG AGTTATCAGT GTTCAATGCC GAGGGGTAT 7560
GTCTGCAAG AGGATGGAAG GACATGCAAA GACCTTGATG AATGTCAAA AAAGCAGCAT 7620
AACTGCCAGT TCCTCTGTGT CAACACCTG GGGGGGTTTA CTTGTAATG TCCACCTGTT 7680
TTTACACAGT ATCAACTGAC TTGTATCGAC AACAACGAAT GTGGGTCTCA ACCTTTGCTT 7740
TGTGAGGAA AGGGAATCTG TCAAAACACT CCAGGCAGTT TCAGCTGTGA ATGCCAAGA 7800
GGGTCTCTC TTGATGCCAC CGGACTGAAC TGTGAAGATG TTGATGAATG TGATGGGAAC 7860
CACAGGTGCC AACACGGCTC CCAGAACATC CTGGGTGGCT ACAGATGTGG CTGCCCCCAA 7920
GGCTACATCC AGCACTACCA GTGGAATCAG TGTGTGATG AGAATGAATG CTCCAATCCC 7980
AATGCTGTG GCTCTGCTTC CTGCTACAA ACCCTGGGGA GTTACAAGTG CGCCTGCCCC 8040
TCGGGGTCTC CTTTGAGCCA GTTCTCCAGT GCCTGCCACG ACGTGAATGA GTGCTCGTCC 8100
TCCAAGAACC CTTGCAATTA CGGCTGCTCT AACACGAGG GGGCTTACCT CTGTGGCTGC 8160
CCCCCTGGGT ATTACAGAGT GGGACAAGGC CACTGTGCTC CAGGAATGGG ATTTAACAAG 8220
GGGCGATACC TGTACTGGA TACAGAGGTC GATGAGGAAA ATGCTCTGTC CCCAGAAGCA 8280
TGCTACAGT GCATAATCAA CGGCTATCCT AAGAAAGACA GCAGGCAGAA GAGAAGTATT 8340
CATGAACCTG ATCCCACTGC TGTGAAACAG ATCAGCCTAG AGAGTGTGCA CATGGACAGC 8400
CCGCTCAACA TGAAGTTCAA CCTCTCCAC CTGCTCTTA AGGAGCACAT CCTGGAAC 8460
AGGCCGCCCA TCCAGCCCTC CAACAACCAC ATCCGTTATG TCATCTCTCA AGGGAACGAT 8520
GACAGCGTCT TCCGATCCCA CCAAGGAAT GGGCTCAGCT ACTTGACAC GGGCAAGAAG 8580
AAGCTCAGTC CGGACACATA CACAAGGAA ATCACTAGCA TCCCTCTCTA CAAGAAGAAG 8640
GAGCTTAAGA AACTGGAAGA GAGCAATGAG GATGACTACC TCCTAGGGGA GCTTGGGGAG 8700
GCTCTCAGAA TGAGGCTGCA GATTGAGTCT TATTAACGTT TCACAGACTT GGGCCCAAGC 8760
TCRAATCCTA GCACAGCCAG TCTGCAAGC CATTTGAAAA GTCAGGACTT AATTTTAAAG 8820
AGGAAAATA ATAATAACTC TTGTTCTTTT CCTCCCTGTC TTAGACTTTG AATGTTGACC 8880
CTACAGGGA GGGATAAATT AGACTCTGGT ATGGCCAAAG ATTTGAGCTC AAAGGCAACC 8940
GTGGTACTG TATTTTTTAT ATAATTCTAT TTTAAATAT ATTTAAAGAA ACCTAAATGT 9000
TCAAGATATC AGCATATGGC ACTAAATGCA CAAAATAAT GTAGCGTTTT TTTTTTTTTT 9060
CCTGTTAGCA CTCTGTAACA CTTTGGGTAT TTTGCTATAG TTGCTAATTA AAAAAATATA 9120
GATGTTTATT TATTTTAAAT GCAGTAATAT ATGAGAAAT GAACAAACTA TGTAAACAAA 9180
AAGGGAACCT CACTGTGTTT TCTTTAGATT TATAAATTG AGCTATTTTT TTAGAGGTG 9240
CTTTTTAAAA ATCAATAGA TACAAGAGAT GTTTCCTTTG GTTTCTGCCC AGTCATCCAG 9300
CTGATACACA CCTGATCGAT TTTAAAGAAA GCCACACAGA GCTGAATCGG GCAGTGCTAA 9360
TCATAATTT AAAAGACATG AATGTCATTA GATCCTTTAT AACGTAGATC GAAGCCAAAG 9420
CAGCTCATTT GTGACACAT TTTATATCAC CAGACACACC AGGCAACAGA AGTGAAGCA 9480
CAACCACTGT AGCAAAATAC CTTGACTGCT TGTGAGACCA TTAGCATGTC AGGCCAAACC 9540
GTACTGTATT TCTTCTCAT AACCTCAAGG AACCATATGT GCTACCCACA ACACCTCATT 9600
CTTACCCAGG GTGGCTGGC TCCTCATGGT ACTGTAGGCA GCTGAAGAAC CGCGTTCCC 9660
TTGAAGGGA ACACCTGGCA TTCTGTGGTG TTTCTGTGCT TCTTAAATAA TGGTGCAATT 9720
ATTATGTTCA AGTTATTTC AAGATTGCCAT ATGTGCAAA ACATCATGCA ATGCAGCCAA 9780
GGAATATATG TTGTTGTTGT TGTTTTAAAC CCAATTTTTT TTTAGAAATT TCATTAATAC 9840
TGATGTTATA CACCATATGC CTATTTTAT CATAGCCTAT TGTGATGAA AGATGTTTGT 9900
ACAATGAATT GATGTTTAGT TTGCTTTAGT CATTTAAAAA GATATTGTAC CAGGATGTGC 9960
TATTAAGAGC AGGTATCCAT TATTTCTCTC AACCAAGAA CCGTTTCTCT GGACCAAGTA 10020
CCAAACCTCA TATGTGAAAT GGCCAAAGCA CATGCAGGCT CCGTGTGTTT CCTCTCAAAC 10080
CTGTGCTGAC CAAAGATTAG TAACCAAGTA TACCAGATAT TTTGAGGTTT TATTGTTTTT 10140
TTAATACTA AAAAAAACT CGTGCC
  
```

Seq ID NO: 162 Protein sequence  
 Protein Accession #: NP\_001990.1

75

80

```

1 11 21 31 41 51
MGRRRRLCLQ LYFLWLGCVV LWAQGTAGQP QPPPPKPPRP QPPFQQVRS TAGSEGGFLA 60
PEYREEGAAY ASRVRRRGQQ DVLRGPNVCG SRFPYSYCCPG WKTLPGGNQC IVPICRNSCG 120
DGFCRPRNMC TCSSSQIIST CGSKSIQCCS VRCMNGTCA DDHCQCKQGY IGTGCGQPV 180
ENGQNGRRC IAQPCACVYG FTGPQCDERY RTGPFCTQVN NQMCQQLTQ IVCTKLCCA 240
TTGRAWGPRC EMCPAQPPPC RRGFIPNIRT GACQDVDEQO AIPGICQGGN CINTVGSFEC 300
RCPAGHKQSE TTQKCEDIDE CSIIPIGICET GECSNTVGSY FCVCPRGVYT STDGSRCIDQ 360
RTGMCPSGLV NGRCAQELFG RMTKMQCCCB PGRCMGIGTI PEACFVRGSE EYRRLCMDGL 420
  
```

5	PMGGIPGSAG	SRPGGTGGNG	FAPSGNGNGY	PGPGTGFIRI	PGNGFSPGV	GGAGVGAGGQ	480
	GPIITGLTIL	NQTIDICKKH	ANLCLNGRCI	PTVSSYRCEC	NMGYKQDANG	DCIDVDECTS	540
	NPCTNGDCVN	TPGSYYCKKH	AGFORTPTKQ	ACIDIDECEI	NGVLCKNGRC	VNSDGSFQCI	600
	CNAGFELTDD	GKNCVDHDEC	TTTNMCLNGM	CINEDGSFCK	ICKPGFVLAP	NGRYCTDVDE	660
	QQTGPGICMNG	HCINSEGSFR	CDPPGLAVG	MDGRVCVDTH	MRSTCYGGIK	KGVCVRPFP	720
	AVTKSECCCA	NPYGFGEPC	QPCPAKNSAE	FHGLCSSGVG	ITVDGRDINE	CALDPDICAN	780
	GICENLRGSY	RQNCNSGYEP	DASGRNCIDI	DECLVNRLLC	DNLGCRNTPG	SYSTCTPPGY	840
	VFRTEETCE	DINECESNPC	VNGACRNNLG	SFNCCECPGS	KLSTGLICI	DSLKGTCLWN	900
10	IQDSRCEVNI	NGATLKSECC	ATLGAANGSP	CERCELDTAC	PRGLARIKGV	TCEVDNCEV	960
	FPGVCPNGRC	VNSKGSFHC	CPEGLTLDGT	GRVCLDIRME	QCYLKWDEDE	CIHPVPGKFR	1020
	MDACCACVGA	AWGTECEEC	KPGTKEYETL	CPRGAGPANR	GDVLTGRPFY	KDINECKAPP	1080
	GMCTYKCRN	TIGSFKCRN	SGFALDMEER	NCTDIDECRI	SPDLGSGGIC	VNTPGSPECE	1140
	CPEGESGFM	MMKNQMDIDG	CERNPLLCRG	GTCTVNTGSE	QCDCLPGLHE	SPSREDCVDI	1200
	NECSLSDNL	RNGKCVNMIG	TYQCSNPGY	QATPDRGGCT	DIDECMIMNG	GCDTQCTNSE	1260
15	GSYECSCSEG	GSYRCFCAAG	ADIDECENNP	DICDGGQCTN	IPGEYRCLCY	DGFMASMDMK	1320
	TCIDVNECDL	NSNICMFGEC	ENTKGSFICH	COLGYSVKKG	TTGCTDVDEC	EIGAHCMDMH	1380
	ASCLNIPGSF	KCSRCRWIG	NGIKCIDLDE	CSNGTHQCSI	NAQCVNTFGS	YRCACSEGFT	1440
	GDGPTCSDVD	ECANENILCE	NGQCLNVPGA	YRCECEMGFT	PASDSRSCQD	IDECSPQNIC	1500
20	VSGTCANLPG	MFHICDDGY	ELDRGTGNCCT	DIDECADPIN	CVNGLCVNTP	GRYECCPPD	1560
	FQNLPTGVC	VDNVNGNCLY	KFGPRGDGSL	SCNTEIGVG	SRSSCCCSLG	KAWGNPCETC	1620
	PPVNSTEYIT	LCPGEGFRP	NPITILEDI	DECQELPGLC	QGGNCINTFG	SPQCECPQGY	1680
	YLSIEDTRICE	DIDECFAHP	VCGPGTCYNT	LGNYTCICPP	EYMQVNGGHN	CHMDRKSEFY	1740
	RSYNGTTCEN	ELPNNVTKRM	CCCTYNVKG	GNKPCCEPCT	PGTADPKTIC	GNIPGFTEDI	1800
25	HTGKAVDIDE	CKEIPICAN	GVCINQIGSF	RCECPTGFSY	NDLLLVCEDI	DECSNGDNLC	1860
	QRNADCNIS	GSYRCFCAAG	FKLSPNGACV	DRNECLEIPN	VCSHGLCVDL	QGSYQCICHN	1920
	GFKASQDQTM	CMWDECEHR	PCNGTCKNT	VGSYNCLCYP	GFEITHNND	LDIDECSSFF	1980
	QOVCRNGRC	NEIGSFKCLC	NEGVELTPDG	KNCIDTNECV	ALPGSCSPGT	CQNLEGSFRC	2040
	ICPPGYEVKS	ENCIDINECD	EDPNICLFGS	CTNTPGGFQC	LCPPGFVLSD	NGRRCFDTRQ	2100
30	SFCPTNFENG	KCSVPKAFNT	TKAKCCSKM	PEGEGWDPE	LCPKDEVAFA	QDLCPYGHGT	2160
	VPSLHDTRED	VNECLQSGY	CSNGQCINTD	GSFRCECPMG	YNLDYTGVR	VDTDECSIGN	2220
	PCNGTCTNV	TGSFECNCE	GFEPPGMNMC	EDINECAQNP	LLCALRCMNT	FGSYECTCPI	2280
	GYALREDQKM	KDLDCECAEG	LHDCESRGM	CQNLIGTFMC	ICPPGMARRP	DGEGCVDENE	2340
	CRTPKGCEN	GRCVNIIGSY	RCECNEGFQS	SSSGTECLDN	RQGLCPAEVL	QTIQCMASSS	2400
35	RNLVTKECC	CDGGRGWGHQ	CELCLPGTA	QYKICPHGP	GYTTDGRDID	ECKVMPNLCT	2460
	NGQCINTMGS	FRCPCKVGYT	TDISGTSID	LDECSQSPKP	CNYICKNTEG	SYQCSCPRGY	2520
	VLOEDGKTCK	DLDEBCTKH	NQFLCVNTL	GGFTCKCPFG	FTQHTACID	NNECGSQPLL	2580
	CGGKIGQNT	PGSFCEBQR	GFSLDATGLN	CEVDDECDGN	HRCQHGQONI	LGGYRCGCPQ	2640
	GYIQHYQWQ	CVDNECSNP	NACGSASCYN	TLGSYKCAP	SGFSFDQFSS	ACHDVNECSS	2700
40	SKNPNYGC	ITEGGYLCG	PPGYRVGQG	HCVSGMGFNK	GGYLSLDETE	DEENALSPEA	2760
	CYCKINGYP	KDQSRQKRSI	HEPDPTAVEQ	ISLESVDMDS	PVNMKFNLSH	LGSKEHILEL	2820
	RPAIQPLNNH	IRYVISQOND	DSVFRIHQRN	GLSYLHTAKK	KLMPGTYYLE	ITSIPLYKKK	2880
	ELKKLEBSNE	DYLLGELGE	ALRMRLQQL	Y			

Seq ID NO: 163 DNA sequence  
Nucleic Acid Accession #: NM\_013372.1  
Coding sequence: 63..617

50	1	11	21	31	41	51	
	GCGGCGGCAC	TCAGCGCCAC	GCGTGAAG	CGCAGGCCCC	GAGGACCCGC	CGCACTGACA	60
	GTATGAGCCG	CACAGCTTAC	ACGGTGGGAG	CCCTGCTTCT	CCTCTTGGGG	ACCTGCTGTC	120
	CGGCTGCTGA	CGGAAAAAG	AAAGGTCCC	AAGGTGCCAT	CCCCCGSCCA	GACAAGGCC	180
	AGCAATGA	CTCAGAGCAG	ACTCAGTCGC	CCCAGCAGCC	TGGCTCCAGG	AACCGGGGCG	240
55	GGGGCAAGG	GGGGGGCACT	GCCATGCCCG	GGGAGGAGGT	GCTGGAGTCC	AGCCAAGAGG	300
	CCCTGCATGT	GACGGAGCGC	AAATACCTGA	AGCGAGACTG	GTGCAAAACC	CAGCCGCTTA	360
	AGCAGACCAT	CCAGAGAGAA	GGCTGCAACA	GTGCAACCAT	CATCAACCGC	TTCTGTACG	420
	GCCAGTGCAA	CTCTTTCTAC	ATCCCCAGGC	ACATCCGGAA	GGAGGAAGGT	TCCTTTCACT	480
	CCTGCTCCTT	CTGCAGGCC	AAGAAATTCA	CTACCATGAT	GGTCACTACT	AAGTGCCTCT	540
60	AATACAGGCC	ACCTACCAAG	AAGAAGAGAG	TCACACGTGT	GAAGCAGTGT	CGTTGCATAT	600
	CCATCGAATT	GGATTAAAGC	AAATCCAGGT	GCACCCAGCA	TGTCTAGGAA	ATGCAGCCCC	660
	AGGAAGTCCC	AGACCTAAAA	CAACAGATT	CTTACTTGCC	TTAAACCTAG	AGGCCAGAAG	720
	AACCCCGCAG	TGCTCTCTGG	CAGGAGCCTG	CTTGTGCGTA	GTTGTGTGTC	ATGAGTGTGG	780
	ATGGGTGCTT	GTGGGTGTTT	TTAGACACCA	GAGAAACAC	AGTCTCTGCT	AGAGAGCACT	840
65	CCCTATTTTG	TAAACATATC	TGCTTTAATG	GGGATGTACC	AGAAACCCAC	CTCACCCCGG	900
	CTCACATCTA	AAGGGGCGGG	GCGGTGGTCT	GGTCTGACT	TTGTGTTTTT	GTGCCCTCCT	960
	GGGGACCCAG	ATCTCTCTTC	GGAATGAATG	TTATGGAAG	AGGCTCCTCT	GAGGGCAAGA	1020
	GACCTGTGTT	AGTGTCTGAT	TGCACATGGA	AAAGTCTTTT	TAACTGTGTC	TTGCATCCTC	1080
	CTTCTCTCCT	CCTCTCTACA	ATCCATCTCT	TCTTAAGTTG	ATAGTGACTA	TGTCAGTCTA	1140
70	ATCTCTGTTT	TGCCAAGGTT	CCTAAATTAA	TTCATTTAAC	CATGATGCAA	ATGTTTTTCA	1200
	TTTTGTGAAG	ACCTTCCAGA	CTCTGGGAGA	GGCTGGTGTG	GGCAAGGACA	AGCAGGATAG	1260
	TGAGTGAGAA	AAGGGAGGGT	GGAGGTGAG	GCCAAATCAG	GTCACGACAA	AGTCAGTAGG	1320
	GACATTGACG	AGCTTTGAAA	GGCCAATACC	AGAACACAGG	CTGATGCTTC	TGAGAAAGTC	1380
	TTTTCTAGT	ATTAAACAGA	ACCCAAGTGA	ACAGAGGAGA	AATGAGATTG	CCAGAAAGTG	1440
75	ATTAACTTTG	GCGGTGTCAA	TCTGCTCAA	CCTAACACCA	AAGTGAAGAA	ATAAATACTG	1500
	ACCACTCTTA	TGTTGGGACC	CAAGCAAGTT	AGCTAAACCA	AACCAACTCC	TCTGCTTTGT	1560
	CCCTCAGGTG	GAAAGAGAG	GTAAGTTAGA	ACTCTCTGCA	TAGGGGTGGG	AATTAATCAA	1620
	AAACCKCAGA	GCTCGAATT	CCTAATACCT	TTCTTTATC	GTGGTTATAG	TCAGCTCATT	1680
	TCCATTCCAC	TATTTCCCAT	AATGCTTCTG	AGAGCCACTA	ACTTGATTGA	TAAAGATCCT	1740
80	GCCTCTGCTG	AGTGTACCTG	ACAGTAAGTC	TAAAGATGAR	AGAGTTTAGG	GACTACTCTG	1800
	TTTTAGCAAG	ARATATTKTG	GGGGTCTTTT	TGTTTAACT	ATTGTGAGGA	GATTGGGCTA	1860
	RAGAGAAAG	CAGCAGAGTA	AGGAAATAAA	GGGATTGCC	TCTGGCTAGA	GAGTAAGTTA	1920
	GGTGTAAATA	CTGTGTAGAA	ATGTAAGGGA	TATGACCTCC	CTTCTTTAT	GTGCTCACTG	1980
	AGGATCTGAG	GGGACCTGT	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCACTCTG	2040
	CTACTGGTTG	GATGACATA	ACTATTGTAA	CTATTGAGTA	TTTACTGGTA	GGCACTGTCC	2100



5 TCTGATTAAA CTTGGCCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160  
 AGGGTGGGTG AACTTTATTG TACTTTGGAT TTGGTTAACC TGTTTTCTTC AAGCCTGAGG 2220  
 TTTTATATAC AAATCCCTCG AATACTCTTT TTGCCTTGTA TCTTCTCAGC CTCTTAGCCA 2280  
 AGTCCTATGT AATATGGAAA ACAAACTG CAGACTTGAG ATTCACTGCG CGATCAAGGC 2340  
 TCTGGCATTG AGAGAACCCT TGCAACTCGA GAAGCTGTTT TTATTTGGTT TTTGTTTTGA 2400  
 TCCAGTGCTC TCCCATCTAA CAACTAAACA GGAGCCATTT CAAGCCGGGA GATATTTTAA 2460  
 ACACCCAAAA TGTGGGTCT GATTTTCAAA CTTTAAACT CACTACTGAT GATTCTCAGC 2520  
 CTAGGCGAAT TTGTCCAAAC ACATAGTGTG TGTGTTTTGT ATACACTGTA TGACCCCAAC 2580  
 10 CCAAATCTTT GTATTGTCCA CATTCTCCA CAATAAAGCA CAGAGTGGAT TTAATTAAGC 2640  
 ACACAAATGC TAAGGCAGAA TTTTGAGGGT GGGAGAGAAG AAAAGGGAAA GAAGCTGAAA 2700  
 ATGTAAACCC ACACCAAGGA GGAATAATGA CATTCAAGAC CAGCAACAC TGAATTTCTC 2760  
 TTGTTGTTTT AACTCTGGCA CAAGAATGCA ATTTGTTAA TGGAGATGAC TTAAGTTGGC 2820  
 AGCAGTAATC TTTCTTAGG AGCTTGTAAC ACAGTCTTGC ACATAAGTGC AGATTGGCT 2880  
 CAAGTAAAGA GAATTTCTCT AACACTAACT TCACTGGGAT AATCAGCAGC GTAATACCC 2940  
 15 TAAAGCATA TCACTAGCCA AAGAGGGAAA TATCTGTCT TCTTACTGTG CCTATATTAA 3000  
 GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTCAATGAA AATGCCATAT CTATACCAT 3060  
 TTTTATTCGA GTCACTGTGT ATGTAATGAT ATATTTTTC ATTATTATAG TAGAATATT 3120  
 TTATGGCAAG ATATTGTGG TCTTGATCAT ACCTATTAAA ATAAAGCCAA ACACCAATA 3180  
 TGAATTTAT GATGTACACT TTGTGCTTGG CATTAAAAGA AAAAACAACA CATCTGGAA 3240  
 20 GTCTGTAAGT TGTGTTTTGT TACTGTAGGT CTTCAAAGTT AAGAGTGTAA GTGAAAATC 3300  
 TGGAGAGAGG GATAATTTCC ACTGTGTGGA ATGTGAATAG TTAATGAAA AGTTATGGTT 3360  
 ATTTAATGTA ATATTACTT CAAATCCTTT GGTCACTGTG ATTTCAAGCA TGTTTCTTT 3420  
 TTCTCCTTTA TTGACTTTT TCTGAGTTGG GCAAGAAGA AGCTGACACA CCGTATGTTG 3480  
 25 TTAGAGTCTT TTATCTGGT AGGGGAAACA AAATCTTGAC CCAGCTGAAC ATGCTCTTCT 3540  
 GAGTCAGTGC CTGAATCTTT ATTTTTTAAA TGAATGTTT CTTAAAGTTT AACATTCTA 3600  
 AAGCAATATT AAGAAGAGCT TTAATGTTA TTTTGAAGA CTTACGATGC ATGTATACAA 3660  
 ACGAATAGCA GATAATGAT ACTAGTTTAC ACATAAAGTC CTTTAAAGGA GAAATCTAA 3720  
 AATGAAAGT GGAATAACAG AACATTTATA AGTGATCAGT TAATGCCTAA GAGTGAAGT 3780  
 30 AGTTCTATTG ACATTCCTCA AGATATTATA TATCAACTGC ATTATGTATT ATGCTCTGCT 3840  
 AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG 3900  
 ATGAAGGGGG AGTTGATAGT CTCATAAAAC TAATTTGGCT TCAAGTTTCA TGAATCTGTA 3960  
 ACTAGAATT AATTTTCAAC CCAATAATGT TCTATATAGC CTTTGTCTAA GAGCAACTAA 4020  
 TAAATTAAC CTATCTTTT AAAAAAAA

35 Seq ID NO: 164 Protein sequence  
 Protein Accession #: NP\_037504.1

40 1 11 21 31 41 51  
 MSRTAYTVGA LLLLLGLLP AAEKKKKGSQ GAIPPPDKAQ HNDSEQTQSP QQPGSRNRGR 60  
 GQGRGTAMPG EEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120  
 QCNFPYIPRH IRKEEGSFQS CSFCKPKKFT TMMVTLCNPE LQPTTKKRV TRVKQCRGIS 180  
 IDLD

45 Seq ID NO: 165 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

50 1 11 21 31 41 51  
 GAATGCAATC GGACAGAGCT TGGCCATGGC CGAGTTGGCG GTGGTTGTGG CACTAACACT 60  
 GCTACGTTTC CGCCTGAGCG TGGACCGAAC GCGCAAGGTG CGGCGGAAGC CGGAGCTCAT 120  
 ACTGCGCAGC GAGAACGGGC TCTGGCTCAA G

55 Seq ID NO: 166 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1650

60 1 11 21 31 41 51  
 ATGCCACCTC TGCCATCCAG AATGTCTCGG GGGCCCTCCT TGGTGACAGG CAGGATGCTG 60  
 CCCATCACAG ACCGCTGTGT GCACCTCCTG GGGCTGGAGA AGACGGCGTT CCGCATATAC 120  
 GCGGTGTCCA CCGTCTCTCT CTCTCTGCTC TTCTTCTGT TCGCTCTGCT GCTGCGGTTC 180  
 65 CTGAGGCTCT GCAGGAGGCT CTACATCACC TGCGCGCGCG TGCGCTGCTT CCGCCAGCCT 240  
 CCGCGCGCCA ACTGGCTGCT GGGCCACCTG GGCATGTACC TTCCAAATGA GCGGGGCTT 300  
 CAAGATGAGA AGAAGGTACT GGACAACATG CACCATGTAC TCTTGTATG GATGGGACCT 360  
 GTCTGTCCGC TGTGTGTTCT GGTGCACCTT GATTACATCA AACCCCTTTT GGGAGCTCA 420  
 GCTGCCATCG CCGCCAAAGG TGACCTCTTC TATGGCTTCC TAAACCTTG GCTAGGGGAT 480  
 GGGCTGTCTG TCAGCAAGG TGACAAGTGG AGCGGCACC GTGCGCTGCT GACACCGGCC 540  
 70 TTCCACTTGG ACATCCTGAA GCCTTACATG AAGATCTTCA ACCAGAGCGC TGACATTATG 600  
 CATGCTAAAT GCGCGCATCT GGCAGAGGGC TCAGCGGTCT CCGTGTATAT GTTTGAGCAT 660  
 ATCAGCCTCA TGACCTTGA CAGTCTTCA AATGTGTCT TCAGCTACAA CAGCAACTGC 720  
 CAAGAGAAGA TGAGTGATTA TATCTCGCT ATCATGAAC TGAGCGCTCT GTCTGTCCGG 780  
 75 CGCCAGTCTT GCTTGCACCA CTACCTCGAC TTCACTTACT ACGCTCTGCG GGATGGGCGG 840  
 AGGTTCGCGC AGGCTGTGTA CATGGTGAC CACTTCACCA CTGAAGTCAT CCAGGAACGG 900  
 CGGCGGGCAC TGGCTGAGCA GGGGGCGGAG GCCTGGCTTA AGGCCAAGCA GGGGAAGACC 960  
 TTGACTTTTA TTGATGTGCT GCTCCTGGCC AGGGATGAAG ATGGAAGGA ACTGTGAGAC 1020  
 GAGGATATCC GAGCGAAGC AGACACCTTC ATGTTTGAGG GTCAAGCAC AACATCCAGT 1080  
 80 GGGATCTCTT GGGATCTGTT CAATTTGGCA AAGTATCCGG AATACAGGA GAAATCCGA 1140  
 GAAGAGATTC AGGAAGTCAT GAAAGGCCGG GAGCTGGAGG AGCTGGAGTG GGACGATCTG 1200  
 ACTCAGCTGC CCTTTACAACT TATGTGCATT AAGGAGAGCC TGGCCAGTA CCCACCTGTC 1260  
 ACTCTGTGCT CTCGCCAATG CACGGAGGAC ATCAAGCTCC CAGATGGGCG CATCATCCCC 1320  
 AAAGGAATCA TCTGCTGGT CAGCATCTAT GGAACCCACC ACAACCCAC AGTGTGGCCT 1380  
 GACTCCAAGG TGTACAACCC CTACCGCTTT GACCCGACA ACCACAGCA GCGCTCTCCA 1440

CTGGCCTATG TGCCCTTCTC TGCAGGACCC AGGAATTGCA TCGGACAGAG CTTGGCCATG 1500  
 GCCGAGTTGC GCGTGGTGTG GGCACCTAACA CTGCTACGTT TCCGCTGAG CGTGGACCGA 1560  
 ACGCGCAAGG TGCGGCGGAA GCCGGAGCTC ATACTGCGCA CGGAGAACGG GCTCTGGCTC 1620  
 AAGGTGGAGC CGCTGCTCC GCGGGCCTGA

Seq ID NO: 167 Protein sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 MPPLPSRMSR GPSLVTRML PITDRLLHLL GLEKTAFRYI AVSTLLLFLL FFLFRLLLRP 60  
 LRLCRSFYIT CRRRLCFPPQ PRRNWLGLHL GMYLPNEAGL QDEKKVLDNM HHVLLVMMGP 120  
 VLPLLVLEVP DYIKPLLGAS AAIAPKDDLF YGFLKPWLG D LLLSKGDKW SRHRRLLTPA 180  
 PHFDILKPYM KIFNQSDIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240  
 QEKMSDYISA IIELSALSVR RQYRLHHYLD FIYRSADGR RFRQACDMVE HFTTEVIQER 300  
 RRALRQQGAE AWLKAQKQKT LDFIDVLLLA RDEDGKELSD EDIRAEADTF MFEGHDTTSS 360  
 GISWMLFNLA KYPEYQEKCR EEIQEVMKGR ELELEWDDL TQLPFTTMC I KESLRQYPPV 420  
 TLVSRQCTED IKLPDGR IIP KGIICLVSIY GTHHNPTVWF DSKVYNPYRF DPDNPQQRSP 480  
 LAYVPFSAGP RNCIGQS FPM AELRVVVALT LLRFRLSVDR TRKVRKPEL ILRTENGLML 540  
 KVEPLPPRA

Seq ID NO: 168 DNA sequence  
 Nucleic Acid Accession #: AK058088.1  
 Coding sequence: 252..1772

1 11 21 31 41 51  
 AGGAAACCAA GGCAAGCTCC CCCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60  
 GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCC AGCTCTCTG 120  
 TAACTCAGAG GCCAGTGTGA TGGGAGTTC TCCACTCAGC ACACCTCCCC TGTAAACACG 180  
 CCTGTGGTGG GCAAAGGGC TTTGGAACGG TTGCTTGTCT TTTCTCTCCT GCGTAATTTT 240  
 CACTTTTATT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAACGC CGGGTCACTG 300  
 GCTCAACCAA CCGGTGGGCT TTGCCCAAAC AGCCTTCTCT TGGGGACCTG CTCTCACTTT 360  
 CCGAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420  
 TATGCAATTC ACAATCCAG AAGTTTCTCT TTGAGAATTT CAAGAACAAG GACATCCAAA 480  
 GTGGGGAAGC AGATGTGATT CTCGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540  
 GGCTTTTTC GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA 600  
 CACACCCCTT GAGGGAGCTG GAGGAGCTTC TGCGAGCTCA ATCCTTAAG AAGACCAAGG 660  
 AAAAAATCCC TGCAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGCTCACTA 720  
 AAGTCGCTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780  
 AAGACCTACT GGGAGTGCTG GCTTCCGCCC ACATCTCTCA GTTCAGTGGC CTGTTTCAAA 840  
 GGTGCGTGGA TGGATGATA GCGAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900  
 CCGGCTGCAA GTACAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATGA 960  
 ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACCTGTCC 1020  
 ACAAGTGCT GAAGTCCCC AGGTATTATTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080  
 TGCTTTTGTG GGTCTCTCTG CAACTGAAT ACAAGATTCA GGCAATTCG ACTTATGAAA 1140  
 CCGTGATGAC ATTTTTAAAG AGCTTTCCTG AGAAGTGTG CTTTCTGGAC CGGGACATAG 1200  
 GACGAGCTT GAGGCGCTC TTCCTCTGCT TGCGCTGCA CGGCATCACC AAGGCAAGG 1260  
 ATCTGGAGGT GCTGCGGCAC CTTAACCTCT TCCAGAGTC ATGGCTCGAC CAGGTTACAG 1320  
 TCAACCATTA CCACGCACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380  
 CCCAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAACCTAT TCGAAAACGA 1440  
 TTGCTCTATA TGGATTCTTC TTTAAGATAA AGGGACTCAA ACATGATACT ACCTCTTATA 1500  
 GTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGAGC 1560  
 ACAACCACT CAGCCTGCGA CGGCAACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620  
 TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACCAAGT CAAGCAGAAG TTTGGGTGA 1680  
 CCACGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG 1740  
 TAAGTTTGGC ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800  
 CCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC

Seq ID NO: 169 Protein sequence  
 Protein Accession #: BAB71658.1

1 11 21 31 41 51  
 MIMSNTHKAR LERVRTGSTN RWRLPKPPFS GDLLSLSQMC KALSIDPEEA LRNPDRLCIS 60  
 QIQKFFFEFEN KNKDIOGSEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQGTHPL 120  
 RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180  
 GVLASAHILQ FSGLFQRCVD VMIAKLKPSI IKQFYAGCK YKEBQLTTCG EKWLEMLNLP 240  
 LGGTQIHLHK IPQDLHLKVL KSPRLFTFSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300  
 FPKSPENCCE FLDRDIGRSL RPLFLCLRHL GITKGDLEV LRHLNFFPES WLDQVTNHY 360  
 HALENGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFPKIKGLK HDTTSYSFYM 420  
 QRIKHTDLES PSAVYEHNHV SLRAARLVKY EIRAEALVDG KMQEFTNQT KQKFGLTSS 480  
 CKSETLKIGT VGIPIVVFA PIPPAS

Seq ID NO: 170 DNA sequence  
 Nucleic Acid Accession #: NM\_007000.1  
 Coding sequence: 1...777

1 11 21 31 41 51  
 ATGGCGTCTG CGGCAGCAGC GGAGGCCGAG AAGGGATCTC CAGTTGTGGT GGGCCTGCTA 60  
 GTTGTGGGCA ATATCATTTAT TCTGCTGTCA GGCTGTCTCC TGTGTGCTGA GACCATATGG 120  
 GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180  
 TTGCTGTGGT CCGTGAATGC CATCTTCTGC GGCTCTCTCT TCTCATGGT AGCCAGTTTT 240

5  
10  
15  
20

```

GGTGTGGGTG CCGCACTCTG CCGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300
CTCATCGTCT ACATCTTCGA GTGCGCCTCC TGATCACAGT CCTACACCCA CCGTGACTAC 360
ATGGTGTCCA ACCCATCCCT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC 420
GACCAGGGCC AGGAGCTGAC CGGCCTCTGG GACCGGCTCA TGATTGAGCA AGAATGCTGT 480
GGCAGATCTG GTCCCATGGA CTGGGTGAAC TTCACGTCAG CCTTCCGGGC GGCCACTCCG 540
GAGGTGGTGT TCCCTTGCCC CCCACTGTGC TGTGCGCGGA OGGGAAACTT CATCCCCCTC 600
AAGAGGAGGG GCTGCCGCCT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660
CAGATCGGCC ACGCCATCGA CAGTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC 720
CTGATGTGGA CGTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA

```

Seq ID NO: 171 Protein sequence  
Protein Accession #: NP\_008931.1

15  
20

```

1 11 21 31 41 51
MASAAAAEAE KGSFVVVGLL VVGNIIILLS GLSLFAETIN VTADQYRVYP LMGVSGKDDV 60
PAGAMIAIFC GPSFFMVASF GVGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY 120
MVSNSPLITK QMLTFYSADT DQGELTRLW DRVMIEQECG GTSGPMDWVN FTSAFRAATP 180
EVVFPWPLC CRRTGNFIPL NEEGCRLGHM DYLFTKGCFE HIGHAIDSYT WGISWFGFAI 240
LMWTLFVMLI AMFYFTML

```

Seq ID NO: 172 DNA sequence  
Nucleic Acid Accession #: NM\_006760.1  
Coding sequence: 39..593

25  
30  
35  
40  
45

```

1 11 21 31 41 51
GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCAGCAT GGCACCCCTG CTGCCCATCC 60
GGACCTTGCC CTGTATCTGT ATTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA 120
ACATCTCAAG CCTCTCTGGT CTGTGTGTCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCCT 180
TGCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGGAGA GCCAATGACA 240
GCAAAAGTGT GACGTCCAGC TTTGTGGTGC TCCTCGTCCG TGGGCGCAGG GAACCTGGTGA 300
GTGTGGTGGG CAGTGGTGTCT GGCTTCACAG TCACTCGGCT CAGTGATATC CAGGTGACAA 360
ACCTCGTGCC AGGAACCAAA TTCTACATT CTACCTAGT GAAGAAGGGG ACAGCCACTG 420
AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC 480
TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTGCCCATGT 540
TCTGTCTGCT GCTGGGCTTC ATCATTGCCG TGGCACTGGG CTCCCGCAAG TAAGGAGGTC 600
TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACA TCCAGCTCCC CAGCCACCT 660
GCTCCAGGC CCCAGGCTGT TGGCTCCCTT GGTGCCCTCG CCTCTCTCTC CTGCCCTCCT 720
CTCCCTAGA GCCCTCTCCT CCCTCTGTCC CTCTCCTTGC CCCAGTGCC TCACCTTCCA 780
ACACTCCATT ATTCTCTCA CCCCCTCTCT GTCCAGATTG ACTTCTCTCC CATTTTACCA 840
CTTTAAACAC CCCATAACA ATTCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900
GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

```

Seq ID NO: 173 Protein sequence  
Protein Accession #: NP\_006751.1

50  
55

```

1 11 21 31 41 51
MAPLLPIRTL FLILLILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL 60
MVRRANDSKV VTSSFVPPC RGRRELVSIV DSGAGFTVTR LSAYQVTLNV PGTKFYISYL 120
VKKGTALESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLL VLGFIIALAL 180
GSRK

```

Seq ID NO: 174 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2733

60  
65  
70  
75  
80

```

1 11 21 31 41 51
ATGAAAGTTG GAGTGTCTGT GCTCATTCTT TTCTTCACT TCACTGACGG CCACGGTGGC 60
TTCTGGGGGA AAAATGATGG CATCAAAACA AAAAAAGAAC TCATTGTGAA TAAGAAAAAA 120
CATCTAGGCC CAGTCGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTCCAAG 180
GAGAAAAAGG ATTTGAGAAA TTTTCTGAAG CTCTTGAAGC CTCCATTATT ATGGTCACAT 240
GGGCTAATTA GAATTATCAG AGCAAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC 300
CTGCAGTGTA CTTGTGAAGA CAGCTACACC TGGTTTCCTC CCTCATGCTT TGATCCCCAG 360
AACTGCTACC TTCACACGGC TGGAGCACTC CCAAGCTGTG AATGTCACTT CAACAACCTC 420
AGCCAGAGTG TCAATTTCTG TGAGAGAACA AAGATTGGG GCACTTTCAA AATTAATGAA 480
AGGTTTACAA ATGACCTTTT GAATTCACT TCTGCTATAT ACTCCAAATA TGCAAAATGA 540
ATTGAAATTC AACTTAAAAA AGCATATGAA AGAATTCAG GTTTTGAGTC GGTTCAGGTC 600
ACCCAATTTC GAAATGGAAG CATCGTGTCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA 660
TCTGAACGTC TGTACGCCAT TGAACATGTT GCGGAGAAGG CTAAGACAGC CCTTCACAAG 720
GTGTTTCCAT TAGAAGACGG CTCTTTCAGA GTGTTGGGAA AAGCCAGTGT TAATGACATT 780
GTCTTTGGAT TGGGTCCAA GGATGATGAA TATACCTGCG CCTGCAGCAG TGGCTACAGG 840
GGAAACATCA CAGCCAAGTG TGAGTCTCTT GGGTGGCAGG TCATCAGGGA GACTTGTGTG 900
CTCTCTCTGC TTGAAGAACT GAACAGAAT TTCAGTATGA TTGTAGGCAA TGCCACTGAG 960
GCAGCTGTGT CATCTCTTGT GCAAAATCTT TCTGTATCA TCGGCAAAA OCCATCAACC 1020
ACAGTGGGGA ATCTGGCTTC GGTGGTGTCT ATTCTGAGCA ATATTTTCAT TCTGTCACTG 1080
GCCAGCCATT TCAGGGGTGC CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT 1140
ATCCTTAATT CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGGGGGAAGA AAAGTATGCC 1200
AGCTCAGGCT TACTAGAGAC ATTGAAAAAC ATCAGCACTC TGGTGCTCC GACAGCTCTT 1260
CCTCTGAATT TTCTCGGAAA ATTCATTGAC TGGAAAGGGA TTCAGTGAA CAAAAGCCAA 1320
CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTCCCATC 1380
AGAGGCCGTG TGTTAATTGG GTCAGACCAA TTCAGAGAT CCCTTCAGA AACTATTATC 1440

```

	AGCATGGCCT	CGTTGACTCT	GGGGAACATT	CTACCCGTTT	CCAAAAATGG	AAATGCTCAG	1500
	GTCAATGGAC	CTGTGATATC	CACGGTTATT	CAAACTATT	CCATAAATGA	AGTTTTCTCA	1560
	TTTTTTTCCA	AGATAGAGTC	AAACCTGAGC	CAGCCTCATT	GTGTGTTTGT	GGATTTCAGT	1620
5	CATTGTGAGT	GGAGAGATGC	AGGCTGCCAC	CTAGTGAATG	AAACTCAGA	CATCGTGAGC	1680
	TGCCAATGTA	CTCACTTGAC	CTCCTTCTCC	ATATTGATGT	CACCTTTTGT	CCCTCTACAC	1740
	ATCTTCCCGG	TTGTAAAATG	GATCACCTAT	GTGGGACTGG	GTATCTCCAT	TGGAAGTCTC	1800
	ATTTTATGCC	TGATCATCGA	GGCTTTGTTT	TGGAAGCAGA	TTAAAAAAG	CCAAACCTCT	1860
	CACACAGTGC	GTATTGTCAT	GGTGAACATA	GCCCTGTCCC	TCTTGATTGC	TGATGTCTGG	1920
10	TTTATTGTTG	GTGCCACAGT	GGACACACAG	GTGAACCCCT	CTGGAGTCTG	CACAGCTGCT	1980
	GTGTTCTTTA	CACACTTCTT	CTACCTCTCT	TTGTTCTTCT	GGATGCTCAT	GCTTGGCATC	2040
	CTGCTGGCTT	ACCGGATCAT	CCTCGTGTTC	CATCACATGG	CCGACGATT	GATGATGGCT	2100
	GTGGGATTTC	GGCTGGGTTA	TGGGTGCCCT	CTCATTATAT	CTGTCAATAC	CATTGCTGTC	2160
	ACGCAACCTA	GCAATACCTA	CAAAAGGAAA	GATGTGTGTT	GGCTTAACCT	GTCCAATGGA	2220
15	AGCAAAACCA	TCCTGGCTTT	TGTTGTCCCT	GCACTGGCTA	TTGTGGCTGT	GAACCTCGTT	2280
	GTGGTGTGTC	TAGTCTCTAC	AAAGCTCTGG	AGGCGGACTG	TTGGGAAAG	ACTGAGTCGG	2340
	GATGACAAGG	CCACCATCAT	CCGCGTGGGG	AAGAGCCTCC	TCACTCTGAC	CCCTCTGCTA	2400
	GGGCTCACCT	GGGGCTTTGG	AATAGGAACA	ATAGTGGACA	GCCAGAATCT	GGCTTGGCAT	2460
	GTTATTTTGT	CTTACTCAAA	TGCATTCCAG	GGATTTTTAA	TCTTATGCTT	TGGAATACTC	2520
20	TTGGACAGTA	AGCTGGGACA	ACTTCTGTTC	AACAAGTTGT	CTGCCCTAAG	TTCTTGGGAG	2580
	CAAAACAGAA	AGCAAAACTC	ATCAGATTTA	TCTGCCAAAC	CCAAATTTCT	AAAGCCTTTC	2640
	AACCCACTGC	AAAAACAAGG	CCATTATGCA	TTTTCTCATA	CTGGAGATTC	CTCCGACAAAC	2700
	ATCATGCTAA	CTCAGTTTGT	CTCAAAATGAA	TAA			

Seq ID NO: 175 Protein sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
30	MKVGVLNLIS	FFTFDGHGG	FLGKNDGIKT	KKELIVNKKK	HLGPVEEYQL	LLQVITYRDSK	60
	EKRDLRNFLK	LLKPLLLWSH	GLIRIIRAKA	TTDCNSLNGV	LQCTCEDSYT	WFPPSCLDFQ	120
	NCYLHTAGAL	PSCECHLNLL	SQSVNFCERT	KIWGTFKINE	RFTNDLLNSS	SAIYSKYANG	180
	IEIQLKKAYE	RIQGFESVQV	TQFRNGSIVA	GVEVVGSSSA	SELLSAIEHV	AEKAKTALHK	240
	LFPLEDGSFR	VFGKAQCNDI	VFGFGSKDDE	YTLPCSSGYR	GNITAKCESS	GWQVIRETCV	300
35	LSLLEELNKN	FSMIVGNATE	AAVSSFVQNL	SVIIRQNPST	TVGNLASVVS	ILSNISSLSL	360
	ASHFRVSNST	MDVISIADN	ILNSASVTNW	TVLLREEKYA	SSRLLETLEN	ISTLVPPPTAL	420
	PLNFSRKFID	WKGIPVKNQS	LKRGYSYQIK	MCPQNTSIPI	RGRVLIGSDQ	QFRLPETII	480
	SMASLTILNI	LPVSKNGNAQ	VNGPVISTVI	QNYISINEVFL	FFSKIESNLS	QPHCFVWDFS	540
	HLQWNDAGCH	LVNETQDIVT	CQCTHLTSFS	ILMSPEVPST	IFPVVKWITY	VGLGISIGSL	600
40	ILCLYIEALF	WKQIKKSQTS	HTRRICMVNI	ALSLLIADWV	FIVGATVDIT	VNPSGVCTAA	660
	VFFTHFFYLS	LEFFWMLMGI	LLAYRIILVF	HHMAQLHMA	VGFCLGYGCP	LIISVITIAV	720
	TQPSNTYKRK	DVCMWNWSNG	SKPLLAFFVP	ALAIIVAVNFV	VLLLVLTCLW	RPTVGERLSR	780
	DDKATIIIRVG	KSLLLILPLL	GLTWGFGIGT	IVDSQNLAWH	VIFALLNAFQ	GFFILFCGIL	840
45	LDSKLRQLLP	NKLSALSSWK	QTEKQNSDDL	SAKPKFSKPF	NPLQNKHYA	FSHTGDSNDN	900
	IMLTQFVSNE						

Seq ID NO: 176 DNA sequence  
Nucleic Acid Accession #: AB035089.1  
Coding sequence: 9845..10219

	1	11	21	31	41	51	
50	GGGCATGCAG	CCATCGGGGA	AAATCCATAG	TGCAGATAAA	GCAAGGAGGA	AGAAGAAGGA	60
	CAGTTCAGT	AAAAAGGAGA	ACATCAATAT	AGGATGTTTC	TTAGCAATAG	AAAAGAAGGG	120
55	CCAAGAGGAA	TTAGGAGAG	AGTTATAAGA	GATCAGCAAG	GGGACAGGGT	TAGATTGGT	180
	TTGGTTTGAA	AGCATACAGT	AAATATGATG	CTGTCTCCCT	GCACTGTTGG	CAGAGTAGGA	240
	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACCTG	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	TTACTGGAGT	TGTTTTCCCT	CATGAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTCT	AGGTGTGTCA	ATGTATACAT	ATCTATATCT	420
60	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAA	480
	AATCTCTCCC	ACTAACCACT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACCTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GGTCCAGGAA	AATCTAGGAG	ATATTCTTTA	ACCAATCTAT	AAAGGCATTA	660
	GTAATGACAG	GATATTTTCT	GAAAGTGTAA	TTTCCCATTG	AGGAATTTGT	TTTAATTTCT	720
65	GGATTCTCTG	AGCCAAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTTGGA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCCTTT	CTAGCCTGTC	TATCACATGC	900
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAAT	GCCTGAAATG	ATTTCTCATT	TGAACCTCAT	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCTTTAAG	1020
70	TTCAACCTTC	AGGGCAAAAC	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATTTCTTT	1080
	CCATAGATTG	GTCCCTCTGA	ACCCCGGTTT	GTCTCAGCTT	GTTATCCTGT	TTTTTTCTTC	1140
	CCTCQATTCC	CAGGATGAGC	TTGTTGCTTC	TGTCCTATGA	GACATTAGAT	TCCTTTTCTT	1200
	TGGTACCCGA	GTAATATCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGATGCAG	ACTCAGCTGA	GAAGACCATT	AITCATTTTT	GGAATTTCTT	ATCTCAGATA	1320
75	TTTCTCTTTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTTAG	TCCATCAAGC	CCCCATTAGT	1380
	CTATTCCTCCG	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTTCAGA	GACTCAAAAC	1440
	ATATATATTT	ATACAGGAGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAATT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTCAG	1560
	CCTATGTGTT	TCTGGCACTT	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTG	ATGTGCTGAG	1620
80	AAAACAAACT	CACGGCTGGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TGGGGAGAAA	1680
	TGTGGAGAAA	TCAGAACTCT	ATTCAAGGTC	GGTTGGAATG	CACACTTGTG	CAGAATTCTA	1740
	TGAGAAAGAG	TCTGGCATTT	CCTCAAAATG	TTAACTCTGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCATTTCAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAACATCAT	TATTCATAAT	AGTAAAAGGA	TGGAACAAAC	ACAAATGTCC	1920
	ATCAACTTAT	GATTAAGAAA	AATCTGGTCT	ATTCTAGAAA	TGGAATATTA	TTGACCACAA	1980

	AAAAGGAATG ATGTACTGAT CCATGCAATG ATGTGGACAA ACCATGAAAA TAACACTAGA	2040
	TTAAAGAAGC CAGTCACAAA AGGACTTACT GTATGATTCC ATTTACCTGA AATGTTTGA	2100
	ATAGGCAAAAT CCATAGAAAAC AGGAGGTAGA TTCTCTGGTTT CCAGGGTCTC CAGGAAGGGA	2160
5	AGAATGAAGT ACAAGATTTC TTTTGGAGGT AGTGAAATTG TTGTGGAATG AGATCATGAT	2220
	GATGATAGCA CAACTTTGTG AATATAATAA AATCATTGAA TTGTACAGTT GAATTTATGG	2280
	TATATAAATT ATATGTTAAT AAAAAGGGGG TCCACAAAAC CCCCTCTCCCT GGCCACAGAC	2340
	TGTCAGGGAG ATATTGGATT AAATGGCCTT GGACAACAAC CCCCTCTCCCT GGCCACAGAC	2400
	ATTCTTCAGA TTACAGATA TTCCAGGGGA AACACTGGAA TGAGTCTGAA GCCAGGTGCT	2460
10	AAACAGAAGG ACCATTGAGA AATGTTGTGA TCCTGACAGG TCAAGCAATT TATTTTTCGG	2520
	CTTCATTTTT AAATGTAAAA TTAGAAAGCT GCCATTAAAA ATGGCCCGTC TGTITCAATT	2580
	GCCTCTCTCA GTGTGAGCCT GTTAACTCAA TGTTTGTAGT TGTITTCATG CTGCTGATAA	2640
	AAACATACCT GAGACTGGCA AGAAAAAGAG GTTTAATTGG GCTTAGAGTT CCACGTGATT	2700
	GGGGAGGCCT CAGAATCACA GTAGGAGGCA AAAGTTATTC TTACATGGTG GCTGCAAGAG	2760
15	AAGATGAGGA AGAAGCAAAA GAAGAAACCC CTGATAAAC CCATCGATCT CCTGAGGCTT	2820
	ATTAACATATC ATGAGAATAG CACAAGAAAG ACCGGCCCCC ATGATTCAAT TACCTCTACC	2880
	TGGGTCCCTC CAATAACATG TGGAAATTCCT GGTAGATACA ATTCAGTTGT AGATTGGGT	2940
	GGGAACACAG CCAAAACCATA TCACCTAGCA AGGCAGATAA CTTTCTCACT GAGCCTATGC	3000
	AACAGAAAAC CATCTGGGAT GGTGTGAAGG GGCACAGGAA GTGACTGGTA GGATCACTGC	3060
20	CAAAGCTGAG CACTCAGGAG AAGGCAATAG AATCCTATTC TCCATAGTAT GCTATAAGAT	3120
	ACTGAAGTAC ACTTCTCTAC TATCTCTTTG GACTTAGAAT TAGCACTACA TTCTTGTITA	3180
	TACAGAAAAA TTACTAAGGA AATTCATAGG ATGCAAAAAA CTTTCAGAAC TGAAAAACAG	3240
	GAAATGTAAG CTTTITAGTT CTTTGGTATT CGAAGTATGC CTAAAAAGACA ATGCAAAATC	3300
	CAAGAAAGA ATGGTGGGGT TTTTGTITGT TTGGTITGT TTTTGTITTA CAGCTGGAGT	3360
25	AGAATACAAA GGGATGGAGT TGAACAAAT GAGAGGAAAT TGGAAATCTA AACTTATTCT	3420
	CATTGGCATT AGAAGGCGAC CTACATGTAT TTCACATGAG CCGGTGACTG CTGACTTGCA	3480
	TTCTTATTTT TTCCCTATAG ATTAAGAAAGG AGGTACAATG GTAGAAGTGT AATCTGAAGT	3540
	TTTGTCTATA ATTTTCTAT TCATAAAGGT GAGTGTTAGC CCGCTTGTGA AATCTGAAGT	3600
	TGAGTAACTT CAAATACATA CCACAGAGGG AAAGGCAGCA AGAGGAGAGG CATAAATTTA	3660
30	GGATCTCACC CTTCATTCCA CAGACACACA CAGCCTCTCT GCCCACTCTT GCTTCTCTTA	3720
	GGAAACACAG TAAGAGCTTC AAGCCTCTCC AGCTTAATAA CATGAATTAT TTTTGAGAAT	3780
	AATAATGATA CTGTGTCTTA TATCATGCAT CTCTGTCATT CTGTCTGATT ATATTTTACT	3840
	TATCTGCCA GAGCAAAAT AAAATACCTA TTTTCTCTGA TTTTCTCTTT ATCTAAATTTG	3900
	CTTAGTCCA AGTAACACAA GGCATTTTGA GGAACACAGA GGGAGAGTGC CTTGCAGCCA	3960
35	GAGAGTCTTG AAGGAGATGT CAGGGACGCA TCTTAACAGC TGTTTGGATG TGATCCACAG	4020
	AGGTCTCTCG TTAGCATTTA TTGTAAGCC ATCCTACCTA GCTCTAGTGT AACCAGCAAT	4080
	GAAAGAAAGA TAAAGAGGGT CGATTACTTA TTTACAATAG TCTTTAAAAA CGTAGTTTGT	4140
	TAAGCCTTCT AATTAGGACA TTAATATATT TAATATATGC ACATTGTAGA AAGATTGAAG	4200
	CGTTAAAAAT AAGAGAAAAA CTTTAAATGT CAAATCTCA CAACCCAGAT ATATCATTTT	4260
40	TTTAAGAAAA TTGACTACA AATACCAT CCAATTATTA AAGTCATTCT GACAGGAATC	4320
	TGATGCTTTT CCAGGAGTTC CAGATCACAT CGAGTTCACC ATGAATTCAC TCAGTGAAGC	4380
	CAACACCAAG TTCATGTTGG ATCTGTTCCA ACAGTTCAGA AAATCAAAAG AGAACAACAT	4440
	CTTCTATTCC CCTATCAGCA TCACATCAGC ATTAGGGATG GTCCTCTTAG GAGCCAAAGA	4500
	CAACACTGCA CAACAAATTA GCAAGGTAGC TATCAGCATC ATTACGTTGT CCTGTTGCAG	4560
45	TTTTTCTCTG GTTCCGTCGG CTAGCAGGCA GATGTTAATA GATGTGGTGG TCTGATGGGT	4620
	AGCACAGGGG GCTGTGCGAG AATCCCATA ACTGTGAGAC CACTGACTTA AACAGATCTT	4680
	TTGAGTAAAG TTTTCTTGTG CCGCTTCTAG TCTCTTCCAG GTTCTTCACT TTGATCAAGT	4740
	CACAGAGAAC ACCACAGAAA AAGCTGCAAC ATATCATGTG AGTCACAGAG CACTCTGATT	4800
	CAGCTTTAGA TCCCTGAACA GGTCAATGTT TAAACCTGGA ACTTCACAAA AACTAAGAAA	4860
50	AGGCCAGTTT TAGGAAAAAT TTCTCTATTT CTGCGTTACT AAAAGACAGT CAGCACTGTA	4920
	TTTATGGCAC ATAAATTATTA TTCTCTATTT CTGCGTTACT AAAAGACAGT CAGCACTGTA	4980
	CCTCAGAGCA TAGGTCTGGA TCAGGATAGG CTGGGTTCCG ACTCCAGCTT TGCTCTTCA	5040
	AAATGATGAA TAAGAGCAGG ACACAACCTG CTGGAGTCCC AGTGACCTCA TCCCAGAAAA	5100
	CTAAGGTTAA GAAAAATCT GACTCAATAC ATGCATAATC ATGCATAATG TTACACACAGT	5160
55	GCCTTGCCCA TAAAGATGTT AATAAATGTT ATTATTATTA TAAAGTAGCT ATAATTATAC	5220
	TAATCATAT ATGTGAAAA TAATTTAATT TTCATTGAGT CATTATAGAG ATTACAGGGA	5280
	ATAAGCACA GTCCCAAGTAT ATTTTGGAAA ATGATTGCTA TGAATATAT TGGTTTAGAG	5340
	CCTTAATAGT GCAAAATGCT TTGCTGGAAG GTAGAAAGTT CTAGATTTAA ACAGGCTTAG	5400
	GTTCAAAACT TGGCACTTCT AATTATATGC TCTATAAACA GGGTTTTTTT CCCCATTCTC	5460
60	TGAGCTTCTT TGTGTTATC TGAATTGAAC TAAAGACTTA GAGTTACCCA TGTAAAGTCC	5520
	TTAGCCATGG ACCTGGCATA CACTCTTCTT ACGTGCAGAG AATGACCATC ATGAGGAAAG	5580
	AGCCACAGAT CAGTCAATGT GTCTTACAG ATAAATAGCAC CAACAGGTAT AACAGGGCTT	5640
	CCTGGCATAA TCTATTAAAA ATATCCAACC TTCAACATAC TCGTATCCTT GATGACTGTT	5700
	AGAAGTGAAA TATGGTCTT GCCCATAAGG AGCTGAGAGT TTAACCTGGA AGCTAAACCT	5760
65	AACCTTTAA ACCAACAGG AGAAAACTA CTGGTAGACA CCGCTGCATC TTTAGTTTCA	5820
	AAGAGAAAAG ATTGCAGTAC GTTAGAGCAA GAAGAATTTT CTGGAAGAAAG TCAATATAA	5880
	GGTGGATTTT GAAGGTATTT TGAGGTGAAA TACACCAATT ATCAGGGAAT AACATCAAG	5940
	GTCTTCAATG AGACTACCAG CATTTAGGGA CTGATCTAAC AGACTTAGCA TGGGTTTAGT	6000
	ATTTACATTG ATACAGCAAT TGAATGATCT CCTTTTTTGA TGTITGAAGG TTGATAGGTC	6060
70	AGGAATGTT CATCCAGT TTCAAAAGCT TCTGACTGAA TTCAACAAAT CCACGTATGC	6120
	ATATGAGCTG AAGATCGCCA ACAAGCTCTT CGGAGAAAAG ACGTATCAAT TTTTACAGGT	6180
	AAATTCACCT GGCCTACCCA CATTTCATTT GCATCTGAT GTCTGTGTCT CTGAGTGGCC	6240
	AAATGGAGGA AAGCAAGGCA GATGAGCCTG GCGGACCCAG GTGGAGAGCA TTTACTCAGA	6300
	GTGCATTAGC TCCATTTCOA CAACTCTCCC CCATCTGGAG GTCCACAGAC CCAACGATAC	6360
75	ATCACTGAAG TGTGGATTTA GGGATAATCT TGTGATAAAA GAGGAGGTTG TGTAAATAG	6420
	TGAGTAAAG TAATAAGTAA TAAGATACCA TCGATAAACT GGCAGTACT CAGTCACATA	6480
	CGATACATCT TGGTGGGAAA TGTATGACTA ATGGGATATT ATTGGAATGG CGAGGCTTGG	6540
	GTGAGTTCTT GAGAAATAGT GAGGAAGTAC CAGGAATAT TGAATGCACA GGATGAAAGA	6600
	CAAAACAAA GATCAGAAAC ATCATGGTTA AAATTTACTG AGAGAAGTCT GAGAGCAAT	6660
80	GAATCTCTCT CAGGGAAGCC TGCTCTGAG TTTGCAAAAC ACAGCTCTT CTGCTTCTG	6720
	CTTTTGGCAA GATGATATTG ACCTTCAGTG ACCTCTTCT TGTGCCAGCC CACATTCCTC	6780
	TTTTGCATTG CCTACATGAC ACCTGTATTA AAATATCCAT GGACAGGAGA TACTGCATCT	6840
	ATTCAGGGTC TGGATTGAGC TTACTGTTGT TACAATAAG TAAGTTTGGT AATATATAGT	6900
	TACATAAATT ACTCCTAATT CCTACTCTT CCTTCATATC TCAAGGAAT ATTTAGATGC	6960
	CATCAAGAAA TTTTACCAGA CCAGTGTGGA ATCTACTGAT TTTGCAAAAT CTCAGAGA	7020

5 AAGTCGAAAG AAGATTAACT CCTGGGTGGA AAGTCAAACG AATGGTAGGA GAGCCACCCA 7080  
 TTATAGAAAC ACCTTTGAGA AACCTATGCC AGTGAGCCTT GTGCTTGACA CTGCATGGGG 7140  
 GAACAGGTGT GGGGATTGAG ATGGGTTTGC AGGGAGGGCT GAAGAGGGCA CTCCAGATGA 7200  
 AGGATTGTGC CAAATGAATA TGAAGAGAGC CTAGGGGAGC CAAGGAGGAA ATCAGAGGAA 7260  
 10 GCCAATTAGA TGGAAACACA TCTGGAGAAT TATTTGCTTA TGGCCCTGCA TGACAATAGC 7320  
 TTTGTGGATC CCCTGTCTCC GCTCAGACCT ATTTTGAGAT CATATCCTTT ACTTTAAATC 7380  
 AGACTCAAAT TTTTATGATG AATATTTAAT AGAAAACATT AGAAAGCGTC TCTCGTCTCC 7440  
 TTTACTAATT GGGAAACAAG CAGCTCTCTG GTAAATCACC CTTTTGTCTC TGAGCTGGAG 7500  
 CTGCTGTGAT CACATCTGTA GCCAATGTGT TCTGCAGGGA TTATCAGACG TCTCTTCCCC 7560  
 15 ATCAAGGGCA AAGAGCTTGA CAAAGTCTCC ATTCTACAGA CATCTTTCTT ACCTCCCAAC 7620  
 TCTCATTACA GGCCAAACTT ACAGCAACTC AACATGAGAG TGAATAGGAA GATACCCCGG 7680  
 GAAGTAGTGT CTGACAGCAC AGSACATGCG TTTCATATTA CAGAGCTCAA GTCACTCATC 7740  
 CTAAAATGCA ATCAGGGCCT CCTTCTCTG AATGGGGACC CCGTAGTTAA AAAAAAATAA 7800  
 AAGTAGGAAG AGGAGGGAGG GAGAAAGGAA AGACACATGT TGGAAAGATA GACAAAATCA 7860  
 20 GTTTACTAGT TGTTCAAATC AGATGATTGG AGACATTCAT ACACAGAGAA CGTGAATCTC 7920  
 TTCTCTATCA CRAAGAAGTA TGTCTCCATC AAGGGTAACT TTATACGACT GGAGCCTTGA 7980  
 AGAAAGCTGC ATCTGGTGAA CCACGTGTCA GTGAGTCTAA CAATTCAAAG ATCAAAGTCA 8040  
 GTGAGTCTCA AGCAGGGATT TGGGTCAATA ATTAACGATC AGTCACGAAC ATTTGCAAAAG 8100  
 CATCTTCCAG ACAAGCCAAT TGTAGCTTGT GTAAAAGACT CTTTATTCTT TTCCCTTGCA 8160  
 25 GAAAAAATTA AAAAACTATT TCTGTATGGG ACTATTGGCA ATGATACGAC ACTGGTTCTT 8220  
 GTGAACGCAA TCTATTTCAA AGGGCAGTGG GAGAATAAAT TTAATAAAGA AAACAATAAA 8280  
 GAGGAAAAAT TTTGGCCAAA CAAGGTATTG TCTATATTTT ATTTATATAG TGTAAATATG 8340  
 TAATACATGG AATGTTAAAC ATTTCTGATG GAATGTAAAC TGATAAGTAA AAAAAAATAA 8400  
 TTGTTCAAGT CTGTATTTTT GTTGTTTTAC TCTTATAACT TTATTTAGTT AGGAATACCT 8460  
 30 GAAAAAATTA TGTTCCTAAT TCAATGGAAT CCTGGGTTAT TTCTTAGAAG AAGAAGGATG 8520  
 TGTGTCTATC TCAATAATAT TATCTTTTTT GTCTTGTGTT TCACGTGTTA TTTGTTGGAC 8580  
 ACATTTGATT ATTCGAGAAT ACATACAAAT CTGTACAGAT GATGAGGCAA TACAATCTCT 8640  
 TTAATTTTGC CTGCTGGAGG GATGTACAGG CCAAGGTCCT GGAATAACCA TACAAGGCA 8700  
 AAGATCTAAG CATGATTGTG CTGCTGCCAA ATGAAATCGA TGGTCTGCAG AAGGTAAAGAA 8760  
 35 CTGTCACTCA CAACCTCTCC TTCTACTGCC GGACATTTTT CCAAGATAC CAAGTTTAAA 8820  
 CAAGGTAAAA GCTTATGACC GAGTTGCCCT AAAATGATGA AAAATTCTAA ATGAGGAATG 8880  
 ATGACTCACC TTCAATTATC AAATATTGGA GCATAGGGCC TGACACAAAC TGAAGAGCTA 8940  
 GTTTTGTGTT GTTGTGTTGT TTTTATTATT ATTATTATAA TACTTTAAGC TTTAGGGTAC 9000  
 ATGTGCACAA TGTGAGGTTT AGTTACATAT GTATACATGT GCCATGCTGG TGTGCTGCAC 9060  
 40 CCATTAATCT GATTCTTATG GTTAGGTATA TCTCCTAATG CTATCCCTCC CCCCTCCCCC 9120  
 CACCCACAAA CAGTCTCTAG AGTGTGATGT TACCTTCTCG TGTCCAAGTG TTCTCATTTG 9180  
 TCAATTCCTA TCTATGATTT AATTCATCTT ATGGCTTAGT TAATGATTAA TTTATTAGAG 9240  
 TTACATGCTT TGGATATCAA TTTGATGATA TTATTATGCA GCAATTTAAA CTGACTGGG 9300  
 AGAAATATAT ACCAATGTGA GGAAGTTTAA CAAATAGGCC GAGTAGAAAA GGAATACAAA 9360  
 45 ATTTAGGAAT TAGGGGAATT ACAATTTAAT AATTGCAATG TGTACTAAAT AATGTATACA 9420  
 GAAAAATATG ATGAGCCTAT TAAAAATTGA CACATGTAGT AGGCTGTTGG CACAAGAAAT 9480  
 AGTGATACAT ACAGTTCATT GTGTACAAAA TAATGTAATC ATATTTTACA TGTGTATCAT 9540  
 ACAGTTGTTT ACATACATAT GTACACATAT ACATATACGT AAAAACATGA TTCTGTTTTT 9600  
 50 ACATACATGT ATATACATAT ACACATATAA CCCAATGTAT TTATATATTC AGGACTCTAT 9660  
 TTTTACCTAT TAGATAATA ATGTCTAATA AAGTGAACTC TCTGTATTTC ACATTTATTG 9720  
 CCAAAATAAC GAATCTCCAC ATAGTCAATT CATTGTTAAG GTGTATTAGA GATCGACAGT 9780  
 TAGTCATATC AGTTTCTTTT TTCCATTGTT ATAGCTTGAA GAGAAACTCA CTGCTGAGAA 9840  
 ATTGATGGAA TGGACAAGTT TGCAGAATAT GAGAGAGACA TGTGTGATTT TACACTTACC 9900  
 TCGGTTCAAA ATGGAAGAGA GCTATGACCT CAAGGACAGG TTGAGAACCA TGGGAATGGT 9960  
 55 GAATATCTCT AATGGGGATG CAGACCTCTC AGGCATGACC TGGAGCCACG GTCTCTCAGT 10020  
 ATCTAAAGTC CTACACAAGG CCTTTGTGGA GGTCACGTAG GAGGGAGTGG AAGCTGCAGC 10080  
 TGCCACCGCT GTAGTAGTAGT TCGAATTATC ATCTCCTTCA ACTAATGAAG AGTCTGTTG 10140  
 TAATCACCTT TTCTTATTCT TCATAAGGCA AAATAAGACC AACAGCATCC TTTCTATGG 10200  
 CAGATTCTCA TCCCATAGA TGCAATTAGT CTGTCACTCC ATTTAGAAAA TGTTCACCTA 10260  
 60 GAGGTGTTCT GGTAAACTGA TTGCTGGCAA CAACAGATTG TCTTGGCTCA TATTTCTTTT 10320  
 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTTA ATGATTAAAA TAGCATGCCT 10380  
 TTCTCTCTTT CTCTTAATAA GCCCACATAT AAATGTACTT TTCCTTCCAG AAAAATTTCC 10440  
 CTTGAGGAAA AATGTCCAGG ATAAGATGAA TCAATTAATA CCGTGTCTTC TAAATTTGAA 10500  
 ATATAATCT GTTCTGACCT TGTTTAAAT GAACCAAAAC AAATCATACT TTCTCTTCAA 10560  
 65 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620  
 GTTCTAAAT TTTGTGATTC TATAAACAC ATCATCAATA AAATAATGAC ATAAATCAT 10680  
 AATTTAGAGA TATATTAATC ATATATAAAG GAAATTAARA AACAGAGTAG TTCATGATGA 10740  
 GCCTGGAGTA GAAGGCATAT CCCAAGACAG GAGGAGCCTT GTAAACCACTA TAGGAACCTC 10800  
 70 CTATTTATG CTAAGGGAT AAGAACTCA TTACAGGCTT TGATGGTTGT TTGTCAAAGA 10860  
 GGGGCATAAA ATTATCATAT CCACATCTAG AAAATACATC TCTGGCTACG CTGATATCAA 10920  
 TGGATGCGAG GAAAGAACAG TGTGGTTACC ATATATAAAT TAGGAATCA TTAGAGTATT 11040  
 GGGAGTGGAA ATGGAGAGAA AGAAAGAGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100  
 AGAAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAAAGATA TCTTGTCTCT 11160  
 75 GAGAGAAAAA AAGACTTTGG GTTTAAATTT GTACTTGATG AATTAAGGTA CTTTAAATAT 11220  
 TCAAATGGAT TTGCTGSCA GGCACITGAA GATATTAGTC TAAATCTCAG AAACAGATA 11280  
 TGATCTGAAG CTCTAAATTT GTGATATTCA ATATAAATAC TTTAGAGTCA TTGGGATAAA 11340  
 TATGGTAGTT GTAGCTAAAA GCAAAAATAA GATACTAGGG AGAAAGGATA AAGTTAGAG 11400  
 AAAGAAGAAAT CTAGAAATGA CCTTGAAGTA TATCAGCATG TGAATAGATC AGGAATTGAT 11460  
 80 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTTACTCC CATAGATTCT 11520  
 TCCC

Seq ID NO: 177 Protein sequence  
 Protein Accession #: BAB21525.1

1 11 21 31 41 51 60 120  
 MNSLSEANTK FMFDLFQQFR KSKENNIFYS PISITSALGM VLLGAKONTA QQISKVLHFD  
 QVTENTTEKA ATYHVDRSGN VHQFQKLLT EPNKSTDAYE LKIANLKFGE KTYQFLQEYL

DAIKKFYQTS VESTDFANAP EESRKKINSW VESQTNEKIK NLFPDGTIGN DTLVLVNAI 180  
 YFKGQWENKF KKENTKEEFK WFNKNTYKSV QMRQYNSFN FALLEDVQAK VLEIPYKGD 240  
 LSMIVLLPNE IDGLQKLEK LTAEKLMWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300  
 TGMVNIIFNG DADLSGHTWS HGLSVSKVLH KAFVEVTEEG VAAAAATAV VVELSSPSTN 360  
 EEFCCNHPFL FFIQNKTN ILFYGRFSSP

Seq ID NO: 178 DNA sequence

Nucleic Acid Accession #: NM\_001910.1

Coding sequence: 50..1240

1 11 21 31 41 51  
 GGAGAGAAGA AAGGAGGGGG CAAGGGAGAA GCTGCTGGTC GGAATCACA TGAACACGCT 60  
 CCTCTCTTTG CTGCTGGTGC TCCTGGAGCT GGGAGAGGCC CAAGGATCCC TTCACAGGGT 120  
 GCCCCTCAGG AGGCATCCGT CCTCAAGAA GAAGCTGGCG GCAAGGAGCC AGCTCTCTGA 180  
 GTTCTGGAAA TCCCATTAAT TGGACATGAT CCAAGTTACC GAGTCTGCT CAATGGACCA 240  
 GAGTGCCAAG GAACCCCTCA TCACTACTT GGATATGGAA TACTTCGGCA CTATCTCCAT 300  
 TGGCTCCCA CCACAGAACT TCACTGTCT CTTCGACACT GGCTCTCCA ACCTCTGGGT 360  
 CCCCTCTGTG TACTGCACTA GCCCAGCCTG CAAGACGCAC AGCAGGTTCC AGCCTTCCCA 420  
 GTCCAGACA TACAGCCAGC CAGGTCAATC TTTCTCCATT CAGTATGGAA CCGGGAGCTT 480  
 GTCCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGGA CTACCGTGG TTGGCCAGCA 540  
 GTTTGGAGAA AGTGTCACAG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT 600  
 TCTGGGCTG CGATACCCCT CCTTGGCTGT GGGAGGAGTG ACTCCAGTAT TTGACAACT 660  
 GATGGCTCAG AACCTGGTGG ACTTGGCGAT GTTTCTGTCT TACATGAGCA GTAACCCAGA 720  
 AGGTGGTGG GGGAGCGAGC TGATTTTGG AGGCTAOCAC CACTCCCAT TCTCTGGGAG 780  
 CCTGAATTGG GTCCAGTCA CCAAGCAAGC TTAAGTGGAG ATTGCATGG ATAACTCCA 840  
 GGTGGGAGGC ACTGTTATGT TCTGCTCCGA GGGCTGCCAG GCCATTGTTG ACACAGGGAC 900  
 TTCCCTCATC TCCCTGCCCT CCGACAAGAT TAAGCAGCTG CAAACGCCCA TTGGGGCAGC 960  
 CCCCTGGAT GGAGAAATAT GTGTGGAGTG TGCCAACTTT AACGTCTATG CGGATGTCTC 1020  
 CTTCATTTCC AGAGAGTCTC CTATACCTC CAGCCCAACT GCCTACACCC TACTGGACTT 1080  
 CGTGGATGGA ATGCAGTTCT GCAGCAGTGG CTTTCAAGGA CTGACATCC ACCTCCAGC 1140  
 TGGGCCCTC TGGATCTCG GGGATGTCTT CATTGACAG TTTTACTCAG TCTTTGACCG 1200  
 TGGGAATAAC CGTGTGGGAC TGGCCCCAGC AGTCCCTTAA GGAGGGGCTT TGTGTCTGTG 1260  
 CCTGCTGCTC TGACAGACCT TGAATATGTT AGGCTGGGGC ATTCTTTACA CCTACAAAAA 1320  
 GTTATTTTCC AGAGATGTA GCTGTTTCCA GGGTTGCAAC TTGAATTAAG ACCAAACAGA 1380  
 ACATGAGAA ACACACACAC ACACACATAT ACACACACAC ACCTTCACA CATACACACC 1440  
 ACTCCACCA CGTCTATGAT GGAGGAATTA CGTTATACAT TCATATTTTG TATTGATTTT 1500  
 TGATTATGAA AATCAAAAAA TTTACATTTT GATTATGAAA ATCTCCAAAC ATATGCACAA 1560  
 GCAGAGTCA TGGTATAATA AATCCCTTTG CAACTCCACT CAGCCCTGAC AACCCATCCA 1620  
 CACACGGCCA GGCCTGTTTA TCTCACTGC TGCCCACTCC TCTCTCCAGC TCCACATGCT 1680  
 GTACCTGAT CATTTCTGAAG CAAATTCGA GCATTACATC ATTTTGTCCA TAAATATTTC 1740  
 TAACATCCTT AAATATACAA TCGGAATTC AAGCATCTCC ATTGTCCAC AAATGTTTGG 1800  
 CTGTTTGTG SLAVGGATG TTTGATTAG GATTCAAGCA AGGCCATAT ATTGCATTTA 1860  
 TTTGAAATGT CTGTAAGTCT CTTTCCATCT ACAGAGTTTA GCACATTGTA ACGTGTCTGG 1920  
 TTGAATGCC AGVCTGTGAT TTGACATGGT TCTCTGAAC TATCTTCTCT ATAAATAGT 1980  
 AGTTAGATCT GGAGGTCTGA TTTTGTGGCA AAAATACCTC CTAGGTGGTG CTGGGTACTT 2040  
 CTGTTGTCAT CTGTCTCAGA GGCAGATAAT GCTGGTGCCT CTCTATTGGT AATGTTAAGA 2100  
 CTGCTGGGTG GGTGTTGAGT TCTTGGCTTT AATCATTAT TACAAAGTTC AGCATTTT

Seq ID NO: 179 Protein sequence

Protein Accession #: NP\_001901.1

1 11 21 31 41 51  
 MKTLLLLLLL LLELGEAQQS LHRVPLRRHP SLKIKLRARS QLSEFWKSHN LDMIQFTESC 60  
 SMDQSAKEPL INVLDMNEYFG TISIGSPPON FTVIFDTGSS NLWVPSVYCT SPACKTHSRF 120  
 QPSQSSTYSQ PGQSFISIYQ TGSLSGIIGA DQVSVEGLTV VGGQFGEVST EPQQTFFVDAE 180  
 FDIILGLGYP SLAVGGATG TTTGATTAG GATTCAAGCA AGGCCATAT ATTGCATTTA 240  
 FGSLSNWVTV TKQAYQIAL DNIQVGGTVM PCSEGGCAIV DTGTSITLTP SDKIKQLQNA 300  
 IGAAPVDGEY AVECANLNVN PDVTFTINGV PYTLSPATY LLDFFVDMQF CSSGFQGLDI 360  
 HPPAGPLWIL GDVFIQRFYS VFDRGNRNVG LAPAVP

Seq ID NO: 180 DNA sequence

Nucleic Acid Accession #: NM\_018058.1

Coding sequence: 319..1575

1 11 21 31 41 51  
 TAAGCGCTGC GGGACCGGCA GGGGAACGCC ATCGGGGTCA CAGCCTGCGA CATCGACGGG 60  
 GACGGCCGGG AGGAGATCTA CTTCCTCAAC ACCAATAATG CCTTCTCGGG GGTGGCCACG 120  
 TACACCGACA AGTTGTTCAA GTTCCGCAAT AACCGGTGGG AAGACATCCT GAGCGATGAG 180  
 GTCAACGTGG CCCGTGGTGT GGCCAGCCTC TTTGCCGGAC GCTCTGTGGC CTGTGTGGAC 240  
 AGAAAGGGCT CTGAGAGCTA CTCTATCTAC ATTGCCAATT AGCCTACGG TAATGTGGGC 300  
 CCTGATGCCC TCATTGAAAT GGACCCCTGAG GCCAGTGACC TCTCCCGGG CATTCTGGCG 360  
 CTCAGAGATG TGGCTGCTGA GGCCTGGGTC AGCAAAATA CAGGGGGCGG AGGCGTCAGC 420  
 GTGGGGCCCA TCCTCAGCAG CAGTGCCTCG GATATCTTCT GCGACAATGA GAATGGGCTT 480  
 AACTTCTTTT TCCACAACCG GGGCGATGGC ACCTTTGTGG ACGCTGCGGC CAGTGTGGT 540  
 GTGAGCGACC CCCACGAGCA TGGGCGAGGT GTCCCGCTGG CTGACTTCAA CCGTGATGGC 600  
 AAAGTGGACA TCGTCTATGG CAACTGGAAT GGGCCCCACC GCCTCTATCT GCAAAATGAGC 660  
 ACCCATGGGA AGGTCCGCTT CCGGACATC GCCTCACCCA AGTTCTCCAT GCCCTCCCTC 720  
 GTCGCAACGG TCATCACCGC CGACTTTGAC AATGACCAGG AGCTGGAGAT CTCTTTCAAC 780  
 AACATTGCTT ACCGCGAGTC CTCAGCCAAC CGCTCTTCC GCGTCTATCC TAGAGAGCAC 840  
 GGAGACGCCC TCATCGAGGA GCTCAATCCC GCGACGCTT TGGAGCTGA GGGCGGGGC 900  
 ACAGGGGGTG TGGTAGCGCA CTTGACGGA GACGGGATGC TGGACCTCAT CTGTGCCAT 960

5 GGAGAGTCCA TGGCTCAGCC GCTGTCGGTC TTCCGGGGCA ATCAGGGCTT CAACAACAAC 1020  
 TGGCTGCGAG TGGTGCCACG CACCCGGGTT GGGGCCCTTG CCAGGGGAGC TAAGGTCTGT 1080  
 CTCTACACCA AGAAGAGTGG GGCCCACTG AGGATCATCG ACGGGGGCTC AGGCTACCTG 1140  
 TGTGAGATGG AGCCCGTGGC ACACCTTGGC CTGGGGGAAG ATGAAGCCAG CAGTGTGGAG 1200  
 10 GTGAGCTGGC CAGATGGCAA GATGGTGAGC CGGAACGTGG CCAGCGGGGA GATGAACCTA 1260  
 GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCAGC CCCACTGGAG 1320  
 ACACCAATGA ATGCATCCAG TTCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380  
 AACCTATGG AAGCTACAGG TGCCGGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA 1440  
 ACGAGGATGG CACAGCTGCG GTGGGGACTC TCGGCCAGTC ACCGGGCCCC GCGCCACCA 1500  
 15 CCCCACCGCG TGCTGCTGCC ACTGCCGCTG CTGCTGCCCG TGCTGGAGCT GCCACTGCTG 1560  
 CACCGGTCTT CGTAGATGGA GATCTCAATC TGGGGTCGGT GGTTAAGGAG AGCTGCGAGC 1620  
 CCACTGCTGT AGCAGGGGTG GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680  
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCTGGGAG CTAGACCCCTC 1740  
 20 CCCCAGCCCA TCCATGCACA TTACTTAGCT AACAAATAGG GAGACTCGTA AGGCCAGGCC 1800  
 CTGTGCTGGG CACATAGCTG TGATCAGAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860  
 ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCCAAGGA GGTGGTGTCA 1920  
 CTGCACAGGA AGTATGAGGA CTTTAGTGTG CTGAGTTCAA ATCCTGATTC AGGAACTCAC 1980  
 AAGCTATGG GACCTTACAC CAGTCACTTA ACTTGTTAGC CATCCATTAT CGCATCTGCA 2040  
 25 AAATGGGGAT TAAGAATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100  
 GACACTTGGC ACAAACCTTG GCACATAGTA AAGGCTCAAT AAAACAAGT GCCTCTCACT 2160  
 GGGCTTTGTC AACACGTG

Seq ID NO: 181 Protein sequence  
 Protein Accession #: NP\_060528.1

25 1 11 21 31 41 51  
 MDPEASDLR GILALRDVAE EAGVSKYTG RGVSVGPILS SSASDIFCDN ENGNFLFHN 60  
 30 RGDGTFVDAA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSHGKVR 120  
 FRDIASPKFS MPSPVRVTIT ADFDNDQELE IFFNNIAYRS SSANRLRVI RREHGDPLIE 180  
 ELNPGDALEP EGRGTGGVVT DFDGDMLDL ILSHGESMAQ PLSVFRGNQV FNNWLRVVP 240  
 RTRVGAFARG AKVVLVTKKS GAHLRIIDGG SGYLCMEPV AHFGLGKDEA SSVETWPDG 300  
 KMSVRNVASG ENNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALET SYPVSTPEAT 360  
 35 GAGPTRSAVG ATSPTRMAQP ANGLSASHRA PAPPPPLLL PLFLLPLLE LPLLRSS

Seq ID NO: 182 DNA sequence  
 Nucleic Acid Accession #: AJ279016  
 Coding sequence: 1..1962

40 1 11 21 31 41 51  
 ATGTCCAGGA TGTACCCTT CTTGCTGCTG CTCTGGTTTC TGCCCATCAC TGAGGGGTCC 60  
 CAGCGGGCTG AACCCATGTT CACTGCAGTC ACCAACTCAG TTCTGCCTCC TGACTATGAC 120  
 45 AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180  
 TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240  
 CAGAAGCGGC TGGTGAAACAT CGCGGTGATG GAGCGCAGCT CACCCCTACT CGCGCTGCGG 300  
 GACCGGCAGG GGAACGCCAT CGGGGTGACA GCGTGGGACA TGACCGGGGA CGGCGGGGAG 360  
 GAGATCTACT TCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG 420  
 50 TTGTTCAAGT TCCGCAATAA CCGGTGGGAA GACATCTGTA GCGATGAGGT CAACGTGGCC 480  
 CGTGGTGTGG CCAGCTCTTT TGCCGGACGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540  
 GAGCGCTACT CTATCTACAT TGCCAATTAC GCCTAAGGTA ATGTGGGGCC TGATGCCCTC 600  
 ATTGAATAG ACCTGAGGCG CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660  
 GCTGCTGAGG CTGGGGTCAG CAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCATC 720  
 55 CTCAGCAGCA GTGCCCTCGA TATCTTCTGC GACAATGAGA ATGGGCCTAA CTCTCTTTC 780  
 CACAACCGGG GCGATGGCAC CTTTGTGGAC GCTGCGGACA GTGCTGGTGT GGACGACCCC 840  
 CACGAGCATG GCGGAGGTGT GCGCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900  
 GTCTATGGCA ACTGGAATGG CCCCCACCG CTCTATCTGC AAATGAGCAC CCATGGGAAG 960  
 GTCCGCTCC GGGACATCGC CTACCCCAAG TTCTCCATGC CCTCCCTGT CCGCACGGTC 1020  
 60 ATCACCGCGG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCCTAC 1080  
 CGCAGCTCCT CAGCCAACCG CCTCTTCCG GTCATCCGTA GAGAGCACGG AGACCCCTC 1140  
 ATGAGGAGC TCAATCCCGG CGAGCCTTG GAGCTGAGG GCGGGGGCAC AGGGGGGTG 1200  
 GTGACCGACT TCGACGGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260  
 GCTCAGCGG CTGCGTCTT CCGGGGCAAT CAGGGCTTCA ACAACAACCT GCTGCGAGTG 1320  
 65 GTGCCACGCA CCGGTTTGG GCGCTTGGC AGGGGAGCTA AGGTCGTGCT CTACACCAAG 1380  
 AAGAGTGGGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440  
 CCGCTGGCAC ACTTGGCTCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500  
 GATGGCAAGA TGGTGAGCGG GAACTGGGCC AGCGGGGAGA TGAACCTCAGT GCTGGAGATC 1560  
 70 CTCTACCCCG GGGATGAGGA CACACTTCAG GACCCAGCCC CACTGGAGTG TGGCCAAGGA 1620  
 TTCTCCACG AGSAAATGG CCAATGATG GACACCAATG AATGCATCCA GTTCCCATTC 1680  
 GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGAGC 1740  
 AACAGAAGAT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT 1800  
 CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCCCACCG CTGCTGCTGC CACTGCGGCT 1860  
 75 GCTGCTGCGG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920  
 CTGGGGTCCG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980  
 CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CTTAGACAGT 2040  
 AGGGATGTAA AGGCTGGGGA GCTAGACCTC CCCCAGCCC ATCCATGCAC ATTACTTAGC 2100  
 TAACAATTAG GGAGACTCGT AAGGCCAGGC CCTGTGCTGG GCACATAGCT GTGATCACAG 2160  
 80 CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCCAGTG GGTCTAATGA CCATATCTTA 2220  
 GGACACAGAT GTGCCCGGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280  
 CCTGAGTTCA AATCTGATT CAGGAATCA CAAAGCTATG TGACCTTACA CCACTCACTT 2340  
 AACTTGTTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAATAG AATCTTGGGG 2400  
 TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460  
 AAAGGCTCAA TAAAAACAAG TGCTCTCAC TGGGCTTGT CAACAGC



Seq ID NO: 183 Protein sequence  
Protein Accession #: CAC08451

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MSRMLPFLLL LWFLPITEGS QRAEPMFTAV TNSVLPPDYD SNPTQLNYGV AVTDVDHGDG 60
FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQNAIGVT ACDIDGDGRE 120
EIYFLTNINA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180
GRYSIIYANY AYGNVGPDAL IEMDFEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
10    LSSASDIPC DNENGNPFLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNDRDKVDI 300
VYGNWNGPHR LYLQMSHTGK VRFRIASPK FSPSPVTV ITADFNDQE LEIFPNNIAY 360
RSSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTFDGDGML DLILSHGESM 420
AQLSVPRGN QGFNNWLRV VPRTRFGAFA RGAQVLYTK KSGAHLRIID GSGVLCME 480
FVAHFLGKD EASSVEVTHP DGKMSVRNVA SGMNSVLEI LYPRDEDTIQ DPAPLECGQG 540
15    FSQENGHCN DTNECIQFPF VCPDRKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT 600
LGQSPGPRPT TPTAAATAA AAAAAGAATA AFVLVDGDLN LGSVVKESCE PSC

```

Seq ID NO: 184 DNA sequence  
Nucleic Acid Accession #: FGENESH1  
Coding sequence: 1..4794

```

20    1      11      21      31      41      51
|      |      |      |      |      |
ATGGCGTGTC CGGGAGGACT CCCAGCCCGT TGCTCTGGTT GGATGGGACT GGGTGGGCCC 60
25    AGCGGCTCCT CCCAGCATC CCCTCCCAT TCCTCCTCCA GGTACAATGG ACCCAACTG 120
GTTCTGAAGT ATGACCGGGC CCAGAAGCGG CTGGTGAACA TCGGGTCGA TGAGCGCAGC 180
TCACCCTACT AGCGCTGGG GGACCGGCGG GGGAAAGCCA TCGGGTCAC AGCCTGCGAC 240
ATCGACGGGAG AGCGCCGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTTCTGGGCG 300
CACAGCAGCT CAGCGCAGGT CCCTTCTGGG CTCCACAGAA ACAGGCGCTGT GCTGAAGCCT 360
30    CCACCTACAA CCCTGTCAGG CCTCTCTGGT CTGCTCCAC TCAGCGGAAG GGACTTTTCC 420
TCCTCCCTGG GTCAGGCTTC TCCGACAGC AGGCAGGGAG AGAGGGTGCC GGTTCCTGTC 480
TGTCCGGGTG GACTGAGACC TACCCATGAA CCAGAACCAT TTCTCTGAG ACCCAATCA 540
GGGCTGGGCA CGTACACCGA CAAGTTGTTT AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
CTGAGCGATG AGGTCAACGT GCGCCGTGGT GTGCCAGCC TCITTGCCGG ACGCTCTGTG 660
35    GCCTGTGTGG ACAGAAAGGG CTCTGGAGCG TACTCTATCT ACATTGCCAA TTAGCCTAC 720
GGTAATGTGG GCCCTGATGC CCTCATTTGA ATGGACCTG AGGCAGTGA CCTCTCCCGG 780
GGCATTTCTG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAATA TACAGAAGGC 840
TTCTCCCACT CTGCTCTTCC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA 900
GGAGGAGACC CAGAGGAGGC AGATGAGGAG CACATGSGGG ATGGAAGCAC CAGCCAACCTG 960
40    TGCCGGCTGG GCTGGAAGGA CGGGCAGTTC AAGGAAGAAG CAGCAGCTTT GGTGGAGGAA 1020
CAGAGGGAGG CTGGGCGAGC TGGCGTGCCC AGAGGAGCTG TTGGAACAGC TCTGCGAGCT 1080
TCCAAAAGCC ATTGGCTGA CAAGAACCTA TTTGGCCACC CATGTTACTA TTCTGTCTGC 1140
GGCGCTTCTC CAGCCACGCC TTTCCTTGCC CGCCAAGCCC CCCAACCTA CCTGTAGACC 1200
45    CCCCTTGTC CACAGCTAAT GACACATGGA CGTCTGGCTG GAAACTAGC CCGGAGTGTG 1260
CCCCACCCC GAGCCCCAGG AATGGACCCC AAATGTAAGG GCCGCCATGC TGAGCCCGGC 1320
CTGATGGCTG AGGCTTTGGG CGCGTGCCCA GCCTCAGCA CCACTGTGGT GCCAGGGGGC 1380
CTGAGAAGCT GGGAGGAAG CAGGCAGAGG GGGCAGGCCA TGTCCAGATG TGCACTCAGG 1440
GAGCTGGGAG GTCCCTGGAG CCAAGCCACA CAGCACTGCT CTGCTAGAGA GCTGTATGAC 1500
50    CTGGGAGAAC CTCCCATTTT ACAAGAACA GACCGAGATC CAGGAGGAG AAGGGACTCG 1560
CCCAAGTCA CACAGAGTG CCATCTAGTG GCCACCATGC CAGCTCTCGG GGGACTCGAG 1620
GGCCCCGGGA GGGTGCCCAA GCGAGAGATT GSGAGAGAGA CTGGGCGAGT AGGAAGACCA 1680
CTCTCCCATC CCCTGTGCCC CAACTTCCCC AGCTGCTTGA GGCTCTTGA AGCCGGGACA 1740
GTGCGGGGAG CTGCGCTGCG TGGGAATCCT GGGAACTGGG TTCTGGACAT GGCCAAAGGC 1800
55    CTGCGCTGGA ACCAGATGGA AAAAGAGGAG GGAAGATTTC ATGGAGACCA TGAGCCCAAG 1860
TTTAGGCTCA GGAAGACAG GGAAGCAGAA TTCCCCCAG GCTCCTCTGA GGAGCCTCTG 1920
CTGCACTTCC CCTCAGGCCT CAGAGGCAGC CCTGTCTTCC AGGTGGGCTT GGGGCTTGCT 1980
TCTGCCACTC ACTGTGGGTC GATGTCTTTT CTAGGGGGCC GAGGCGTCAG CGTGGGCCCC 2040
ATCCTCAGCA GCAGTGCCCT GGATATCTTC TGGACAAATG AGAATGGGCC TAACCTCTTT 2100
TTCCACAACC GGGGOGATGG CACCTTTGTG GACGCTGCGG CCAGTGTGTA ACGTGTGTTA 2160
60    GCCTTCATCG TTCACCTCAA ATATCACCTC TGCAAGATT TTCTCACTC CCTGTGCCAC 2220
CTAGCAGAAA CTGGTCTCTC CTCTCTCTG TGCCGCTGGC ATGCACGTCT TCTTCAGGCT 2280
CCACATGGCC ATCATGGTTT GTCTATGAGC TTTACAAGGA CCGGTCACG GTTCTATTCA 2340
TTCTTGACGC AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT 2400
CAGGGGGCCC CACCTGCTC TCTGGCAAGA GCTCCTGTG TCTGGGGTCT TCTGATCCCC 2460
65    ACTGCCTATT ACATTGTCTT GTGGTCTGCC ATCCAGAGA GCTGATGAC CCACAGCTAT 2520
TTGTCTCTG AAAGAGTCAA CGTGGGTGTG GACGACCCCC ACCAGCATGG GCGAGGTGTC 2580
GCCCTGGCTG ACTTCAACCG TGATGGCAAA GTGGACATCG TCTATGGCAA CTGGAATGGC 2640
CCCCACGCC TCTATCTGCA AATGAGCACC CATGGGAAGG TCGCTTCCG GGACATCGCC 2700
TCACCAAGT TCTCATGCC CTCCCTGTG CGCAGGCTCA TCACGCGCA CTTTGACAAT 2760
70    GACCAGGAGC TGGAGATCTT CTTCAACAAC ATTGCTTACC GCAGCTCTCT AGCCAACCGC 2820
CTCTTCOGAT GCTCCATCTT GGCTCGTGGC TCTTCTATCT TGACAGCTGG TGGGAGGAAC 2880
GGTCAGGGAG AAGGTTTAAG AATCAGAAGG GAGGGGTTC CAGGGCCAGG GGGTCAGGCC 2940
AAGTCAACA CAGTCCCTCT GATGAAGAAA CAGAAAGGAA GGAAGGACGA GGAATGGGCA 3000
AGAGGCTGTG GGAATGTCAG GCAAAGCCTG GCCAAGGAGC CGGCTCTGCT TATTGCAAGG 3060
75    AAAGGGAAGG GAAATGTGGC CCAAAGTGTG CCAAGAACCC AAGCGCACA AGATACAAAG 3120
CCACACTACC ACAAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAGG GGGCTACGGG 3180
GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC ACTACCAGGA AAAGGGGCTA 3240
CGGGGTCCAA TCACTACGAG GAAAAGGGGC TACGGGTGCC AATCACTACC AGGAAAAGGG 3300
GCTACGGGCT CCAATCACTA CCAGGAAAGG GGGCTACAGG GTCCAATCAC TACCAGGAAA 3360
80    AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGCTA CAGGGTCCAA TCACTACCAC 3420
AGAAAGGGGC TACGGGCTCC AATCACTACC AGGAAAAGGG GCTACGGGT CCAATCACTA 3480
CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC 3540
ACTACCAGGA AAAGGGGCTA CGGGCTCCAA TCACTACCAG GAAAAGGGGC TACGGGTGCC 3600
AATCACTACC AGGAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAGG GGGCTACAGG 3660

```

5  
10  
15  
20

GTCCAATCAC TACCACAGAA AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGGCTA 3720  
CGGGGTCCAA TCACTACCAG GAAAAGGGGG TACGGGCTCC AATCACTACC AGGAAAAGAG 3780  
GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA 3840  
AGGGGCTATG GGGTCCAATC ACTACCAGAG AAAGGGGGCTA CGGGGTCCAA CGTCATCCGT 3900  
AGAGAGCAGC GAGACCCCTT CATCGAGGAG CTCAATCCCG GCGACGCCCT GGAGCCTGAG 3960  
GGCCGGGGCA CAGGGGGTGT GGTGACCGAC TTGACCGGAG ACGGGATGCT GGACCTCATC 4020  
TTGTCCCATG GAGAGTCCAT GGCTCAGCCG CTGTCCGTCT TCGGGGGCAA TCAGGGCTTC 4080  
AACAACAACT GGCTCGAGT GGTGCCAGC ACCCGGTTTG GGGCTTTGC CAGGGGAGCT 4140  
AAGGTCGTG TCTACACCAA GAAGAGTGGG GCCCACCTGA GGATCATCGA CGGGGGCTCA 4200  
GGCTACCTGT GTGAGATGGA GCCCGTGCCA CACTTTGGCC TGGGAAGGA TGAAGCCAGC 4260  
AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAACGTGGC CAGCGGGGAG 4320  
ATGAACTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC 4380  
CCACTGGAGT GTGGCCAAGG ATTCTCCAG CAGGAAAATG GCCATTGCAT GGACACCAAT 4440  
GAATGCATCC AGTTCCCATT CGTGTGCCCT CGAGACAAGC CCGTATGTGT CAACACCTAT 4500  
GGAAGCTACA GTGTCCGGAC CAACAAGAG TGCACTGGG GCTACGAGCC CAACGAGGAT 4560  
GGCAGAGCTG TGAGCTAGGC TCTAGGCATA CAATGACGTG GAAACCAAGG 4620  
CCCAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCAACC CGTCTGGTC CTTTTCCTG 4680  
CCGGTGTGCC GGTCTGCTCT CAAAAGAGCT CAGCTCCAGG CTGCTCCAG CACCTTCTC 4740  
CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA

Seq ID NO: 185 Protein sequence  
Protein Accession #: FGENESHH

25  
30  
35  
40  
45  
50

1 11 21 31 41 51  
MACPGGLPAR CSGWMGLGPP SGSSPASPPH SSSRYNGPNL VLKYDRAQKR LVNIAVDERS 60  
SPYYALRDRQ GNAIGVTACD IDGDGREEIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP 120  
PFTTFAGLLG LPLSLGRDFS SSLGQASPD S RQGERVVPVC CRGGLRPTHE PEPFLLRPKS 180  
GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKSGSR YSIYIANYAY 240  
GNVGPDALIE MDPEASDLRS GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE 300  
GGDPEADEEE HSGDGGSTSQL CRLGWKDGQF KEEAALVEE QREAGAAGVP RGRVRTALQT 360  
SKSHLADKNL FGPPCYYSVC APSPAHFPPA RQAPQHYPVA PLVTQLMTHG RLAGKLARSV 420  
PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESROK GOAMSRCALR 480  
ELGGPWSQAT QHLPARELYD LGEPPILOQT DGDPRRRDS PKVTQECHLV ATPMALGGLE 540  
GPGRVAKREI GRETAGVGRF LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA 600  
LAWNQMEKEE KITHGDHEPR FRLRKAREAE FPPGSSEEP LQPPSGLRGS PVLQVGLGLA 660  
SATHCGSMGF LGGRGVSVGP ILSSASDIF CNENGNPNFL FHNRGDGTFFV DAAASAERRL 720  
AFIVHLKYHL CRDFGPHSLCH LAETGPSSSC CFWHARLLQA PHCHHGLSMS FTRTGSRFYS 780  
FLTQGLASSA HRRTLSLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840  
LSSERVNVGV DDPHQHGRGV ALADFNDRDGK VDIVYGNWNG PHRLYLQMS T HGKVRFRDIA 900  
SEKFSMSPV RTVITADFDN DQELEIFPNN IAYRSSSANR LFRCSILARG SSSLTAGGRN 960  
GQGBGLRIRR GGFPGPGQQA KVTNGLPMKK QKGRKDEWA RGCGNAGQSL AKEPASAIAI 1020  
KKGKGVQSDV PRTQAPQDTH PHYHKKGLQG PITTRKRGYV VQSLPGKGAT GSNHYQEKGL 1080  
RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH 1140  
RKGLRAPITT RKRGYGVQSL PGKGATGSNH YQEKGLRGPI TTRKRGYGLQ SLPGKGATGS 1200  
NHYQEKGLQG PITTRKRGYV VQSLPGKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260  
AMGSNHYQEK GLRAPITTRK RGYGVQSLPG KGATGSNVIR REEGDPLIEE LNPDALEPE 1320  
GRGTGGVVD FGDGMDLDLI LSHGESMAQP LSVFRGNQGF NNNWLVRVPR TRGFAPARGA 1380  
KWLYTKKSG AHLRIIDGGS GYLCEMEPVA HFCLGKDEAS SVEVTFPDGK MVRNVASGE 1440  
MNSVLEILYP RDEDTLQDPA PLECGGFSQ QENGHCMDTN ECIQFFVFCP RDKPVCVNTY 1500  
GSYRCRINKK CSRGYEPNED GTACVGTGLG SRHTMTWKPR PKKELQLSQG ICTPVWSFFL 1560  
PGCRLLLKRA QLQAPSTLL QKAPGIPEAQ VYEQDQE

55  
Seq ID NO: 186 DNA sequence  
Nucleic Acid Accession #: NM\_000584.1  
Coding sequence: 75..374

60  
65  
70  
75  
80

1 11 21 31 41 51  
AGCAGAGCAC ACAAGCTTCT AGGACAAGAG CCAGGAAGAA ACCACCGGAA GSAACCATCT 60  
CACTGTGTGT AAACATGACT TCCAAGCTGG CCGTGGCTCT CTGGGCAGCC TTCTGATT 120  
CTGCAGCTCT GTGTGAAGGT GCAGTTTTGC CAAGGAGTGC TAAAGAACTT AGATGTCAGT 180  
GCATAAAGAC ATACTCCAAA CCTTCCACC CCAAATTTAT CAAAGAACTG AGAGTGATTG 240  
AGAGTGGACC ACATGCGGCC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300  
TCTGTCTGGA CCCCAGGAAA AACTGGGTGC AGAGGGTTGT GGAGAAGTTT TGAAGAGGG 360  
CTGAGAATTC ATAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT 420  
GAAACTTCAA GCAATCTACT TTCAACACTT CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480  
CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTCA GTAAACAATG AATAGTTTTT 540  
CATGTATACA TGAATATACC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA 600  
CAAAAAACAA CAAATAATTT TTAATATATA GGATTTTCCT AGATATTGCA CGGGAGAATA 660  
TACAATAGC AAAATTGAGC CAAGGGCCAA GAGAATATCC GAACCTTAAT TTCAGGAATT 720  
GAATGGGTTT GCTAGAATGT GATATTGAA GCATCACATA AAAATGATG GACAATAAAT 780  
TTTGGCATAA GTACCAATTT AGCTGGAAAT CCTGGATTTT TTTCTGTTAA ATCTGGCAAC 840  
CCTAGTCTGC TAGCCAGGAT CCACAGTCC TTGTCCACT GTGCCTTGGT TTCTCCTTTA 900  
TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTACCTCAC AGTGATGTTG TGAGGACATG 960  
TGAAGCACT TTAAGTTTTT TCATCATAAC ATAAATTATT TCAAGTGA ACTTATTAAC 1020  
CTATTATTA TTTATGTAAT TATTAAAGCA TCAAATATT GTGCAAGAA TTTGAAAAAT 1080  
AGAAGATGAA TCATGTATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTA 1140  
GATATTAAAT GATGTTTTAT TAGATAAATT TCAATCAGGG TTTTATGATT AAACAAAGAA 1200  
ACAAATGGGT ACCCAGTTAA ATTTTCATTT CAGATAAACA ACATAAAT TTTTAGTATA 1260  
AGTACATTAT TGTTTATCTG AAAGTTTTAA TTGAACATAA AATCCTAGT TGATACTCCC 1320  
AGTCTGTGCA TTGCCAGCTG TGTGTGAGT GCTGTGTGTA ATTACGGAAT AATGAGTTAG 1380  
AATATATAA ACAGCCAAA CTCCACAGTC AATATTAGTA ATTTCTGTGT GGTGAAACT 1440  
TGTTTATTAT GTACAAATAG ATTCCTATAA TATTATTATA ATGACTGCAT TTTTAAATAC 1500

AAGGCTTTAT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTACTGT 1560  
 TTCTGATTGT ATGGAATAT AAAAGTAAAT ATGAACATT TAAATATATA TTTGTGTCA 1620  
 AAGTAAAAA AAAAAAAA

5 Seq ID NO: 187 Protein sequence  
 Protein Accession #: NP\_000575.1

10 1 11 21 31 41 51  
 | | | | |  
 MTSKLAVALL AAFILISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60  
 CANTEIIVKL SDGRELCIDP KENWVQRVVE KFLKRAENS

15 Seq ID NO: 188 DNA sequence  
 Nucleic Acid Accession #: NM\_003661.1  
 Coding sequence: 1..1152

20 1 11 21 31 41 51  
 | | | | |  
 ATGAGTGCAC TTTTCCTTGG TGTGGGAGTG AGGCAGAGG AAGCTGGAGC GAGGGTGCAA 60  
 CAAAACGTTT CAAGTGGGAC AGATACITGA GATCCTCAAA GTAAGCCCTT CGGTGACTGG 120  
 GCTGCTGGCA CCAATGGACC AGAGAGCAGT ATCTTTATTT AGGATGCCAT TAAGTATTTT 180  
 AAGGAAAAG TGAGCACACA GAATCTGCTA CTCTGCTGTA CTGATAATGA GGCCTGGAAC 240  
 GGATTCTGTG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300  
 GACAACTTGG CAAGACAAT GATCATGAAA GACAAAACT GGCACGATAA AGGCCAGCAG 360  
 25 TACAGAACTT GGTTCCTGAA AGAGTTTCCT CGGTTGAAAA GTGAGCTTGA GGATAACATA 420  
 AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAAGGCAC CACCATCGCC 480  
 AATGTGGTGT CTGGCTCTCT CAGCAATTCC TCTGGCATCC TGACCTCGT CGGCATGGGT 540  
 CTGGCACCTT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600  
 ATCACAGCCG CTTTGACCGG GATTACAGC AGTACCATGG ACTACGGAAA GAAGTGGTGG 660  
 30 ACACAAGCCC AAGCCACAGA CCTGGTCATC AAAAGCCTTG ACAAATTGAA GGAGTGAGG 720  
 GAGTTTTTGG GTGAGAACAT ATCCAACTTT CTTTCCTTAG CTGGCAATAC TTACCACTC 780  
 ACACAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840  
 GTACCCGATG CCTCAGCCTC ACGCCCCGGG GTCAGTGGC CAATCTCAGC TGAAAGCGGT 900  
 35 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAA TGAGCAGAGG AGTCAAGCTC 960  
 ACGGATGTGG CCCCTGTAAG CTCTTTCTT GTGTGGATG TAGTCTACCT CGTGTACGAA 1020  
 TCAAAGCACT TACATGAGGG GGCAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080  
 CAGGAGCTGG AGGAGAAGCT AAACATTCTC AACAATAATT ATAAGATTCT GCAGGCGGAC 1140  
 CAAGAAGTGT GA

40 Seq ID NO: 189 Protein sequence  
 Protein Accession #: NP\_003652.1

45 1 11 21 31 41 51  
 | | | | |  
 MSALFLGVGV RAEAEAGARVQ QNVPSGTDG DPQSKPLGDW AAGTMDPES IFIEDAIKYF 60  
 KEKVSTQNL LLLTDNEAWN GFVAAELPR NEADELRKAL DNLARQMIMK DKNWHDKGQ 120  
 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLIS SGILLVGMG 180  
 LAPFTEGSL VLEPGMELG ITAALTGITS TMDYKKWW TQAQHLVI KSLDKLKEVR 240  
 50 EPLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPIAESG 300  
 EQVERVNEPS ILEMSRGVKL TDVAPVSFPL VLDVVLVYE SKHLHEGAKS ETAEELKKVA 360  
 QLELEKLAIL NNNYKILQAD QEL

55 Seq ID NO: 190 DNA sequence  
 Nucleic Acid Accession #: NM\_014452.1  
 Coding sequence: 1..1968

60 1 11 21 31 41 51  
 | | | | |  
 ATGGGGACCT CTCGAGCAG CAGCACCGCC CTGSCCTCTT GCAGCGCAT CGCCCGCCGA 60  
 GCCACAGCCA CGATGATCG GGGCTCCCTT CTCTGCTTGG GATTCCCTAG CACCACCACA 120  
 GCTCAGCCAG AACAGAAGGC CTGGAATCTC ATTGGACAT ACCGCCATGT TGACCGTGCC 180  
 ACCGGCCAGG TGCTAACCTG TGACAAGTGT CCAGCAGGAA CCTATGTCTC TGAGCATTGT 240  
 ACCAACACAA GCGTGCAGGT CTGCAGCAGT TGCCCTGTGG GGAACCTTAC CAGGCATGAG 300  
 65 AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA 360  
 TTACCTTGTG CTGCTTGGAC TGACCGAGAA TGCACTTGCC CACTGGCAT GTTCCAGTCT 420  
 AACGCTACCT GTGCCCCCA TACGGTGTGT CCTGTGGGTT GGGGTGTGGC GAAGAAAGGG 480  
 ACAGAGACTG AGGATGTGCG GTGTAGCAG TGTGCTGGG GTACCTTCTC AGATGTGCTT 540  
 TCTAGTGTGA TGAATGCAA AGCATAACA GACTGTCTGA GTCAGAACCT GGTGGTGATC 600  
 70 AAGCCGGGGA CCAAGGAGAC AGACAAGTCT TGTGGCACAC TCCGCTCCTT CTCCAGCTCC 660  
 ACCTCACCTT CCCTTGGCAC AGCCATCTTT CACGCGCTG AGCACATGGA AACCCATGAA 720  
 GTCCCTTCTT CCCTTATGT TCCCAAAGGC ATGAACCTCA CAGAATCCAA CTCTTCTGCC 780  
 TCTGTAGAC CAAAGGTACT GAGTAGCATC CAGGAAGGGA CAGTCCCTGA CAACACAGC 840  
 TCAGCAAGGG GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCAC 900  
 75 CAGCAAGGCC CCCACACAG ACACATCCTG AAGCTGTGTC GGTCCATGGA GGCCACTGGG 960  
 GGCAGAGAGT CCAGCAGGCC CATCAAGGCC CCCAAGAGGG GACATCTAG ACAGAACTTA 1020  
 CACAAGCATT TTGACATCAA TGAGCATTG CCCTGGATGA TTGTGCTTTT CTGTCTGCTG 1080  
 GTGCTTGTGG TGATTGTGGT GTGCAGTATC CGGAAAAGCT CGAGGACTCT GAAAAGGGG 1140  
 80 CCGCGGAGG ATCCAGTGC CATTGTGGA AAGGCAGGGC TGAAGAAATC CATGACTCCA 1200  
 ACCCAGAAC GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATCGA TATCCTGAAG 1260  
 CTTGTAGCAG CCCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC 1320  
 AGTGAGAGGG AGGTTGCTGC TTTCTCCAAT GGGTACACAG CCGACCACGA CGGGCCTTAC 1380  
 GCAGCTCTGC AGCACTGGAG CATCCGGGGC CCGAGGCCA GCCTCGCCA GCTAATTAGC 1440  
 GCCCTGCGC AGCACCGGAG AAACGATGTT GTGAGAGAAGA TCGTGGGCT GATGGAAGAC 1500  
 ACCCCCCAGC TGGAACTGA CAACTAGCT CTCCGATGA GCCCAGGCC GCTTAGCCCG 1560

5 AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCOG CTCTCCTGAC GGTGGAGCCT 1620  
 TCCCCACAGG ACAAGAACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCTC TCTCCGCTGT 1680  
 GACTCTACAT CCAGCGGCTC CTCGCGCTG AGCAGGAACG GTTCCTTAT TACCAAGAA 1740  
 AAGAAGGACA CAGTGTTCGC GCAGGTACGC CTGACCCCT GTGACTTGCA GCCTATCTTT 1800  
 GATGACATGC TCCACTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG 1860  
 GCTGAGGACA AACTAGACCG GCTATTGAA ATTATTGAG TCAAGAGCCA GGAAGCCAGC 1920  
 CAGACCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG

10 Seq ID NO: 191 Protein sequence  
 Protein Accession #: NP\_055267.1

15 1 11 21 31 41 51  
 | | | | | |  
 MGTSPSSSTA LASCRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTYRHVDRA 60  
 TGQVLTCDCX PAGTYVSEHC TINTSLRVCS CPVGTFTRHE NGIEKCHDCS QPCPWPMEIK 120  
 LPCAALDRE CTCFPMFQV NATCAPHTVC PVGWGVKKKG TETEDVRCKQ CARGTFSDVP 180  
 SSVMKCKAYT DCLSNLVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPERMETHE 240  
 VPSSTYVPKG MNSTESNSSA SVRPKVLSSI QEGTVFDNTS SARGKEDVNK TLPNLQVNH 300  
 QQGPPIHRL KLLPSMEATG GEKSSTPIKG PKRGHPRQNL HKHFDINEHL PWMIVLFLLL 360  
 20 VLVVIVVCSI KRSRRLTKKG PRQDPSAIVE KAGLKKSMTP TQNREKIYY CNGHGIDILK 420  
 LVAAQVGSQ KDIYQFLCNA SEREVAAFSN GYTADHERAY AALQHWITRG PEASLAQLIS 480  
 ALRQHRNDV VEKIRGLMED TQLETDKLA LPMSPSPSP SPIPSNAKL ENSALLTVEP 540  
 SPQDNKNGFF VDESEPLLR DSTSSGSSAL SRNGSFITKE KEDTVLRQVR LDPCLQPIF 600  
 25 DDMHLHFNPE ELRVIEEIPQ AEDKLDRLFE IIGVKSQEAS QTLSDSVYSH LPDLL

Seq ID NO: 192 DNA sequence  
 Nucleic Acid Accession #: XM\_044533  
 Coding sequence: 238..2751

30 1 11 21 31 41 51  
 | | | | | |  
 GCTCTGCCCA AGCCGAGGCT GCGGGGCGGG CGCGGGCGGG AGGACTCGCG TGCCCCGCGG 60  
 AGGGGCTGAG TTGSCCAGGG CCACTTGAC CCGTTTCCC ACCTCCGCGC CCCAGGTCC 120  
 35 GGAGGCGGGG GCCCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCCCGCGGTG 180  
 AGTCCGCGCG AGCCACTTGA GCCCGAGCGG CGGGACACCG TCGCTCTCGC TCTCCGAATG 240  
 CTGCGCACCG CGATGGGCTT GAGGAGCTGG CTGCGCGCCC CATGGGCGCG GCTGCGCGCT 300  
 CGGCCACCGC TGCTGCTGCT CCGTCTGCTG CTGCTCTCGC TGCAGCGCGC GCCTCCGACC 360  
 TGGGCGCTCA GCCCCCGGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGGC ATTCTCAGA 420  
 40 TTGAAGCTG AACACATCTC CAACACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC 480  
 CTGTAGCTGG GTGCTGAGGA GGCCTCTTTC GCACTCAGTA GCAACCTCAG CTTCCTGCCA 540  
 GGGGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCG AGAAGAAACA GCAGTGACAG 600  
 TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAACTACA TCAAGATCCT CCTGCCGCTC 660  
 AGCGGCAGTC ACCTGTTTCA CTGTGGCACA GCAGCCTTCA GCGCCATGTG TACCTACATC 720  
 45 AACATGGAGA ACTTACCCTT GGCAAGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780  
 AAGGGCGGTT GTCCCTTCGA CCGCAATTTT AAGTCCACTG CCCTGGTGGT TGATGGGGAG 840  
 CTCTACACTG GAACAGTCAG CAGCTTCCAA GGAATGACC CGGCCATCTC GCGGAGCCAA 900  
 AGCCTTCGCG CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG 960  
 GCGTCAGCTC ACATTCTCTG GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020  
 50 TTTTCTTCA GCGAGACTGG CCAGGAATTT GAGTCTTTG AGAACACCAT TGTGTCCCGC 1080  
 ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC 1140  
 TCCTTCTCA GCGCCAGCTG GCTGTCTCTA CGGCCCGAOG ATGGCTTCCC CTTCACGCTG 1200  
 CTGCAGGATG TCTTACGCTG GAGCCCGAGC CCGCAGGACT GCGGTGACAC CCTTTTCTAT 1260  
 GGGGTCTTCA CTTCCTAGTG GCACAGGGGA ACTACAGAAG GCTCTGCGCT CTGTGTCTTC 1320  
 55 ACAAAGAAGG ATGTGCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA 1380  
 CAGCAGTGGT ACACCGTGAC CCACCCGGTG CCCACACCCC GGCCTGGAGC GTGCATCACC 1440  
 AACAGTGGCC GGAAGAAGAA GATCAACTCA TCCCTGCAGC TCCAGACCG CGTGCTGAAC 1500  
 TTCTCAAGG ACCACTTCTT GATGGAAGGG CAGGTCCGAA GCGCGATGCT GCTGTGACG 1560  
 CCCAGGCTC GCTACCAAGC GGTGGCTGTA CACCGGTGCC CTGGCTGACA CCACACTTAC 1620  
 60 GATGTCTCTT TCTTGGGCAC TGTGACGGC CGGCTCCACA AGGCAGTGAO GTGGGCGCCC 1680  
 CGGGTGACA TCATTGAGGA GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAATCTG 1740  
 CTCTGTGACA CCCACAGGGG GCTGTGTAT GCGGCTCAC ACTCGGCGT AGTCCAGGTG 1800  
 CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGACT GCGCTCTCGC CCGGACCCCG 1860  
 TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CAGCTCAGCC TCTACAGGCC TCAGCTGGCC 1920  
 65 ACCAGGCGGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGGTCTT 1980  
 TCGGTGTGTG CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040  
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC 2100  
 TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCTCCTT GCCAGTGTCT ACCACTGGG 2160  
 GACCTGTCTG TGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGTGTGTC ACTAGAGGAG 2220  
 70 GGCTTCCAGC AGCTGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280  
 CAAACAGATG AGGGTGGCAG TGTACCGGTC ATTATCAGCA CATGGGTGTG GAGTGACCA 2340  
 GCTGGTGGCA AGGCCAGCTG GGGTGCAGAC AGTCTTACT GGAAGGAGTT CCGGTGTATG 2400  
 TGCACTGTCT TGTGTGTCG CGTGTCTGTC CAGTTTTAT TCTTGTCTTA CCGGACCCGG 2460  
 AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA GCGTGACCCC CAAGACTCTG 2520  
 75 CCTGTGTGTC TGCCCCCTGA GACCCGCCCA CTCAACGCC TAGGGCCCCC TAGCACCCCG 2580  
 CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640  
 GAGTCAAGGA AGAGCCCACT CAGCATCCAA GACAGCTTGG TGGAGGTATC CCGAGTGTGC 2700  
 CCGGCCCCCG GGGTCCCGCT TGGCTCGGAG ATCGGTGACT CTGTGTGTG AGAGCTGACT 2760  
 80 TCCAGAGGAG GTGCGCTGCT CTTAGGGGCG TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820  
 TCCCTCCGCG TCTGCTCTTC GTGGAACAG ACCGTGGTGC CCGGCCCTTG GAGGCTTGG 2880  
 GGCCAGCTGG CCGTCTGCTC TCCAGTCAAG TAGCGAAGCT CTAACACCCC AGACACCCAA 2940  
 ACAGCGGTGG CCGGAGAGGT CCTGGCCAAA TATGGGGGCC TGCTAGGTT GGTGGAACAG 3000  
 TGCTCTTAT GTAACTGAG CCCTTTGTTT AAAAAAAT TCCAAATGTG AAATAGAAAT 3060  
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACAAGGCTG CTCCAGTTCA TGGCTTCCA 3120  
 GGGGTGCTGG GGATGCATCC AAAGTGGTGT TGTGAGACAG AGTGTGAAAC CCTCACCAAC 3180

5  
10  
TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCTGTCTC ACTGCAGATT 3240  
CAGGACCAAGC TTGGGCTGCG TGCGTCTGCG CTGCGCAGTC AGCCGAGGAT GTAGTTGTGTG 3300  
CTGCGTGTGT CCCACCACTC CAGGGACCAAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360  
GGTCTCGGGC TCGGACCCAA CTCTCGGACC TTTCAGCCT GTATCAGGCT GTGGCCACAC 3420  
GAGAGGACAG CGCGAGCTCA GGAGAGATT CTGACAATG TACGCTTTC CCTCAGAATT 3480  
CAGGGAAAGAG ACTGTGCGCT GCCTTCTCC GTTGTTCGT GAGAACCCT GTGCCCTTC 3540  
CCACCATATC CACCTCGCT CCATCTTTGA ACTCAAACAG GAGGAACATA CTGCACCCCTG 3600  
GTCCTCTCCC CAGTCCCAGG TTCACCTCC ATCCCTCACC TTCTCCACT CTAAGGGATA 3660  
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTAATAAAG 3720  
ATGCACITTA TGTCAITTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 193 Protein sequence  
Protein Accession #: XP\_044533.3

15  
20  
25  
30  
1 11 21 31 41 51  
MLRTAMGLRS WLAAPWALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60  
RFEAEHISNY TALLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELW GADAEKKQCC 120  
SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180  
GKGRCPFFPN FKSTALVVDG ELYTGVSSF QGNDPAISRS QSLRPTKTES SIWNLQDPAP 240  
VASAYIPESL GSLQDDDKI YFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300  
TSFLKAQLLC SRPDGFPFN VLQDVFTLSP SPQDWRDLTF YGVFTSQWHR GTTEGSAVCV 360  
FTMKDVQRVF SGLYKEVNR TQQWYVTHP VTPRPGACI TNSARERKIN SSLQLPDRVL 420  
NFLKDHFLMD GQVSRMRLL QPQARYQVVA VHRVPLGHT YDVLFLGTGD GRLHKAVSVG 480  
PRVHIEELQ IFSSQGPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540  
PYCAWSGSSC KHVSLYQPL ATRPWIQDIE GASAKDLCAS SSVVSPSPFV TGEKPCQVQ 600  
FQPNVTNTLA CPLLSNLATR LWRNGAFVN ASASCHVLP GDLLLVGTQQ LGFEQCWSLE 660  
EGFQQLVASV CEPVEDGVA DQTEGGSPV VIISTSRVSA PAGGKASWGA DRSYWKFLV 720  
MCTLFVLAFL LPVFLFLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780  
PLDHRGYQLS SDSPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 194 DNA sequence  
Nucleic Acid Accession #: NM\_022819.1  
Coding sequence: 1..635

35  
40  
45  
1 11 21 31 41 51  
ATGGCAGATG GGGCAAAGGC CAACCCCAAA GGTTTCAAAA AGAAGGTGCT GGATAGATGC 60  
TTCTCTGGGT GAGGGGGCCC ACGCTTCGGG GCCTCCTGTC CTTCAGAAC CTCCAGGTCT 120  
AGCCTGGGTA TGAAGAAGTT CTTACCGTG GCCATCCTG CTGGCAGCGT TCTGTCCACA 180  
GCTCAGCGCA GCCTGCTCAA CCTGAAGGCC ATGTTGGAGG CCGTCACAGG GAGGAGCGCC 240  
ATCCTGTCCT TCGTGGGCTA CGTTTGTCTG TGTGGGCTGG GGGGCGGTGG CCAGCCCAAG 300  
GATGAGTGG ACTGGTGTCT CCACGCCAC GACTGCTGCT ACCAGGAAC CTCTTGACCA 360  
GGCTGTACCC CCTATGTGGA CCACTATGAT CACACCATCG AGAACACAC TGAGATAGTC 420  
TGCAGTGACC TCAACAGAGC AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480  
GTCTGTGCTC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCTC CAATGTCTAC 540  
TGCCAGGGCC CCACGCCCAA CTGCAGCATC TATGAACCGC CCGCTGAGGA GGTCACTGTC 600  
AGTACCAAT CCCCAGCGCC CCCCAGCGCT CCCTAG

Seq ID NO: 195 Protein sequence  
Protein Accession #: NP\_073730

55  
60  
1 11 21 31 41 51  
MADGAKANFK GFKKKVLDR FSGWRGPRFG ASCPSRTSRS SLGMKKFFTV AILAGSVLST 60  
AHGSLNLLKA MVEAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDWCHAH DCCYQELFDQ 120  
GCHPYVDHYD HTIENNTIEV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EBYRGLFNVY 180  
CQGPTEPCSI YEPPPEEVT SHQSPAPPAP P

Seq ID NO: 196 DNA sequence  
Nucleic Acid Accession #: XM\_028196.1  
Coding sequence: 1315..1791

65  
70  
75  
80  
1 11 21 31 41 51  
GGCATGTATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60  
GTGTGTGTGT GTCTGGAGTC ATGGCAGGCT CCCTTCTGT CTGTCTCCTT GCTCTGCCCG 120  
AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180  
ATGGCCTGGG CTGGGCCCCC GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAAG 240  
CTCTTGTGGG CAAAGCAGGG GAGGCGCCAA TGTGAGGAA CAGAGTCTCC TGGCTGGCTG 300  
CTGCTCTCTG GAGCGGGTGG AGTCAGGGA GAGCTGAGCT GGGGAGTCAC CTGGGGCTG 360  
GGGTACCGT AGGCCCATG TAGCACCTG GTTCCCTGTC CTGTAGGTGA CAGGAGCCAG 420  
CCAGCCCATG TGTCTCCCT CCCCAGGCC TAGGCAGCG GGTACAGGG CCAGCAGCTG 480  
CGCCCGCCCC ACCTTCTTTC CCACCCACAT GCGAAGGGT GGCCAGGCA GCAGGTGGAC 540  
GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGAATGTTC TGGCGCTCC CAGCTGCACC 600  
CTGCCCTAC CTGCCACCAC CTCACCTTCA TCCTCAGGCG CTGGGGCCCT GAGCCCTGTC 660  
CAGGAATGCA CCTTAGCCCC AGGCCTGCTC AGTGAGCTCC GCGCACAGCC AGCCCTGCTC 720  
CTCCGCCCAT TGTCTCCCT ACCCTCTGG GCTTCCAGT TCTTGGGGC TGCAGTGAAC 780  
ATGCTCACC TGCATGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT 840  
AGAGGCAAGG TAGTGATGG ACCGCAGAGA TGAGACCCC AGGGATGAGA TGGGACCCCC 900  
AGGCAGGGCC CAGGTCACG GGCACAGGAG AGAGAAGCAG GAGAGGAGAG AGCTTCTCTG 960  
TGGAGGACGC ATCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020  
AGGCTGCCCA GGCCTGCCCT GCTTGGCTGG GGCTGGGGG TGTCTGGAGG TGGCTGGGAG 1080  
GCTGGGCGCT GGCAGCTAAG CTGGAGCTTT GGCCAGGCTC CAGAGCCTCC CTCCCTTCA 1140

5 CTTCCTGCTG CACAGAACCCT TCGCCCTGG CCACCCCGTG CTGCCTCCTT GCCCTGGCAG 1200  
 ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCGGGA GGGGCCACCC 1260  
 TCCCAGCTGA CCCAGCCTCC TGGCCCGCTT CTTCACAAAC AGCAGGGTAG AAAGATGGGG 1320  
 CACCCACAGC TCTCTCCAGG TGCCCGGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGGCTT 1380  
 ATTCAGAGC TTGTCGCGG GACCCCTGT GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440  
 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500  
 CCAGGGGCCCC GCTGGGCTCT CATTGCGGC GCCCTTGCCG CGGGGCTCCT CCTGCTCTCC 1560  
 TGCTCTCTCT GTGCTGCTGCT CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAAG 1620  
 GAGTCCGTTG GTCTGGGCGG TGCCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680  
 10 TCCTTGCTCA CTAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740  
 GGGCAGTTCA GCCCCAGGGA TGGTTAAACC CCCACAGAGG CAGGGCGTTG AGGACCTTCC 1800  
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCAT 1860  
 GGGCCCGAGG GAGCCACAGC GGGTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCAGT 1920  
 TTTGGGTGGG TTTGGCGGCT CTCACAGAGC GAAGCCGACG ATTTGTGCTT GTTGGGTGGC 1980  
 15 CTGCGCTGCA GCGGGGGGGT CTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCAGGG 2040  
 CTCTGATGAG GCATGATGTC AGCACCACCT GCCCCTGTGC CCACTCACT CCAGGTGCAA 2100  
 CCTGATGTGG ATGCGCTGAG GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCGTGCAG 2160  
 CTCTCCCTGG AGTTCGACTT TGAAGGCCAG GAGGTGAAGG GCCCGCTGTC GCAGGACCAG 2220  
 CGGTTCTGCG AGTTTCGGGA AAGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280  
 20 TGGGAGCTG ACAGGGCAGG GGGCCTTGGC TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340  
 GTGGGCTCTA GGCAGGCAGC GCACTGAGG CCGTGGGGCA CCGTGGACCC CTATGCCCGG 2400  
 GTACAGGCTT CCACCCAGG CCGACACAGA CATGAGACAA AAGTGCACCG AGGCACGCTC 2460  
 TGCCCGCTGT TTGACGAGC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGCTGGGTGG 2520  
 25 GCTTGGACGG CTGATGGGC CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCTGGGCA 2580  
 GCTGGGTGGG CTGAGCTAG GGCAGCAGGG CCGCTGCAC GCGCTGCTC CAGATCCCGC 2640  
 AGGCGGAGCT GCGAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700  
 GGCATGAGCC CCGGTGAGG CTGCTGCTG CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760  
 TGGAGCACTG GTACCTGCTG GCGCCGCGCG CTGCCACTCA GGTGAGGTGC TGGTCAACAG 2820  
 GCCACAGCCC AAGGCAGAGT TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC 2880  
 30 CTGATGGCTA CCAATTTTCG GGGTCTGAGC CCAACTCGG CAGAAATCAC CCTCCCGGGC 2940  
 TGAAGCCCTT CTGCTGCCC ACAGCCCGAG CAGGTGCGGG AGCTGTGCTT CTCTCTCCGG 3000  
 TACGTGCCCA GCTCAGGCG GCTGACCGTG GTGGTGTGG AGGCTGAGG CCGCTGCTCA 3060  
 GGAATGTCAG AGCCCTACGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG 3120  
 35 AGAAGACAG CCACCAAAAA GGGCAGCGCG GCCCCTACT TCAATGAGGC CTTCACCTTC 3180  
 CTGGTGGCCT TCAGCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGACCGCAGC 3240  
 CTGCGCTGCC GAACGTGAGC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300  
 CCGCTGACGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GCGCCATTCG CCAGCGGCAC 3360  
 CCGCTGCGGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCCG CCTTCGCTCG 3420  
 40 CGCCTGCCCT TGCCCACTC CTGAATGCAC CACATGCCCT TGCTCTCCCG CTGAGCCAG 3480  
 GCATCTGCCC AGGCGGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

Seq ID NO: 197 Protein sequence

Protein Accession #: XP\_028196.1

45 1 11 21 31 41 51  
 MGHPPVSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQBG GSDNPAKWGL QLSTDALSLSA 60  
 STPGPRWALI AGALAAAGVLL VSCLLCAACC CRRHRKKKPR DKESVGLGSA RGTTTTLHVR 120  
 50 SGLLTQSRRE GLKSLRLQSPG QRGEPSPRDG LTPTEAGR

Seq ID NO: 198 DNA sequence

Nucleic Acid Accession #: NM\_000612.2

Coding sequence: 553..1095

55 1 11 21 31 41 51  
 TTCTCCCGCA ACCTTCCCTT CGTCCCTCC CGTCCCGCCC AGCTCCTAGC CTCGACTCC 60  
 CTCCTCCCTT CAGCCCGGCC CTCTCGCTT CGCCGAACCA AAGTGGATTA ATTACAGCT 120  
 60 TTCTGTTTCT CTCGTGCTG TTCTCTCCCG CTGTGCGGCT GCGCGCTCT CTCTGCTCTC 180  
 TCTCCCTCTT GCGCTCTCTT CGGCCCGCCC CTCTCAGTCT CACTCTGCTC CTCCACTAT 240  
 CTCTGCCCCC CTCTATCCTT GATACCAACG CTGACCTCAT TTCCGATAC CTCTTCCCCC 300  
 CCGAAAGTGA CAACATCTGG CCGCCCGCCG CCGGAAGACA GCGCGTCTC CTGGACAAT 360  
 CAGACGAATT CTCCCCCCCC CCCCCAAAAA AAAAGCCATC CCCCCGCTCT GCGCCGTCGC 420  
 65 ACATTGCGCC CCGCGACTC GCGCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG 480  
 CCAACGCGCG CTGTTCCGTT TGGCAGACGC AGCAGGGAGG TGGGCGGCAG CGTCGCGGCG 540  
 TTCCAGACAC CAATGGGAAT CCAATGGGGG AAGTCGATGC TGGTGTCTCT CACCTTCTTG 600  
 GCCTTGCCCT CGTCTGCTAT TGCTGCTTAC GCGCCCATG AGACCTGTG CCGCGGGGAG 660  
 CTGGTGGACA CCTTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCGCGA 720  
 70 AGCGGTGTGA GCGGTGCGAG CGGTGGCATC GTTAGGAGGT GCTGTTTCCG CAGCTGTGAC 780  
 CTGGCCCTCC TGGAGACGTA CTGTGCTACC CCGCCCAAGT CCGAGAGGGA CGTGTGAC 840  
 CCTCGGACCG TGCTTCCGGA CAACTTCCCC AGATACCCCG TGGGCAAGTT CTTCATAT 900  
 GACACTGGA AGCATCTCA CAGGCGCTG GCGAGGGGCC TGCCCTGCTT CCTGCTGCTC 960  
 CGCCGGGGTC ACGTGTCTGC CAAAGAGCTC GAGGCGTTCA GGGAGGCCAA ACGTCACCGT 1020  
 75 CCGCTGATTG CTCTACCCAC CCAAGACCCC GCGCCCGGGG GCGCCCGCCC AGAGATGGCC 1080  
 AGCAATCGGA AGTGGACAAA ACTGCCGCAA GTCTGACGCC CCGCGCACCC ATCCTGCAGC 1140  
 CTCTCTCTGA CCAAGGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACGT 1200  
 CCGCTGCGGC CTCTCTCTGA CCAAGTCCCC GTGCCCGGCC TCCCGAAGAC AGGCTACTCT 1260  
 80 CCTCGGCCCC CTCCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC 1320  
 GATTGGCTTT AAACACCTTT CACATACCTT CCCCCC

Seq ID NO: 199 Protein sequence

Protein Accession #: NP\_000603.1

1 11 21 31 41 51

MGIPMGKSM L VLLTFLAFAS CCIAAYRPSE TLGGELVDLT LQFVCGDRGF YFSRPASRVS 60  
 RRSRGIVEEC CFRSCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPYPYV GKFFQYDTWK 120  
 QSTQRLRRGL PALRLARRGH VLAKELEAFR EAKRHRPLIA LPTQDPAHGG APPEMASNRK

Seq ID NO: 200 DNA sequence  
 Nucleic Acid Accession #: AK057131.1  
 Coding sequence: 61..1146

1 11 21 31 41 51  
 AGTCTGGGCG TTTAGGTCAG AACTACCCCG GTAGCCTGAC AGCAGGAGCT CGAGAGAAGC 60  
 ATGGCTCAGC GGTGCGTTTG CGTGCTGGCC CTGGTGGCTA TGCTGCTCCT AGTTTTCCTT 120  
 ACCGTCTCCA GATCGATGGG CCGAGGAGC GGGAGGATC AAAGGGCGTC GCGAATCCCT 180  
 TCTCAGTTCA GCAAAGAGGA ACGCGTCGCG ATGAAAGAGG CGCTGAAAGG TGCCATCCAG 240  
 ATTOCAACAG TGACTTTTAG CTCTGAGAAG TCCAATACTA CAGCCCTGGC TGAGTTCGGA 300  
 AAATACATTC ATAAAGTCTT TCCTACAGTG GTCAGCACCA GCCTTATCCA GCATGAAGTC 360  
 GTGGAAGAGT ATAGCCACCT GTTCACTATC CAAGGCTCGG ACCCCAGCTT GCAGCCCTAC 420  
 CTGCTGATGG CTCACCTTGA TGTGGTGCTT GCCCTGAAG AAGGCTGGGA GGTGCCCCCA 480  
 TCTCTGGGT TGGAGCGTGA TGGCGTCATC TATGTTGGG GCACACTGGA CGACAAGAAC 540  
 TCTGTGATGG CATTACTGCA GGCCTTGGAG CTCCTGCTGA TCAGGAAGTA CATCCCCGGA 600  
 AGATCTTTCT TCATTCTCTT GGGCCATGAT GAGGAGTCAT CAGGGACAGG GGCCTCAGAGG 660  
 ATCTCAGCCC TGTACAGTCT AAGGGGCGTC CAGCTAGCCT TCATTGTGGA CGAGGGGGGC 720  
 TTCATCTTGG ATGATTTTCA TCCTAACTTC AAGAAGCCCA TCGCCTTGAT TGCAGTCTCA 780  
 GAGAAGGGTT CCATGAACCT CATGCTGCAA GTAAACATGA CTTCAGGCCA CTCCTCAGCT 840  
 CCTCCAAAGG AGACAAGCAT TGGCATCCTT GCAGCTGCTG TCAGCCGATT GGAGCAGACA 900  
 CCAATGCCTA TCATATTGGG AAGCGGGACA GTGGTGACTG TATTGCAGCA ACTGGCAAT 960  
 GAGGTTTATG GCTAGAAATC CCTTAACCAA TGCAATAATC AGGACACCA CGGCACTCAC 1020  
 CATATTCAA CGAGGGGTCA AGTTCAATGT CATCCCCCA GTGGCCGAGG CCACAGTCAA 1080  
 TCTCCGGAT CACCCTGGAC AGACAGTCCA AGAGGTCTTA GAACTCAGCA AGAATCTGT 1140  
 GGCTGATAAC AGAGTCCAGT TCCATGTGTT GAGTGCCTTT GACCCCTCC CCGTCAGCCC 1200  
 TTCTGTGATC AAGGCTTGG GCTACAGCTT GCTCCGCGAG ACCGTACAGT CCGTCTTCCC 1260  
 GGAAGTCAAT ATTACTGCCC CAGTTACTTC TATTGGCAAC ACAGACAGCG GATTCTTTAC 1320  
 AAACCTCACC ACTGGCATCT ACAGGTTCTA CCCCATCTAC ATACAGCCTG AAGACTTCAA 1380  
 ACGCATCCAT GGAGTCAACG AGAAAATCTC AGTCCAAGCC TATGAGACCC AAGTGAAATT 1440  
 CATCTTTGAG TTGATTGAGA ATGCTGACAC AGACCAGGAG CCACTTTCTC ACCTGCACAA 1500  
 ACTGTGAGGT CAAGGGGCTT GCTGGGTTAG GCATGCCGGA CCCGGGACA GGAATAACCC 1560  
 AAGGGGGAAA GCTAGTGTG ATGAACTTT TGATCAAAAC CACATTGTAA AACATTGCC 1620  
 ATCTGCTTGG CTCACCTTAA AACTCTCCCA AGAACCAAGG CGGGTAAGG TAAAGTCAGC 1680  
 AGAAATCTGG CTCTCTCCCT CTTCCGACA TCTGCATCCC TTGATCCACT GGCATTGTCT 1740  
 GCGCTCTGT CCCTTATCTG TCTTAGCTG GTTATTTTAC TGCTTCACCT TCCAGGCTTG 1800  
 ACTTAACAAA TGTAGATTGG AGAAATCTCA ACCAGTTGTT ACCTGATAGG AGTCTTTAAT 1860  
 TTAGGCGACT TTGCTGGGGA TGCTTTCTCC AGAGCTTATA TATTCTCTCT TACTAGAACT 1920  
 TTCTTCCCCC TTTTATTTCC CTCTCTTCTT GGACTCATGA GCTGCTCTTT CATCTCTCCT 1980  
 CTCTCTCTG CATCTCTCCC CTTACTCTTC AATTTATTCT ACTTCTGGAC CTGGAATTAC 2040  
 CCAAAGTGTG ATACTACCAT AATTGTCAAC ATAATCAGTC AAATAAAGTG ATCTGTGCAT 2100  
 C

Seq ID NO: 201 Protein sequence  
 Protein Accession #: BAB71368.1

1 11 21 31 41 51  
 MAQRVCVLA LVAMLLLVFP TVSRSMGPRS GEHQRASRIP SQFSKEERVA MKEALKGAIQ 60  
 IPTVTFSSEK SNTTALAEPG KYIHKVFPPTV VSTSPHQHEV VEEYSHLFTI QGSDPSLQPY 120  
 LLMAHFDVVP APEEGHEVPP FSGLERDGVY YGWTGLDDKN SVMALLQALE LLLIRKYIPR 180  
 RSFFISLGHG EESSGTGAQR ISALLQSRGV QLAFTVDEGG FILDFFIPNP KKPIALIAVS 240  
 EKGSMMLAQ VNMTSGHSSA PPKETSIGIL AAASRLQET PMPIIFGSGT VVTVLQQLAN 300  
 EVYGEKSLAQ CNQDHHGTH HIQSRGQVQC HPPSGPGHSQ LPDSFPWTDSP RGPRTHEHC 360  
 G

Seq ID NO: 202 DNA sequence  
 Nucleic Acid Accession #: NM\_004217.1  
 Coding sequence: 58..1092

1 11 21 31 41 51  
 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG 60  
 GCCCAGAAGG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120  
 AGCACCTCTG CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180  
 ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCTGGCC AGAAGGTGAT GGAGAATAGC 240  
 AGTGGGACAC CCGACATCTT AACCGGGCAC TTCACAAATG ATGACTTTGA GATTGGGCGT 300  
 CCTCTGGGCA AAGGCAAGTT TGGAAACGTC TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360  
 ATCGTGGCCG TCAAGTCTCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420  
 CTGCGCAGAG AGATCGAAAT CCAGGCCAC CAGCACCATC CCAACATCTT CGCTCTCTAC 480  
 AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540  
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG 600  
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660  
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG 720  
 TCTGTGCATG CGCCCTCCTT GAGGAGGAAG ACAATGTGTG GCACCTCGGA CTACCTGCC 780  
 CCAGAGATGA TTGAGGGGCG CATGCACAAAT GAGAAGGTGG ATCTGTGGTG CATTGGAGTG 840  
 CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCTTTGAGA GTGCATCACA CAACGAGACC 900  
 TATCGCCGCA TCGTCAAGGT GGACCTAAGG TTCCCGCTT CTGTGCCAC GGGAGCCGAC 960  
 GACCTCATCT CCAACTGCTC CAGGCATAAC CCTCGGAAC GGCCTGCCCT GGCACAGTCT 1020

TCAGCCACC CTGGGTCG GGCACACTCT CGGAGGGTGC TGCCCTCCCTC TGCCCTTCAA 1080  
 TCTGTGCGCT GATGGTCCTC GTCACTTCACT CGGGTGCCTG TGTITGTATG TCTGTGTATG 1140  
 TATAGGGGAA AGAAGGGATC CCTAAGCTGT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200  
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 203 Protein sequence  
 Protein Accession #: NP\_004208

1 11 21 31 41 51  
 MAQKENSYPW PYGRQTAPSG LSTLPQVRVLR KÉPVTPSALV LMSRSNVQPT AAPGQKVMEN 60  
 SSGTPIIDLTR HFTIDDFEIG RPLGKGFN VYLAREKSH FIVALKVLFK SQIEKEGVEH 120  
 QLRRRIEIQH HLHHPNILLR YNYFYDRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180  
 MEELADALMY CHGKKVIRHD IKPENLLGL KGEIKIADFG WSVHAPSLLR KTMCGTLDYL 240  
 PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA 300  
 QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPSPAL QSVA

Seq ID NO: 204 DNA sequence  
 Nucleic Acid Accession #: AK055663  
 Coding sequence: 38..1423

1 11 21 31 41 51  
 AGAACGGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTG 60  
 AAAACACCAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120  
 CCGAAGGTCC TGGAGATAC TGCTCTTTGG TGTAAATAAC TTGATATGTA CTGGCTCTCT 180  
 GCTTATGTGG TGCAGTCTTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT 240  
 TTTTGATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC 300  
 TAGCCCTGTC TATTCAATTG GGTITGAAAG ATTAGAAGTC CTGGCTGTAT TTGCTCCAC 360  
 AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAAGAA AGTGCAGAAC GCTTTTGGGA 420  
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTGGTACT TTTGTGGCTC TTTGTTTCAA 480  
 CCTGTTCAGC ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540  
 TACGAGCTGG CTTCAGAGC ATGTTGCAGA TCTTAGTCTG AGCTTGTGTG GAATTATTCC 600  
 GGGACTTAGC AGTATCTTCC TTCCCGCAAT GAATCCATTT GTTTGTATG ATCTGTCTGG 660  
 AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCGGTAGA 720  
 CACTGCCTCT GCTATAGCTA TTGCTGTGAT GACATTGGGC ACTATGTATC CCATGAGTGT 780  
 GTACAGTGGG AAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATGTGTC AGTGGACAA 840  
 ACTCATCAGA TTTAGTATCTA CCTTAGATGG AGTTTATGAA GTCCGAAATG AACATTTTTG 900  
 GACCTAGTGT TTTGGCTCAT TGGCTGGATC AGTGCAATGA AGAATTGACG GAGATGCCAA 960  
 TGAACAAATG GAGTCTGCTA ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC 1020  
 TGTTCAAATT TTCAAGGATC ACTGGATTAG GCCTGCCTTA TTGCTGCGGC CTGTTGCAGC 1080  
 CAATGCTCTA AACTTTTCAG ATCATCAGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140  
 TGATTTGAAC CAATTTACTT CAATCCAGC TAACCTAGT AGTCCACCTC CAGAATTTTC 1200  
 ATTTAACAAT CCTGGGAAAT ATGTGAACCC AGTATTCTT CTAAACACAC AAACAAGGCC 1260  
 TTATGGCTGT GGTCTCAATC ATGGACACAC ACCCTACAGC AGCATGCTTA ATCAAGGACT 1320  
 TGGAGTTCCA GGAATTGGAG CAATCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380  
 TAGATATGGA ACTAATAATA GAATGGACA ACCAGACCA TGATAGACTC TAATTTATT 1440  
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTAG TAATCCAAT TTGCATTGAC 1500  
 TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC 1560  
 TATGAACTA TATTTTTGA AAATGTATT GTGACAGTGA AATCCTGTGA AATGTTAAG 1620  
 GCTTTAATA GGCCTCTCTT AGAAAATGTG TTTCTTTAAA TTTGATTTT GGTATCTTTG 1680  
 GTTTTGTAGT TGACTGCAGT GTGATGTGAC CTACCTTTA TAAGAGCCAC TTGATGGAGT 1740  
 AGATCTGCA CAATTAAG ATACGATATT TCTTTTTTTT TCCGAGACGG AGTCTGTCTC 1800  
 TGCCACTGTG CCGGCGCAAT ACATTATAT TAACCTAAGG CTGACTTTA TTAAGGCTTC 1860  
 CTTAGTTTTT GTTTTGTGTT GTTTTTGAG ATGGAGTCTC ACTCTGTGCG CCAGGCTGGA 1920  
 ATGCAGTGGC ATGATCTCAG CTCACCTGCA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC 1980  
 TGCCCTAGCC TCCGAGTAG CTGGGATTAC AGGCACCTGC CACCAAGCCC AGCTAATTTT 2040  
 TGTATTTTGA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAATCCTG 2100  
 ACCTCATGAT CCACCCCACT TAGCCTCCCA AAGTGTCTGG ATTAGGTGTG AGCCACCGCA 2160  
 CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATA TACACATTTT 2220  
 GGGAAACGGA AAAATGTCTG TTCAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT 2280  
 AATTGCTAAA TTTTCTTTG AGGTCTCTCT GAATTATGTC TTACAACTA AAAGCAAAA 2340  
 TTTTATGACA AAATTTTGA ATACATTCTA TCTAGCACAA TTTGAATTT TAATTATCAA 2400  
 GATTTTGTG AAAGTTTCTC TCCTTTAAA ATTTAGTAC ATTTGTAAT

Seq ID NO: 205 Protein sequence  
 Protein Accession #: BAB70980.1

1 11 21 31 41 51  
 MGTIHLFRKP QRSFFGKLLR EPRLVAADRR SWKILLFGVI NLICTGFLM WCSSTNSIAL 60  
 TAYTYLTIFD LPSLMTCLIS YWVTLRKPS VYSFGFERLE VLAVFASTVL AQLGALFILK 120  
 ESAERFLQEP EIHTGRLLVG TFVALCFNL TMLSRNKP AYVSEAASTS WLQEHVADLS 180  
 RSLCGIIFGL SSIFLPRMNP FVLIDLAPG ALCITYMLIE INNYFAVDTA SAIAIALMTF 240  
 GLTMYPMVSYS GKVLQITTP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH 300  
 VRIRRDANEQ MYLAHVNTNRL YTLVSTLTIV IFKDDWIRPA LLSGPVAANV LNFSDRHVIP 360  
 MPLLKGTDDL NPVTSTPAKP SSPPPPEFSN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY 420  
 SSMLNQGLGV PGIGATQGLR TGFTNIPSRY GTNNRIGQPR P

Seq ID NO: 206 DNA sequence  
 Nucleic Acid Accession #: NM\_016361.1  
 Coding sequence: 397..1662

1 11 21 31 41 51



5  
10  
15  
20  
25  
30

	GGAACTCAGG		GCCGGCTCCT		GTTCCTTCAA		GAGTGTCTGA		GGCCAAACTT		GAATACAAG	60
	TTTAATGTTT		CTCGTCGGGC		AAAAGATAAG		GATCCGATCT		CCCCCGGCC		GGTGTGCAGC	120
	AGGAGCGACC		AACCCCGACC		CGGGTTAAAA		CTCCAGGGA		CTCTCGCTG		CTGCCACCTC	180
	TTGTTCTCTC		CCCCGTTCCC		ACTCGGGGTC		TCCCTCAGGG		CGGGAGGCA		CAGCGGTCCC	240
	TGCTTGTCTG		AGGGCTGGAT		GTACGCATCC		GCAGGTTCCC		GCGGACTTGG		GGGCGCCCGC	300
	TGAGCCCCGG		CGCCCGCAGA		AGACTTGTGT		TTGCCCTCTG		CAGCCTCAAC		CCGGAGGCGAG	360
	CGAGGGCCTA		CCACCATGAT		CACTGGTGTG		TTACGATGC		GCTTGTGAC		CCAGTGGGC	420
	GTCTGACCTT		CGCTGGCGTA		CTGCCTGCAC		CAGCGCGGGG		TGGCCTGGC		CGAGCTGCAG	480
	GAGGCGGATG		GCCAGTGTCC		GGTCGACCGC		AGCCTGTCTG		AGTTGAAAT		GGTGCAGTTC	540
	GTGTTTCGAC		ACGGGGCTCG		GAGTCTCTC		AAGCGCTCC		CGCTGGAGGA		GCAGGTAGAG	600
	TGGAACCCCC		AGCTATTAGA		GGTCCACCC		CAAACTCAGT		TTGATTACAC		AGTCACCAAT	660
	CTAGCTGGTG		TGCCGAAACC		ATATTCTCCT		TACGACTCTC		AATACCATGA		GACCAACCTG	720
	AAGGGGGGCA		TGTTTGTCTG		GCAGCTGACC		AAGGTGGGCA		TGCAGCAAT		GTTCGCTTGT	780
	GGAGAGAGAC		TGAGGAAGAA		CTATGTGGAA		GACATTCCCT		TTCTTTCACC		AACCTTCAAC	840
	CCACAGGAGG		TCTTTATTGG		TTCCACTAAC		ATTTTTCGGA		ATCTGGAGTC		CACCCGTTGT	900
	TTGCTGGCTG		GGCTTTTCCA		GTGTGAGAAA		GAAGGACCCA		TCATCATCCA		CAGTGTGAAA	960
	GCAGATTGAG		AAGTCTTGTA		TCCCAACTAC		CAAGCTGCT		GGAGCCTGAG		GCAGAGAACCC	1020
	AGAGGCCGGA		GGCAGACTGC		CTCTTTACAG		CCAGGAATCT		CAGAGGATT		GAAGAGGTG	1080
	AAGGACAGGA		TGGGCATTGA		CAGTAGTGAT		AAAGTGGACT		TCTTCATCCT		CCTGGACAAC	1140
	GTGGCTGCGG		AGCAGGCACA		CAACCTCCCA		AGCTGCCCA		TGCTGAAGAG		ATTGTCACGG	1200
	ATGATCGAAC		AGAGAGCTGT		GGACACATCC		TTGTACATAC		TGCCCAAGGA		AGACAGGGAA	1260
	AGTCTTCAGA		TGGCAGTAGG		CCCATTCCTC		CACATCCTAG		AGAGCAACCT		GCTGAAAGCC	1320
	ATGGACTCTG		CCACTGCCCC		CGACAAGATC		AGAAAGCTGT		ATCTCTATGC		GGCTCATGAT	1380
	GTGACCTTCA		TACCCTCTT		AATGACCCCTG		GGGATTTTGT		ACCACAAATG		GCCACCGTTT	1440
	GCTGTGTACC		TGACCATGGA		ACTTTACCGA		CACCTGGAAT		CTAAGGAGTG		GTTTGTGCAG	1500
	CTCTATTACC		ACGGGAAGGA		GCAGGTGCCG		AGAGGTTGCC		CTGATGGGCT		CTGCCCCGCTG	1560
	GACATGTTCT		TGAATGCCAT		GTCAGTTTAT		ACCTTAAGCC		CAGAAAAATA		CCATGCACTC	1620
	TGCTCTCAAA		CTCAGGTGAT		GGAAGTTGGA		AATGAAGAGT		AACGTATTTA		TAAAAGCAGG	1680
	ATGTGTTGAT		TTTAAATATA		AGTGCCTTTA		TACAAAAAAA		AAAAAATAA		A	

Seq ID NO: 207 Protein sequence  
Protein Accession #: NP\_057445.1

35  
40  
45

	1		11		21		31		41		51	
	MRLWTFVGL		TSLAYCLHQ		RVALAELQEA		DGQCFVDRSL		LKLKMQVQVF		RHGARSPLKP	60
	LPLEQVEVNN		PQLEVPPT		QFDYTVNL		GGPKPYSPYD		SOYHETTLKG		GMFAGQLTKV	120
	GMQMFALGE		RLRKQYVEDI		PFLSPTNPQ		EVFIRSTNIF		RNLESTRCLL		AGLFQCKKEG	180
	PIIHTDEAD		SEVLVYNYQS		CNSLRQRTG		RQQTASLQPG		ISEDLLKVKD		RMGIDSSDKV	240
	DFIILLDNVA		AEQAHNLPSC		PMLKRPFARM		EQRAVDTSLY		ILPKEDRESL		QMAVGPFLLHI	300
	LESNLLKAMD		SATAPDKIRK		LYLYAAHDVT		FIPLMLTGI		FDHKWPPFAV		DLTMELYQHL	360
	ESKEWFVQLY		YHKEBQVPRG		CPDGLCLPDM		FLNAMSVTYL		SPEKYHALCS		QTQVMEVGENE	420
	E											

Seq ID NO: 208 DNA sequence  
Nucleic Acid Accession #: CAT cluster

50  
55  
60

	1		11		21		31		41		51	
	TTTGAGGGGG		TGGTGGGGCG		AGTTTAATTC		ATAAAGAAGC		CTCCTGATCA		GAAGGGGGCC	60
	TACAGCGCTG		CCCTTGAGAG		GAAGTCCTTC		CTTGAGGATA		AGGCCTCCCA		GGGGAGGAGG	120
	TGCTGGGGCG		CAGTGTAGG		CTTCAGGCCA		TCCCTGGAGG		CCAGTCCTGT		GCTCAGCAAG	180
	TAGTGGCAGA		GCCTGGAGTG		ATGAGTGGGA		TGGCCTTCTC		AGGTACAGGA		CTGTGCTGCT	240
	TCTGGCTGCT		CTTGCAATTG		CATTTGCCAC		TCAGAACTGC		CGGATCCCA		GCAATGGCCA	300
	GGAGCCCTCC		GCAGATCAGT		CCGCTCAGCT		GCAGGTTTTT		CCAGTCATAG		TAGAAGGGAT	360
	CGTCTTTATT		GGCAAAATGG		TCATTGGCTT		CCAAGGCAGT		CAGGCCAACT		GTGTGACTCT	420
	GCAGGTTCTT		CACTGCTCCT		TCACCAAGTG		CCTGCGAGST		CACCTTGGCG		AGGGCTCACC	480
	TGAGCTGGCA		GCGCAG									

Seq ID NO: 209 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..564

65  
70  
75  
80

	1		11		21		31		41		51	
	ATGGAGCCCT		GGGCGTGCTT		GCAGGGTTTA		AAGAGCCGAC		CCACGTGCCC		AGCAGCCTCC	60
	TCAGATCCGT		TCTCTGCGCT		GCCAGCTCAG		GACACTGGTG		AAGGAGCAGT		GAGGAACCTG	120
	CAGAGTCACA		CAGTTGGCCT		GACTGCCTTG		GAAGCCCAATG		ACCCATTTCG		CAATAAGAC	180
	GATCCCTTCT		ACTATGACTG		GAAGAACCTG		CAGCTGAGCG		GACTGATCTG		CGGAGGGCTC	240
	CTGGCCATMG		CTGGGATCGC		GGCAGTTCTG		AGTGGCAAAT		GCAATGCAAA		GAGCAGCCAG	300
	AAGCAGCACA		GTCTGTATCC		TGAGAAGGCC		ATCCCACTCA		TCACTCCAGG		CAGATTCTCT	360
	ACCTTGGCCA		AATCAAAATA		ACCTTTATCT		CCAAGCACCT		TTGTCTTGGT		GTTTGGCATC	420
	AGCTACACAT		CAGTCTTCCG		AGTGCCTCTT		TCTGCGTCCC		TGTACCCCTG		CATTCTCTGT	480
	GATGCTGCTG		CCCTCACATC		AGGCCATCCA		AGCATGACA		ACATAAGCAT		GCAGAACACT	540
	GGAACGAAGG		GCTGTACCTA		ATGA							

Seq ID NO: 210 Protein sequence  
Protein Accession #: FGENESH predicted

	1		11		21		31		41		51	
	MEPWANLQGL		KSRPTCPAAS		SDPFSALPAQ		DTGEGAVRNL		QSHTVGLTAL		EANDPFANKD	60
	DPFFYDWKNL		QLSLGICGGL		LAIAGIAAVL		SGKCKCKSSQ		KQHSFVPEKA		IPLITPGRFL	120

TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSGHP SMQNISMQNT 180  
GKKGCT

5 Seq ID NO: 211 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..318

```

1      11      21      31      41      51
|      |      |      |      |      |
10 ATGCCCGGCC ACCCGCTCTG TGAAGTGAGG AGCACCTCTG CCGGCTGCC CCGTCTGGGA 60
    AGTGAGGAGC GGCTCTGCCC GGCTGCCACC CCGTCTGTGA GTGCCTGCTG CGCTGGGCCC 120
    AGGCGCGCCG TGCCCTGCCA GGCCCTCCGG CCCCCACCT TCCACCCAG GGCCTGTCTC 180
    TCACCCAGG GTTCCATCTC CTTAGTTTCC ACCAGAGACT GGGTCTTCAT TCTCACCTCG 240
    CTACACAGCC CCTACCAGAA CGTTCTGAAA TGCAAACTTA ACAACTGTCT CACCCAGCA 300
15 GGAAACTCCC CAGGCTCCCG GGCCCCCTGC GGGTTGCGAG GCCTCACTCT TCGCGCCCAT 360
    CCCTCGCCCC TGACCGCCCT GAGCTCGCCC CCAAGTGTGG CCCTTCAGCT CCAGTTATCC 420
    CTCCAGCCT CCAAGGTCCC CGTTACCGAA GACCGCCACC ATCAACGACAT AGCGCAGCAC 480
    ATATGGGACA CTGGTGAAGG AGCAGTGAGG AACCTGCAGA GTCAACAGT TGGCCTGACT 540
    GCCTTGAAG CCAATGACCC ATTTGCCAAT AAAGACGATC CTTTCTACTA TGACTGGAAA 600
20 AACCTGCAGC TGAGCGGACT GATCTGCGGA GGGCTCCTGG CCATTGCTGG GATCGCGGCA 660
    GTTCTGAGTG GCAATATGCA ATGCAAGAGC AGCCAGAAAG AGCACAGTCC TGTAACCTGAG 720
    AAGGCCATCC CACTCATCAC TCCAGGCAGA TTTCTCACCT TGGCCAAATC AAATAAACCT 780
    TTATCTCAA GCACCTTTGT CTGTGTGTTT GGCATCAGCT ACACATCAGT CTTCCGAGTG 840
    CCTCTTCTG CGTCCCTGTA CCCTGCCATT CTTGGTGATG CTGCTGCCCT CACATCAGGC 900
25 CATCCAGCA TGCAGAACAT AAGCATGCAG AACACTGGAA CGAAGGGCTG TACCTAA

```

Seq ID NO: 212 Protein sequence  
Protein Accession #: FGENESH predicted

```

30 1      11      21      31      41      51
    |      |      |      |      |      |
    MPGHVCEVR STSARLPRLG SEERLCPAAT PSVSACCAGP RPPVPCQALR PPTFHPRACS 60
    SPQGSISLVS TRDWFILTL LHSFYQNLK CKENNCLETA GNSPGRAPC GVAGLTLRAH 120
35 PSALTALSSP PVLALHVQLS LPASKVPVTE DRHHHDIAQH IWDTEGAVR NLQSHTVGLT 180
    ALEANDPFAN KDDPFYYDWK NLQLSGLICG GLLAIAAGIAA VLSGKCKCKS SQKHSPVPE 240
    KAIPILITPGR FILTAKSNKP LSPSTFVLVF GISYTSVFRV PLSASLYPAI PGDAAALTSG 300
    HPSMQNISMQ NTGTGKCT

```

40 Seq ID NO: 213 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1758

```

1      11      21      31      41      51
|      |      |      |      |      |
45 ATGATGGGGT CTCAATGTTG CCAGGCTGGT CTTGAAGTCC TGGGCTCGAG TGACCCTCCT 60
    GCCTTGGCCT CGAAAGATGC TGGGATTACA GGAAGTGTAT TACAGGAATC CATAACACTG 120
    GAGGATGTGG CTGTGGACTT CACTTGGGAG GAGTGGCAAC TCCTGGGCGC TGCTCAGAAG 180
    GACCTGTACC GGGATGTGAT GTTGGAGAAC TACAGCAACC TGGTGGCAGT GGGGTATCAA 240
    GCCAGCAAAC CGGATGCACT CTTCAAGTTG GAACAAGGAG AACAACTGTG GACAATTGAA 300
50 GATGGAATCC ACAGTGGAGC CTGTTCAAGT TCTCCAAAGG TCCCGTTCTC CATTTTCTCA 360
    TCTGTGCCCT TCACCTCTCA AAATTGCCCT CATTCTAACA TATGGAAAGT TGATCATGTG 420
    CTGGAGCGCT TGCAGAGTGA AAGCCTGGTG AACAGAAGGA AACCATGTCA TGAACATGAT 480
    GCATTTGAAA ATATTGTTC TGCAGCAAAA AGTCAGTTTC TGTTAGGGCA AAATCATGAT 540
    ATATTGACT TACGTGAAA AAGTTTGAAA TCCAATTAA CTTTAGTTAA CCAGAGCAAA 600
55 GGCTATGAAA TAAAGAATCT TGTGTAGTTT ACTGGAATG GGGACTCCTT TCTTCATGCT 660
    AACCATGAAC GACTTCATAC TGCAATTAAA TTCCTTGCAA GTCAAAAACCT CATCAGCACT 720
    AAGTCCCAAT TACTCAGTCC CAAGCATCAG AAAACACGAA AATTAGAGAA GCATCATGTG 780
    TGCAGTGAAT GTGGGAAAGC CTTTCATCAG AAGTCTTGGC TAACTGATCA CCAGGTAATG 840
    CATACAGGAG AGAAACCCCA CAGATGTAGT CTATGTGAGA AAGCCTTCTC CAGAAAGTTC 900
60 ATGCTTACTG AACATCAGCG AACTCATACA GGAGAAAAAC CTTATGAATG CCCTGAATGT 960
    GGCAAGCCTT TTCTCAAGAA ATCAGGCTC AACATACATC AGAAAACACA TACCGGAGAG 1020
    AAACCCCTATA TATGCAAGTA ATGTGAAAAA GGCTTCATCC AGAAAGGAAA TCTCATTGTA 1080
    CACCAAGCGAA TTCATACAGG TGAGAAACCT TATATATGCA ATGAATGTGG AAAAGGCTTC 1140
    ATTCAGAAGA CGTGTCTCAT AGCATCAG AGATTTCACA CAGGAAAGAC GCCCTTTGTG 1200
65 TGCAGTGAAT GTGAAAAATC CTGTTCTCAG AAATCAGGTC TCATTAAACA TCAAAGAAAT 1260
    CACACAGGAG AGAAACCCCT TGAATGTAGT GAATGTGGGA AAGCCTTTAG CACAAAGCAA 1320
    AAGCTCATTT TCCATCAAAG GACTCATAA GGAGAGAGAC CCTATGGCTG TAACGAGTGT 1380
    GGGAAAGCGT TTGCGTATAT GTCGTGTCTG GTTAAGCATA AGAGAATACA CACAAGGGAG 1440
    AAACAAGAGG CAGCCAGGT GGAAATCCT CTTGCAGAGA GGCACAGCTC ATTACACACC 1500
70 AGTGATGTCA TGCAGGAGAA AAATCTGCT AACGGGGCGA CTACACAAGT GCGTCTGTG 1560
    GCCCTCAGA CATCATTAAT CATCAGCGGC CTCTCGCAA ACAGGAACGT AGTCTTGTG 1620
    GGACAGCCAG TGGTCAGATG TGCAGCCTCA GGAGATAACA GAGGATTGTC ACAGGACGA 1680
    AACCTTGTGA ATGCAGTGAA TGTGGTTGTG CCTTCCGTGA TCAATTATGT CTTATTTTAT 1740
75 GTTACAGAAA ACCCATAG

```

Seq ID NO: 214 Protein sequence  
Protein Accession #: FGENESH predicted

```

80 1      11      21      31      41      51
    |      |      |      |      |      |
    MMGSVHAQAG LELLGSSDPP ALASESAGIT GLLQESITL EDVAVDFTWE EWQLLGAQK 60
    DLYRDVMLEN YSNLVAVGYQ ASKPDALFKL EQGEQLWTIE DGIHSGACSG SPRKVPFSIFS 120
    SVPPTLQNC LHSNIKWVDEH LERLQSESLV NRRKPCHEHD AFENIVECSK SQFLLQNH 180
    IFDLRGKSLK SNLTLVNQSK GYEIKNSVEF TQNGDSFLHA NHERLHTAIK FPASQKLIST 240

```

5 KSFQISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQM HTGEKPHRCS LCEKAFSRKF 300  
 MLTEHQRTHT GEKPYECPEC GKAFLEKSRK NIHQKTHTGE KPYICSECGK GFIOKGNLIV 360  
 HQRHTHTEKP YICNECGKGF IQKTCLIAHQ RFHTGKTPFV CSECGKSCSQ KSGLIKHQRI 420  
 HTGEKPFECB ECKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VKHKRIHTRE 480  
 KQEAARKVENP PAERHSSSLHT SDVMQEKNSA NGATTQVPSV APOTSLNISG LLANRNVVLV 540  
 GQPVVRCAAS GDNRGFAQDR NLVNAVNVVV PSVINYLFLY VTEHP

Seq ID NO: 215 DNA sequence  
 Nucleic Acid Accession #: NM\_032190.1  
 Coding sequence: 502..1332

15 1 11 21 31 41 51  
 GATTCCGTGT TCTTGGCCAT GTTAGCCATA ATATCCTGTG CAGTATGTTT TTCTGTGCA 60  
 GAGGCAAAAA CATATTGGGC ATATGTTCCC AAGCCCCCAG CAGTATGACC CACTATTGG 120  
 AGTGACACTC CTCCTAAGAT TTATCATGAT TAAGGAGCAT GGGCTCCAGG ACCCTTAAC 180  
 CCACCTGACA TAGAACAGTT AGACTCTCAG AATAATGTCA TTAATTATAC CGCTCCATTG 240  
 GAAGGACTTC CTTTGTGTGT CACCACAAAG ACATCACTCA GCCATAGCTG TCTTACAGTT 300  
 CAAGCTCACA CATGGTTGAG TCACTATGGG AAAATCATGT ACTTATTAAG TCTTGGTTAT 360  
 20 ATTAATGTAA CCGGTGTGCT AACCAACCAT TCCTGGCCCA ATCGCCTTCA TTGTGCTGAC 420  
 TATACAGAAT GGATTCCCTT CAATAGTTC TACCCCCCTC CATAGACCCA GTGTCTTGGC 480  
 CCACCTGGTA GAAACAAATC TATGTTAACT GGAGACATTG TGGATTGGGG ACCTAAAGGC 540  
 CAATTAGATG GAAAGAAAGA AAATCAGAAA TCGTGGCACA AACTTTGCTG GCATTGGTGG 600  
 CAAGCTTTTA ATGCTTCTTC TTTATATAAC ACTGGGATCC AATCCAGTGC GGCCGCCCAG 660  
 25 ATTGCTTGGC ATGGAGCAGG CTTTAGCCCG CCTCTCTCTC AGTGGCATT TCTAGGAGG 720  
 AAAGGACCAA TTCAAAAGAT GATATGGAAG GCAGCATTC CATTATGAA TGGCAACATC 780  
 TGGGTGCCA TAATACTATC CAATAATAGC AATAGTAAGC AACACAGTCT TAATGTTACA 840  
 TTTGTAAAGA ATATCACAC TCAATTTACA GTTTGTGTTT TTAATCCTTA TGTGTTTTTG 900  
 GCAGCTAAGA AGGACCAGCT CCAGGTAAAC AATACCCAAAT TGACCTGTAA ATCTTGCCAG 960  
 30 TTATATCATC GCATTAATCA TAGCACATTG CAAACACATA ATATCTCTAC TTTGATGATT 1020  
 TTAGGTTGCA TCCCTGGGCT ATGGATTCTT GTTAATCTGT CTGAGCCATG GGCTGCCACA 1080  
 ATTGCTTTAC ATTTGTGAAA ACTTCTCTTA ACTCAGTTTA CTCATTGTGT CCGTAGAGGC 1140  
 TTAGGCATGA TAATTTTGTG TATTGTTTAC TTGGTCACAC TAATAATTTC TGTGTGTGAT 1200  
 TCCTCTGTAG CTTTGCATAG TTCTATTCAA ACAGCTCAGT ATGTGGAGAA CTGGACACGC 1260  
 35 ACAGTCAACC AAGGCTGGCT ACTTGAGAAT AAAATTAACA CTGAGTTACA AACTGAAGTG 1320  
 GCAGTGTAT AATCCACGAT TCTATGGTTA GGGGAACAG TACAAGCTT GCAATTGCAG 1380  
 CAGTAATTGT GTTGTCAATT TAATCACACT CATATTTGTG TAACCAACTT AGAATATAAC 1440  
 CAAAGTAGAT ATCCATGGGA TCTTGTGAAA GCCCATTTC AGGGAGCTTT CACATCCGAC 1500  
 ATCACCTTTG ATATTGGTGA ATTACAAAAC AAAATCTCTG ATTTAAATAA ACAAAATCCA 1560  
 40 GAGTTTCAGC CTTCTTTAGA AGACTGSACT GAATTCACG AAGGCTGGA GAGCGTCAAC 1620  
 CCTTGGACCT ATCAAAGCA CCACATTAAC ATCTTATATA TAGTCTCTGG AATAATGTTG 1680  
 TTTTGTCTCT GTCTCTCTGT CATAGTCTGT AAAATCGGAT GGACTGCCAA TCGGAGAAATG 1740  
 AAAGCTACCC AGCCTGGCCT TACATCTCTT CACTTAATAC ATAAACAAGA AGGGGGAAT 1800  
 GTTGGGAGCC AAAAGGCCA AAGGGATGTT GACCAACTCA GCATTCACCT GGAGGCTACA 1860  
 45 TGATCAACA GCAAACTGTT TATCATGAAT ACAGAAATGT GGCAAACTCG CTTCTGTGCC 1920  
 TGCCAGAAAG GTTGTCTGAG GGCCATGCT CCTGGCCCC GGCTCCTTGA GGTATCTAC 1980  
 TGGGACATCT AGAGCTTATT GTTCAGGAAA TGCAGTCTTG CAAGCCTACT CTGGACGAG 2040  
 CAGCTGACCT CTTCTTCCAC ACCCTTCTC ACTATCTCTT TTGCTTAATA AATATGGAGG 2100  
 50 GCTGTGTAAA GCTCAGGGCC CTTGTCCACT AGAGGCAAGG TGTCCCTGTA CCCTTCTTCC 2160  
 AAACAT

Seq ID NO: 216 Protein sequence  
 Protein Accession #: NP\_115566.1

55 1 11 21 31 41 51  
 MLTGDIVDWG PKQLDQKEE NQKSWHKLCW HWWQAFNASS LYNTGIQSQS AAQIAWHGAG 60  
 FSPPLQWHY LGRKGPQIKM IWKAFFPMN GNIWVAILLS NNSNSKQHSI NVTFVKNITT 120  
 60 QFTVCFNFPY VFLAAKDKQL QVNTQLTCK SCQLYHCINH SLQTHENIST LMILGCIPLG 180  
 WIPVNLSEPW AATIALHFVK LLLTQFTHCV RRLGMIIFA IVYLVTLIIS VVMSSVALHS 240  
 SIQTAYQVEN WRTVNGGWL LENKINTELO TEVAVL

Seq ID NO: 217 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1566

70 1 11 21 31 41 51  
 ATGGTGAACC CCAATTCAC TTCTCCCTC TTCAGGTTAT GTTTTTGCT CCTGAGGAGT 60  
 CAGAACCTGT GGGTTGAAGA GCAAAATCAA TGCAAAAACA TATTGGGCAT ATGTTCCCAA 120  
 TCCCCAGCA GTATGGCCTA TACTTTGGAG CTCCTCTCTC CTGAGATTTA TCACGATCAG 180  
 GGAGAGTGGG CTCAGGAGCC CCAACTCCCT CGTGACATAG AAAAGTTAGA CTCTCAGAAC 240  
 AATGTCAATTA ATTAACCCAC TCCACTGGAA GGACTCCCTT TGTTTATCAC CACAAGAACG 300  
 75 TCGCTCAGCC ATAGCTGTCT TGCAATTCAA GCTCAAAATC GGTGTAGTCA CTATGGAAAA 360  
 ATTATGTACT TATTAGGTCT TGGTCTATT AATGTAACG GTGTGCTAAC CAATCATTCC 420  
 CAGTCCAGTC ACCCTAATTG TGCTGATTAT ACAGAAATGA TTCCATTCAA TAGTCTCTAC 480  
 CCCACTCTGT GGACCCAGTG TCTTGATCCA CTGGCTAGTA AACAATATAT GTCAACTGAA 540  
 GACACTGTGG ATTGGGAACC TAAAGGTCAA TTAGATGGAA AAGGTGAAG TCAGAAATCA 600  
 80 TGGCACAAC TTCCTGGCA TTGGCGGCAA GCTTTTAATG CTTCTCTCTT ATACAACAGC 660  
 AGAATCCAAT CCCAGTCTGC TGCTCAGATT GCTTGGCATG GAGCAGGCTT TAGCCACCT 720  
 CTTCTCAGT TGCATTATCT GGGGAGGAAA GGACCAATTC AAGAACTAT ATGGAAGGCA 780  
 GCATCCCAT TTATGAATGG CAACATCTGG ATTGGAAAC TGCTAATATA TAGCAATAGT 840  
 AAGCAACACA GTCTTAATGT TGCAATTGTA AAGAATATCA CCACTCAGTT TACAGTTTGT 900  
 GTTTTAAATC CTTATGCCTT TTTGGCAGCT AAGAAGAAC AGCTTCAGT GGAGAACTGG 960

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

ACACGCACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020
GAAGTGGCAA TGTTGAAATC CATGGTTCTG TGGTTAGGAG AACAGGTACA AAGCTTGCAG 1080
TTGCAGCAGC AATTCGGTCA TCATTTTAAT CACATTCTATA TTTGCGTAAC TAACTCAGAA 1140
TATAACCAA GTGAGTATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTCACA 1200
TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAA TTATTGATT AAATAGGCAA 1260
ACTCAAGAA TTCAGCCTTC TTTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC 1320
CTCAACCCCT GGACCTATCT AAGGCACCAC ATTAACATCT TATATGTAGT TCTTGAATA 1380
ATGTTGTTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440
AGAATGAGAG CCTCCAGCC CAGCCTTACA TTCTTTCAAT TAATACATA ACAGAAAGGG 1500
GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATTCT GCTGGAGGCT 1560
ATATGA

```

Seq ID NO: 218 Protein sequence  
Protein Accession #: FGENESH predicted

15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
MVNPKSTSSL FRLCFLLLRS QNLWVEEQIQ CKNILGICSQ SPSSMAYTLE LTPPEIYHDO 60
GEWAPGLTP RDIEKLDSON NVINYTTPL E GLPLFITTKT SLSSHCLAIO AQTWLSHYGK 120
IMYLLGLGSI NVTGVLNTHS QSSHPNCADY TENIPFNSSY PTLWTQCLDP LASKQYMSTE 180
DTVDWEPKQG LDGKGESQKS WHKLHWHWRQ AFNASSLYNS RIQSQSAAQI AWHGAGFSPP 240
LPQLHYLGRK GPIQETIWK A ALPFMNGNIW IGTLSNNSNS KQHSLNVAEV KNITTQFTVC 300
VENPYALAA KINQLQVENW TRTADQARLL QNKINTELQT EVAMLKSMVL WLGEQVQSLQ 360
LQQQLRHHFN HIHICVTNSE YNQSEYPWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNRO 420
TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW 480
RMRASQPSLT FFQLIHKQKG GYAGSQRPVG RDQLSILLEA I

```

Seq ID NO: 219 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..900

30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGGGCGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGCGACGGC 120
GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTCTGT AOGTACGTTT AATCGCCCGT CGCGCGCGCT 240
GGCTGCGGCG GGGCTGTGCA CCGGGGAGCT GGGGCGGGCG TCTCGGCGGG AGGGCGCAGA 300
GGACCCCGGG GAGGAGACTG GAGCAGGCCG CGAGGTGGCG CTGTTGCGGC CCAGGACGCT 360
CTTCTAACT CAGGCTCTCC CCGCCCCCGC CCTGCAGTGC AAGTCTGTGT GGATGGAGCT 420
CCGGTGGGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTCTC 480
CTTTGCTACC CGGATACCGA TGTCTTCTGT GCGTGTCTCA GCGTGGTGCA GCCCAGCTCC 540
TTTCAAAACA TCACAGAGAA ATGGCTGCCC GAGATCCGCA CGCACAAACC CCAGGCGCCT 600
GTGCTGCTGG TGGSCACCCA GCGCGACCTG AGGGACGATG TCAACGTACT AATTCAGCTG 660
GACCAAGGGG GCGGGGAGGG CCCCGTGCCC CAACCCAGG CTCAGGCTCT GGCCGAGAAG 720
ATCCGAGCCT GCTGTCTACT TGAGTGTCTA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
GCCAAAGGTG TGGCACCCCT CTCCCGCTGC CGCTGGAAGA AGTTCCTCTG CTTCGTTTGA

```

Seq ID NO: 220 Protein sequence  
Protein Accession #: FGENESH predicted

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVKSSSLIVS YTCNGYPARY 60
RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120
LPNNGSPRPA PAVQVLVDGA PVRIELMDTA GQEDFDRLRS LCYPTDVFLL ACFSVVQPSS 180
FQNIETKWL EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGFVP QPQAQGLAEK 240
IRACCYLECS ALTQKNLKEV FDSAILSABE HKARLEKLN AKGVRTL SRC RWKFFCFV

```

Seq ID NO: 221 DNA sequence  
Nucleic Acid Accession #: XM\_063832.2  
Coding sequence: 1..711

65  
70  
75  
80

```

1 11 21 31 41 51
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGGGCGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGTCTGT GGGCGACGGC 120
GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTCTGT CAAGTCTCTG TGGATGGAGC TCCGTTGCGC 240
ATTGAGCTCT TGGACACAGC GGGACAGGAG GATTTTGACC GACTTGTGTC CCTTTGCTAC 300
CCGGATACCG ATGTCTTCTT GCGGTGCTTC AGCGTGGTGC AGCCAGCTTC CTTCACAAAC 360
ATCACAGAGA AATGGCTGCG CGAGATCCGC ACGCACAAAC CCAGGCGGCC TGTGCTGCTG 420
GTGGGACACC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTCAGCT GGACCGAGGG 480
GGCCGGGAGG GCGCCGTGCC CCAACCCAG GCTCAGGTC TGGCCGAGAA GATCCGAGCC 540
TGCTGTACCT TTGAGTGTCT AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
GCTATTCTCA GTCCATTGA GCACAAAGCC CGCTGGAGA AGAAACTGAA TGCCAAAGGT 660
GTGGCACACC TCTCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTCGTTTG A

```

Seq ID NO: 222 Protein sequence  
Protein Accession #: XP\_063832.1

1 11 21 31 41 51

MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60  
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRRLSLCY PDTDVFLACF SVVQPSSEFN 120  
 ITEKWLPEIR THNQAPVLL VGTQADLRDD VNVLIQLDQG GREGVPVQPQ AQGLAEKIRA 180  
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAKG VRTLSRCRWK KFFCFV

5

Seq ID NO: 223 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1161

10

1	11	21	31	41	51	
ATGAATCGGC	ACCATCTGCA	GGATCACTTT	CTGGAAATAG	ACAAGAAGAA	CTGCTGTGTG	60
TTCCGAGATG	ACTTCATTGC	CAAGGTGTTG	CGCCCGGTGT	TGGGGCTGGA	GTTTATCTTT	120
GGGCTTCTGG	GCAATGGCCT	TGCCCTGTGG	ATTTTCTGTT	TCCACCTCAA	GTCCTGGAAA	180
15						
TCCAGCCGGA	TTTTCTGTT	CAACCTGGCA	GTAGCTGACT	TTCTACTGAT	CATCTGCCCTG	240
CGTTCTGTGA	TGGACTACTA	TGTGGGGCGT	TCAGACTGGA	AGTTTGGGGA	CATCCCTTGC	300
CGGCTGTGTC	TCTTCATGTT	TGCCATGAAC	CGCCAGGGCA	GCATCATCTT	CCTCACGGTG	360
GTGGCGGTAG	ACAGGTATTT	CGGGGTGGTC	CATCCCCACC	ACGCCCTGAA	CAAGATCTCC	420
AATTGGACAG	CAGCCATCAT	CTCTTGCTTT	CTGTGGGGCA	TCACTGTGTT	CCTAACAGTC	480
20						
CACCTCTCTG	AGAAGAAGTT	GCTGATCCAG	AATGCCCTCG	CAATGTGTGT	CATCAGCTTC	540
AGCATCTGCC	ATACCTTCCG	GTGGCAGGAA	GCTATGTTCC	TCCTGGAGTT	CCTCTGCCCC	600
CTGGGCATCA	TCCTGTTCTG	CTCAGCCAGA	ATTATCTGGA	GCCTGCGGCA	GAGACAAATG	660
GACCGGCATG	CCAAGATCAA	GAGAGCCATC	ACCTTCATCA	TGGTGGTGGC	CATCGTCTTT	720
GTCTCTGCT	TCCTTCCGAG	CGTGGTGTGT	CGGATCCGCA	TCTTCTGGCT	CCTGCACACT	780
25						
TCGGGCACGC	AGAATTGTGA	AGTGTACCGC	TCGGTGGACC	TGGCGTTCTT	TATCACTCTC	840
AGCTTCACCT	ACATGAACAG	CATGCTGGAC	CCCGTGGTGT	ACTACTTCTC	CAGCCCATCC	900
TTTCCCAACT	TCTTCTCCAC	TTTGATCAAC	CGCTGCCTCC	AGAGGAAGAT	GACAGGTGAG	960
CCAGATAATA	ACCGCAGCAC	GAGCGTCGAG	CTCACAGGGG	ACCCCAACAA	AACCAGAGGC	1020
GCTCCAGAGG	CGTTAATGGC	CAACTCCGGT	GAGCCATGGA	GCCCCCTTTA	TCTGGGCCCA	1080
30						
ACCTCAAATA	ACCATTCCAA	GAAGGGACAT	TGTCACCAAG	AACCAGCATC	TCTGGAGAAA	1140
CAGTTGGGAT	GTTGCATCGA	G				

Seq ID NO: 224 Protein sequence

Protein Accession #: Eos sequence

35

1	11	21	31	41	51	
MNRHHLQDHF	LEIDKKKNCV	FRDDFIKVL	PPVLGLEFIF	GLLGNGLALW	IFCPHLKSWK	60
SSRIFLFLNLA	VADFLLIICL	PFVMDYYVRR	SDWKFGDIPC	RLVLFMPAMN	RQGSIIPLTV	120
40						
VAVDYRFRV	HPHHLNKLIS	NWTAALISCL	LWGIVTGLTV	HLKKKLLLIQ	NGPANVCISF	180
SICHTFRWHE	AMFLLEFLLP	LGIIILFCSAR	IIWSLRQRQM	DRHAKIKRAI	TFIMVVAIVF	240
VICFLPSVVV	RIRIFWLLHT	SGTQNCVYR	SVDLAFFITL	SFTYMNMSLD	PVVYFSSPS	300
FPNFFSTLIN	RCLQRKMTGE	PDNNRSTSV	LTGDPNKTGR	APALMANSG	EPWSPSYLGP	360
45						
TSNHSKXKH	CHQEPASLEK	QLGCCIE				

Seq ID NO: 225 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1092

50

1	11	21	31	41	51	
ATGAATCGGC	ACCATCTGCA	GGATCACTTT	CTGGAAATAG	ACAAGAAGAA	CTGCTGTGTG	60
TTCCGAGATG	ACTTCATTGT	CAAGGTGTTG	CGCCCGGTGT	TGGGGCTGGA	GTTTATCTTC	120
GGGCTTCTGG	GCAATGGCCT	TGCCCTGTGG	ATTTTCTGTT	TCCACCTCAA	GTCCTGGAAA	180
55						
TCCAGCCGGA	TTTTCTGTT	CAACCTGGCA	GTGGCTGACT	TTCTACTGAT	CATCTGCCCTG	240
CCCTTCTCTG	TGGACCAACTA	TGTGAGGCGT	TGGGACTGGA	AGTTTGGGGA	CATCCCTTGC	300
CGGCTGATGC	TCTTCATGTT	GGCTATGAAC	CGCCAGGGCA	GCATCATCTT	CCTCACGGTG	360
GTGGCGGTAG	ACAGGTATTT	CGGGGTGGTC	CATCCCCACC	ACGCCCTGAA	CAAGATCTCC	420
AATCGGACAG	CAGCCATCAT	CTCTTGCTTT	CTGTGGGGCA	TCACTATTGG	CCTGACAGTC	480
60						
CACCTCTCTG	AGAAGAAGAT	GCCGATCCAG	AATGGCGGTG	CAATTTGTG	CAGCAGCTTC	540
AGCATCTGCC	ATACCTTCCA	GTGGCAGGAA	GCCATGTTCC	TCCTGGAGTT	CTTCTGCCCC	600
CTGGGCATCA	TCCTGTTCTG	CTCAGCCAGA	ATTATCTGGA	GCCTGCGGCA	GAGACAAATG	660
GACCGGCATG	CCAAGATCAA	GAGAGCCATC	ACCTTCATCA	TGGTGGTGGC	CATCGTCTTT	720
GTCTCTGCT	TCCTTCCGAG	CGTGGTGTGT	CGGATCCGCA	TCTTCTGGCT	CCTGCACACT	780
65						
TCGGGCACGC	AGAATTGTGA	AGTGTACCGC	TCGGTGGACC	TGGGTTCTTT	TATCACTCTC	840
AGCTTCACCT	ACATGAACAG	CATGCTGGAC	CCCGTGGTGT	ACTACTTCTC	CAGCCCATCC	900
TTTCCCAACT	TCTTCTCCAC	TTTGATCAAC	CGCTGCCTCC	AGAGGAAGAT	GACAGGTGAG	960
CCAGATAATA	ACCGCAGCAC	GAGCGTCGAG	CTCACAGGGG	ACCCCAACAA	AACCAGAGGC	1020
70						
GCTCCAGAGG	CGTTAATGGC	CAACTCCGGT	GAGCCATGGA	GCCCCCTTTA	TCTGGGCCCA	1080

Seq ID NO: 226 Protein sequence

Protein Accession #: Eos sequence

75

1	11	21	31	41	51	
MNRHHLQDHF	LEIDKKKNCV	FRDDFIVKVL	PPVLGLEFIF	GLLGNGLALW	IFCPHLKSWK	60
SSRIFLFLNLA	VADFLLIICL	PFLMDNYVRR	WDWKFGDIPC	RLMLFMLAMN	RQGSIIPLTV	120
78						
VAVDYRFRV	HPHHLNKLIS	NRTAALISCL	LWGITIGLTV	HLKKKMPIQ	NGGANLCSSE	180
SICHTFQWHE	AMFLLEFLFP	LGIIILFCSAR	IIWSLRQRQM	DRHAKIKRAI	TFIMVVAIVF	240
VICFLPSVVV	RIRIFWLLHT	SGTQNCVYR	SVDLAFFITL	SFTYMNMSLD	PVVYFSSPS	300
FPNFFSTLIN	RCLQRKMTGE	PDNNRSTSV	LTGDPNKTGR	APALMANSG	EPWSPSYLGP	360
TSP						

Seq ID NO: 227 DNA sequence  
Nucleic Acid Accession #: NM\_006018  
Coding sequence: 61..1224

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
CGCCACTTGT CTGGAGCATT CACTAGGCGA GCGCTCCAT CGGACTCACT AGCCGCACTC 60
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 120
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT 180
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCGTGAAA 240
TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCGT 300
CGGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 360
CGGCTGTGTC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCAGGGTG 420
GTGGCGGTAG ACAGGTATTT CCGGTGGTTC CATCCCCACC AGCCCTGAA CAAGATCTCC 480
AATTGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTGTGG CCTAACAGTC 540
CACCTCACTA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 600
AGCATCTGCC ATACCTTCCG GTGGCAGCAA GCTATGTTC TCCTGGAGTT CCTCCTGCC 660
CTGGGCATCA TCCGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGGGCA GAGACAAATG 720
GACCCGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGG CATCGTCTTT 780
GTCACTGTCT TCCCTCCAGC CGTGGTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 840
TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 900
AGCTTCACCT ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTCTC CAGCCCATCC 960
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 1020
CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACAGAGGC 1080
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCGCTCTTAA TCTGGGCCCA 1140
ACCTCAATAA ACCATTCCAA GAAGGGACAT TGTACCAAG AACCAAGCAT CTCGGAGAAA 1200
CAGTTGGGCT GTTGATCGA GTAATGTAC TGGACTCGGC CTAAGTTTC CTGGAACCTC 1260
CAGATTGAGA GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG 1320
GTGTGACCAC AGGAATCTCT GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAACCTTGC 1380
TTCACTCTCT AGCTTCGAG GACTGAAGAT GGGCAAATG TAGGCGTTTC TGCTGAGCAG 1440
AGTTGGAGCC AGAGATCTAC TTGTGACTTG TTGGCTTCT TCCACATCT CCTCAGACT 1500
GGGGGGGGCT CAGCTCCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG 1560
GAGAGCTGAG ATTGGAGGGA ATTGTGTTG TCCTGGAGGA AGCCAGGCA TCATTAAACA 1620
AGCCAGTAGG TCACCTGCTC TCCGTGGACC AATTCATCTT TCAGACAAGC TTTAGAGAAA 1680
TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCGG TGGGTGTAAT 1740
AGGGGATTAG CCCCAGAAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAAATGGCA 1800
TTGCTGCTTT CAACAGCGA CTAATGCAAT CCATTCTCT CTGTTTATA GTAATCTAAG 1860
GGTTGAGCAG TTAACAACGG TTCAGGATAG AAGCTGTTT CCCACCTGTT TCGTTTACC 1920
ATTAAAGGG AAACGTGCCT CTCGCCACG GGTAGAGGGG GTGCAGCTTC CTCCTGGTTC 1980
CTTCGCTGT GTTCTGTAC TTACCAAAAA TCTACCACTT CAATAAATTT TGATAGGAGA 2040
CAAAAAAAAA A
```

Seq ID NO: 228 Protein sequence  
Protein Accession #: NP\_006009.1

```
45      1      11      21      31      41      51
      |      |      |      |      |      |
MNRHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
SSRIPLFNLA VADFLLIICL PFVMDYYVRR SDWNFGDIPC RLVLFMFAMN RQSSIIFLTV 120
VAVDRYFRV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKKLIQ NGPANVCISF 180
SICHTFRWHE AMFLLEFLIP LGIILFCSAR IWSLRQRQM DRHAKIKRAI TFIWVAIVE 240
VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNMLD PVVYFSSPS 300
FPNFFSTLIN RCLQRKMTGE PDNNRSTSV LITGDPNKTRG APEALMANS EWSFSPYLGP 360
TSNNHKKGH CHQEPASLEK QLGCIE
```

Seq ID NO: 229 DNA sequence  
Nucleic Acid Accession #: NM\_014398.1  
Coding sequence: 64..1314

```
60      1      11      21      31      41      51
      |      |      |      |      |      |
GGCACCGATT CGGGGCTGTC CCGGACTTCG CGCACGCTG CAGAACCTCG CCCAGCGCCC 60
ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
CAGATGGCCA GTCAATGAG AGCAAAAGCA TTTCAGAAA CCAGAGATTA TTCTCAACT 180
ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACCAGC TAAGCAAGCA 240
CCTCACCAA CTTTAGCAGC AAGATTCTAT GATGGTCATA TCACCTTTC AACAGCGGCC 300
ACAGTAAAAA TTCAACAAC TACCCAGCA ACTACAAAA ACATGCAAC CACGAGCCCA 360
ATTACCTACA CCTGGTCACT AACCCAGGCC ACACCAACA ACTCACAC AGCTCCTCCA 420
GTTACTGAAG TTACAGTCGG CCTAGCTTA GCGCTTATT CACTGCCACC CACCATCACC 480
CCACAGCTC ATACAGCTGG AACCAATTCA TCAACCGTCA GCCACACA TGGGAACACC 540
ACTCAACCA GTAACCAAG CACCTTCCA GCAACTTTAT CGATAGCACT GCACAAAGC 600
ACAACCGGT AGAAGCTTGA TCAACCAACC CATGCCCGAG GAACAACGGC AGCTGCCAC 660
AATACCAACC CCACAGCTGC ACCTGCCCTC ACGTTCTCTG GCGCCACCTT TGCACTCAG 720
CCATGCTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
TACTTCAACA GTACCCCAAC CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA 960
TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
CAAGGAATCA AACATGCGGT GGTGATGTT CAGACAGCAG TCGGCATTC CTTCAGTGC 1080
GTGAGTGAAC AGAGCCTCCA GTTGTACGCC CACCTGCAGG TGAACCAAC CGATGTCCAA 1140
CTTCAAGCTT TTGATTTTGA AGATGACCAC TTGGAAATG TGGATGAGTG CTGCTCTGAC 1200
TACACAAATT TGCTTCTGCT GATTGGGGCC ATCGTGGTTG GTCTCTGCTT TATGGGTATG 1260
GGGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAA CTAAATGTTG 1320
CCCCGGGGGA ATGAAATAA TGAATTTAG AGAATCTTT CATCCCTTCC AGGATGGATG 1380
```

5 TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440  
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACCTTTT 1500  
 GTTTATTTTA TGAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560  
 GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620  
 AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680  
 ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCITTG TTATCAAATG GACTTTCAGT 1740  
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800  
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAC GGAGTTTCAC TCTGTCCACC 1860  
 10 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCCGCTTCC CGGTTTCAAG 1920  
 TGATTTCTCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTCG 1980  
 GCTAATTTT GTATTTTAT TATAGACGGG TTCCACCATG TTGGCCAGAC TGGTCTTGAA 2040  
 CTCTGACCT CAGGTGATCC ACCCACTTCA GCCTCCCAAA GTGCTGGGAT TACAGGCATG 2100  
 AGCCATTGCG CCCGGCTTAA AATGTTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160  
 GTTGTCTAAG TGTTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220  
 15 CTTGATGACT CCTGCTCCAG AATGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280  
 CTAACAATA AGCAGAGAC AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC 2340  
 TAGGCTAAGC ACTTATCTA TATCTCATT CATTCTACA ACTTATAAGT GAATGAGTAA 2400  
 ACTGAGACTT AAGGGAAGT AATCATTAA ATGTCACCTG GCTAATCTAT GGCAGAGCCA 2460  
 20 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520  
 CCTACAAGAA CAATGACACC ACACCTCTGC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580  
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640  
 AGCTTTCAG ATACAAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700  
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTGA TGGGATTGCT TAGCTGGGCT 2760  
 25 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTTTGA TAATAGAGAA 2820  
 ACTTCGCTAA CCACTCTTTC TTTCTTGAGT GTATAGCCCC ATCTGTGTGT AACTGTCTGC 2880  
 TCTGCACTT CATATCCATA TTTCTTATG TTCACCTTAT TCTGTAGAGC AGCCTGCCAA 2940  
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000  
 AGAAAAGTCC ACATAACCTT AGAATCTTGA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060  
 30 CCATGTTGAC TTTCTCATG TGTTCCTTGA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120  
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP\_055213.1

35 1 11 21 31 41 51  
 | | | | |  
 MPRLSAAAA LFASLAVILH DGSQMRKAP PETRDYSQPT AAATVQDIKK PVQPAKQAP 60  
 HQTLAARFMD GHITFQTAAT VKIPTTTPAT TONTATTSPI TYTLVTTQAT PNNSHAPPV 120  
 40 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNWT QPSNQITLPA TLSIALHKST 180  
 TQKQPDQPTH APGTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNSRLCIKA 240  
 EMGILQIVOD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLFTFKDEES 300  
 YYSISVGYL TVSDPEYVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTTDVQL 360  
 QAFDFEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMSGM VYKIRLRQCS SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM\_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51  
 | | | | |  
 TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60  
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120  
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180  
 55 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240  
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAA 300  
 AAGAGCAAC GAGTCCAGCA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360  
 GAAAGAAAGA ATTTTAAAT ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420  
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAACTG 480  
 60 AGACTTTTCT ATGGTTTGT GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540  
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA 600  
 CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660  
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCITAC TTGTTGTATT ATACATTCAT 720  
 GCATTTCTAG CTTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780  
 65 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTATGCT ATATTACTAT 840  
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900  
 CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAAATACAC ACTTCTTTCC 960  
 CCAAAATACA TTGAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTGGGTTTGT 1020  
 TTTATAACCA ATCTATTAAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080  
 70 TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT 1140  
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200  
 TGTACTTTTT GTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTTGAAA 1260  
 TACAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320  
 75 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380  
 TGTTCATGC CTATATACTG TAAATTTAG GTATACCTCA GACTAGTTTA AAGAATCAAA 1440  
 GTCATTTTTT TCTTAATAA ACTACCACA CTTTCTTTT TTAATAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP\_005400.1

80 1 11 21 31 41 51  
 | | | | |  
 MSVKGMAIAL AVILCATVVO GPFMFKRGRG LCIGPGVKAV KVADIEKASI MYPNNCDKI 60  
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 233 DNA sequence  
Nucleic Acid Accession #: NM\_000577.1  
Coding sequence: 41..520

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
GGCACCAGGGG GAAGACCTCC TGTCTATCA GGCCTCCCC ATGGCTTTAG AGACGATCTG 60
CCGACCTCTCT GGGAGAAAAA CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACCA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAAATGT 180
10    CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
CATCGCTACA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCGCCTGCC CCGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
15    GGTCTGCTGC ACCAAATCTT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCCTGT 540
TCCCATTTCT GATGTCGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGCTCCCG 600
GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAAACA 660
CTGTGGTACA GAGCTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC TCCAGAAATG 720
GTCCTTTCAA TGTGTGAATC AGAGCACAGC AGCCCTGCA CAAAGCCCTT CCATGTCCGC 780
20    TCTGCATTCA GGATCAAACC CCGACCACCT GCCCAACCTG CTCTCCTCTT GCCACTGCCT 840
CTTCTCCCTT CATTCACCTT TCCCATGCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
ACCAAGTGGC TCCACACCCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
TTTAAGGGTT TGTGGAAAAT GAAAATTAGG ATTTTCATGAT TTTTITTTTT CAGTCCCGT 1020
GAAGGAGAGC CCTTCATTGT GAGATTATGT TCTTCCGGG AGAGGCTGAG GACTTAAAT 1080
25    ATTCTGCTAT TGTGAAATG ATGGTGAAG TAAGTGGTAG CTTTCCCTT CTTTCTCTT 1140
TTTTTTTGTG ATGTCCCAAC TTGTAATAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGACT CCTCTGTCCA GGCAGTGTCT 1260
CCGAGCTCAC AAGCTCCATC TCCACTCCAG ATTTTITACA GCTGCCTGCA GTACTTTACC 1320
TCCTATCAGA AGTTTCTCAG CTCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGTTCTT 1380
30    TCTTCTCTG CTGAAGGAAT AAATGTCTCC TTGACATTGT AGAGCTTCTG GCAGTGGAG 1440
ACTTGTATGA AAGATGGCTG TGCTCTGCC TGCTCCCCC ACCAGGCTGG GAGCTCTGCA 1500
GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAACA CCTAGCCTCG 1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAGT TCCCTACTTC 1620
35    CTGTGACTTC AGCTCTGTT TACAATAAAA TCTTGAATAT GCCTAAAAAA AAAAAAAA 1680
AAAAAAA AAAA AAAA AAAA
```

Seq ID NO: 234 Protein sequence  
Protein Accession #: NP\_000568.1

```
40      1      11      21      31      41      51
      |      |      |      |      |      |
MALETICRPS GRKSSRMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPFEP 60
HALFLGIHGG KMCLSCVKSQ DETRLQLEAV NITDLSENK QDKRPAFIRS DSGPTTSFES 120
AACPGWFLCT AMEADQPVSL TNMPDEGMV TKFYFQED
```

Seq ID NO: 235 DNA sequence  
Nucleic Acid Accession #: NM\_001840.1  
Coding sequence: 149..1567

```
50      1      11      21      31      41      51
      |      |      |      |      |      |
GGGGACTACG GAGAGCTCTG CAGGGAGCCG AGGCCCCCGC CCGGGCCAAG GGAGCTTCTG 60
TCCGAGGAC CAGGGGATGC GAAGGGATTG CCCCTGTGG GTCACTTTCT CAGTCATTTT 120
GAGCTCAGCC TAATCAAGA CTGAGGTTAT GAAGTGGATC CTAGATGGCC TTGAGATAC 180
55    CACCTTCCGC ACCATCACCA CTGACCTCCT GTAAGTGGC TCAAATGACA TTCAGTACGA 240
AGACATCAAA GGTGACATGG CATCCAAAT AGGCTACTTC CCACAGAAAT TCCCTTTAAC 300
TTCTTTTAGG GGAAGTCCCT TCCAAGAGAA GATGACTCGG GGAGACAACC CCCAGCTAGT 360
CCGAGCAGAC CAGGTGAACA TTACAGAATT TTACAACAAG TCTCTCTCGT CTTTCAAGGA 420
GAATGAGGAG AACATCCAGT GTGGGAGAA CTTTATGGAC ATAGAGTGT TCATGGTCTC 480
60    GAACCCAGC CAGCAGCTGG CCAATGCACT CCTGTCCCTC ACGCTGGSCA CCTTCACGGT 540
CTGGAGAAC CTCCTGGTGC TGTGCGTCAI CCTCCACTCC CGCAGCCTCC GCTGCAGGCC 600
TTCTACCAAC TTATCGGCA GCCTGGCGGT GGCAGACCTC CTGGGAGTGC TCATTTTGT 660
CTACAGCTTC ATTGACTTCC ACGTGTTC CAAGCAAGAT AGCCGCAACG TGTTCCTGTT 720
65    CAACTGGGT GGGGTCAAG CCTCCTTCA TGCCTCGTG GGCAGCTGT TCCTCAGAC 780
CATCGACAGG TACATATCCA TTCACAGCC CCTGGCTAT AAGAGATTG TCACAGGCC 840
CAAGGCGGTG GTGGCGTTT GCCTGATGT GACCATAGCC ATTGTGATG CCGTGTGCC 900
TCTCTGGGC TGAACCTGC AGAAACTGCA ATCTGTTGC TCAGACATT TCCACACAT 960
TGATGAAACC TACCTGATGT TCTGGATCG GGTCAACAGC GTACTGCTTC TGTTCATCGT 1020
70    GTATGCTAG ATGTATATTC TCTGGAAGGC TCACAGCCAC GCGCTCCGCA TGATTCAGCG 1080
TGGCACCCAG AAGAGCATCA TCATCCACAC GTCTGAGGAT GGAAGGTAC AGGTGACCG 1140
GCCAGCCAA GCCGCAATG ACATTAGGTT AGCCAAGACC CTGGTCTGTA TCCTGGTGGT 1200
GTTGATCATC TGCTGGGGCC CTCTGCTTGC AATCATGGTG TATGATGCT TTGGGAAGAT 1260
GAACAAGCTC ATTGAACGG TGTGTGATT CTGAGTATG CTCTGCTGC TGAACCTCAC 1320
75    CGTGAACCCC ATCATCTATG CTCTGAGGAG TAAGGACCTG CGACACGCTT TCCGAGCAT 1380
GTTTCCCTCT TGTGAAGGCA CTGCGCAGCC TCTGGATAAC AGCATGGGG ACTCGGACTG 1440
CCTGCACAAA CACGCAACCA ATGCAGCCAG TGTTCACAGG GCCGAGAAA GCTGCATCAA 1500
GAGCAGGCTC AAGATTGCCA AGGTAACCAT GTCTGTGTCC ACAGACAGT CTGCGAGGCC 1560
TCTGTAGAGC TGATGCTTCC CTGGCAGCAC AGGAAAAGAA TTTTITTTTT TAAGCTCAAA 1620
80    ATCTAGAGA GTCTATGTCT TCCTTGGTTA TATTTTITTA ACTTTACCAT GCTCAATGAA 1680
AAGTGATTG CCACATGTCA CTTATTGTCT TAGTTCCGT TTGGCTAAT CTTCCGGGGT 1740
TGTAGGAAA CTTT
```

Seq ID NO: 236 Protein sequence  
Protein Accession #: NP\_001831.1



```

1      11      21      31      41      51
|      |      |      |      |      |
5  MKSILDGLAD TTFRTITDDL LYVGSNDIQY EDIKGDMASK LGYFPQKFPL TSFRGSPFQE 60
   KMTAGDNPOL VPADQVNITE FYNKLSSEFK ENZENIQCGE NFMIDIECFMV LNPSQOLAIA 120
   VLSLTGTFIT VLENLVLVCV ILHSRSLRCR PSYHPIGSLA VADLLGSVIP VYSFIDFHFV 180
   HRKDSRNVEL FKLGGVTASF TASVGSFLT AIDRYISIRH PLAYKRIVTR PRVAVAFCLM 240
   WTIAIVIAVL PLLGWNCEKL QSVCSDFPH IDETYLMFWI GVTSVLLLPF VYAYMYILWK 300
   AHSHAVRMIQ RGTQKSIH TSEDGVQVT RPDQARMDIR LAKTLVLILV VLIICWGPLL 360
10  AIMVYDVFGK MNKLIKTVFA FCSMLCLNS TVNPIIYALR SKDLRHAFRS MFPSCGTAQ 420
   PLDMSMGDSO CLHKHANNA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL

```

Seq ID NO: 237 DNA sequence  
 Nucleic Acid Accession #: NM\_016083.2  
 Coding sequence: 64..1482

```

1      11      21      31      41      51
|      |      |      |      |      |
20 GATTGCCCCC TGTGGGTAC TTTCTCAGTC ATTTTGAGCT CAGCCTAATC AAAGACTGAG 60
   GTATGAAGT CGATCCTAGA TGGCCTTGCA GATACCACCT TCOGCACCAT CACCACTGAC 120
   CTCCTGACG TGGGCTCAAA TGACATTCAG TACGAAGACA TCAAGGTGA CATGGCATCC 180
   AAATTAGGGT ACTTCCACA GAAATTCCT TTAACCTCCT TTAGGGGAAG TCCCTTCCAA 240
   GAGAAGATGA CTGCGGAGAG CAACCCCGAG CTAGTCCCAG CAGACCAGGT GAACATTACA 300
   GAATTTTACA ACAAGTCTCT CTGCTCCTTC AAGGAGAATG AGGAGAACAT CCAGTGTGGG 360
25 GAGAATCTCA TSGACATAGA GTGTTTCATG GTCCTGAACC CCAGCCAGCA GCTGGCCATT 420
   GCACTCCTGT CCTCAGCGCT GGGCACCTTC ACGGTCTGG AGAACCTCCT GGTGCTGTGC 480
   GTCATCCTCC ACTCCCGCAG CCTCCGCTGC AGGCCTTCCT ACCACTTCAT CGGCAGCCTG 540
   CGCGTGGCAG ACCTCCTGGG GAGTGTCAIT TTTGTCTACA GCTTCATTGA CTCCACGTG 600
   TTCCACCGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT CACGGCCTCC 660
30 CTCACCTGCT CCGTGGCAG CCTGTTCTCT ACAGCCATCG ACAGGTACGT ATCCATTAC 720
   AGGCCCTCG CCTATAGAG GATTGTCAAC AGGCCCAAGG CGTGGTGGC GTTTTGCTCG 780
   ATGTGGACCA TAGCCATTGC GATCGCGTGC CTGCTCTCC TGGGCTGGAA CTGCGAGAAA 840
   CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT GATGTTCTGG 900
   ATCGGGGTCA CCAAGCTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA TATTCTCTGG 960
35 AAGGCTCACA GCCACGCCGT CCGCATGATT CAGCGTGGCA CCCAGAAGAG CATCATCATC 1020
   CACACGCTCG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG CATGGACATT 1080
   AGGTATGCCA AGACCCCTGT CCTGATCCTG GTGGTGTGTA TCATCTGCTG GGGCCCTTTG 1140
   CTTGCAATCT TGGCTATAGA TGTCTTTGGG AAGATGAACA AGCTCATTA GACGGTGTGT 1200
   GCATTCTGCA GTATGCTCTG CCGTCTGAAC TCCACCGTGA ACCCATCAT CTATGCTCTG 1260
40 AGGAGTAAGG ACCTGCGACA CGCTTTCCGG AGCATGTTTC CCTCTTGTA AGGCACTGCG 1320
   CAGCCTCTCG ATAACAGCAT GGGGGACTCG GACTGCTGTC ACAAACAGCG AAACAATGCA 1380
   GCCAGTGTTC ACAGGGCGCG AGAAGCTGTC ATCAAGAGCA CGGTCAAGAT TGCCAAGGTA 1440
   ACCATATCTG TGTCCACAGA CACGCTCGCC GAGGCTCTGT GAGCCTGATG CCTCCCTGGC 1500
   AGCACAGGAA AAGAAATTTT TTTTAAAGC TCAAAATCTA GAAGAGTCTA TTGTCTCCTT 1560
45 GGTATATATT TTTAACTTT ACCATGCTCA ATGAAAAGGT GATTGTCAAC ATGATCACTT 1620
   ATCAGTTTGC TAATGTTTCC ATAGTTTAGG TACTCAAACT CCATTCTCCA GGGGTTTACA 1680
   GTGAAGAAAG CCTGTGTTT AAGTGACTGA ACGATCCTTC AAAGTCTCAA TGAATAGGA 1740
   GGGAAACCTT TGGCTACAGA ATTGGAAGTC TAAGAAACCCA TGGAAAAATG CCATCAAATG 1800
   AATAATGCCT TTGTAAACCA AACTTTCACT ATAATGTGAA ATGTAACTGT CCGTAGTATC 1860
50 AGAGATGTCC ATTTTACAA GTTATAGTAC TAGAGATATT TTGTAAAATG TATTATGTCC 1920
   TGTGAGATGT GTATCAGTGT TTATGTGCTA TTAATATTG TTAGTTTCA CAAACTGAA 1980
   AGGTAGACTT TTATGAGAAC AATGGAACAG CAGTGATATC GTGTCAATGT GTGCACTTTT 2040
   TTTCTATATT TTGCTGACT ATATAACTTT AGAAATAAAC CTTAATATT CTTCAAATAT 2100
   CTCTATTAA TTTTGACAT GAAATAACCG TAAAGGTTTA TTTTCTGTT ACCTCAACAA 2160
55 GAAGAATTGG AGACTTCAA AATATTGAGC AGAATTCATT CATCTTAAA AATTTATTAG 2220
   CCTGCACTT TCATAGGAAG ACACATTATC TTCTGGACTA TAGCTGTTCT AATGGATTAT 2280
   AATCAGAAAT GAAGAGAGAA AGCATATTGA CTTTTTTTGA GCGACATCTC TGACTTTCTT 2340
   TAGTCTTTAG CTATTACTGG ATCTCTTAAG ACAGCATGTG TTAATCTTAA TGTATATCGT 2400
   TATCACTGTG CAGTGTGCTG TTAATTTAAT AGTATTGTGT TCCTATATTC CAGGTTTAAG 2460
60 TAGATTTCAT GCCTGGGTGG CCAACACACA GTCTTCATT TTTTAAATG AAAAGAGTA 2520
   GTGCTGTGAT CAGTAAATTT ATACTGTGTG TGAGTGTGAA TATAAATGTG TGTATGTGTG 2580
   TTTCTGTCCG TAACGTGTAC AGTAATGTCA TAAAGTGAGA AAACGTGTAC CAGATATAAA 2640
   CTTTTACCAC TTGCTGCACT CTGCAATG GATTCACTTT CTAAATTTGA GTTCTTCTGT 2700
   TAATCTGTGT GATAAAATA CTGACTCCAA CCATTCAAAA ATTTCAACCC ATCCCTCCTT 2760
65 AAGAGATTGG ATCAAGTATT ACTAAATTGA CCTTAGGTA TTACACAAGA CAGTGCTTAA 2820
   GCAAAAATA ATGACAGGCA TCCAAGGAAG GGATGTATT GTAGTGTAT TGCCAGGAAA 2880
   GGAGAGTACT TTGGTTTCTG AGCACCGAAT ATTGAGCAAT ATGTGAGTCA CTAAAGGAAA 2940
   GACAGTTCTA CAGAAAACA AATGGTAACA TTTTCAATA GCGTGTGTAG ATAGTATGCA 3000
   CTATATACAT CACGTTAAAG TAGGACTATC ACACCCAGCC CATGTGGCTA AAAAGCTGA 3060
70 ATCAGACAGT GGATGAGACA CACAACGGCA GTGAAGAAC GATACACTTG GCATTGACGT 3120
   CTAGCTATGC TGTATCTGTG CTTTGGCCAC ATGCCCTTGG TGACAGCTGA GCACCCAGCT 3180
   CTGTCTGTGT AGGTTTGGCG TAAGGAACAA ATCTCTCTCT TGCTGTGTGT TAGCAAGATA 3240
   CACTCAAGCA TGAAGATAAA CACAGCTGCT TTCTCTTAC ACCTCGGTCT CATGCTCCTT 3300
   AATGGGCCCA TGGGTGCTTG TGGGCGCTTT TTCCAGTAAG GAATGATATT GCTGAAGAAT 3360
75 CACTTAAAC CTGACAAATT TTAATTATA TCTCTTCTTA TACAGATAAA ACATGACTCC 3420
   TACAAGGCC CAAGTTTAC ATAGTCTGAA GTGAAGTACA GAGCTGGCAT CTATCTGGTG 3480
   ATTTCTAGCT CTCGAGATAC CCAAGCAGCC TGATGGGGCA GTTCCCTTTC TTACGGTTCA 3540
   CGCTCAAGG CAGGATGTGG CTTATGAGAT ACTTTCATT GTCTGTCTGC ACACCTTGAA 3600
   TCTGCTGCT GGCTCCCTTA CTTTACCTCT CTGTCAATGT CAGATGAAGG CTCAGGGTGC 3660
80 TAGAGGATTA TAGGAACTC TTTCTAAAGA CAGGAGAGAT TATTTACAG AAGAAGCTCAC 3720
   CAGGGTTTAG TTTGCATTAA AGAATTGCCA GTCTTTTGTG CTGCATCATC TTGAACATTA 3780
   ATCCACATGT TTCAGAGCTC ACCAGGCAGT ACCAATGTCT TTTTCAAGC TATGAAGAGC 3840
   TAGAGAAAT CTGTTATAGG TAGAAAAATT TCACGGTTCA TTTTGAAGC TGCAATTGTG 3900
   CGTATGCAGT GTAGATTTTA TAGTGTGTG TGCTTCAAG ATCTAAATCA TATATAATAA 3960

```

5 ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020  
 TCTGTGAAAT ATCATCACGT ATGTTATACA ACCTTCATTT AAAAAGGTTT AAAACTAGTT 4080  
 AGATTCACTT TGACACTTTT CATATCATT CTTAACCCAA GTGACGAAAA CATTGTCCCC 4140  
 AATGAATATA CTCATTAGAA TTACCATTGG TTAATATCAC TCATTAATTA ACCCCATAAT 4200  
 TAGATCCATT AATTAAATG ATTTAAATTT AAGTAAGTTT TATAAGGTCT GACATCAGAG 4260  
 GTATCTTACT TTCTCTGAG GATGATGTAC TTGCCCTGAC CATGCATTTT ACCATCACAC 4320  
 ATGTTAGAAA AGGGCCAAAT TCCCAACCTG CTCATTTTTT TTTTATCAG AGTCATGATG 4380  
 AATCAGTCTT AGAATGTTT ATTTGCACAA GTAGGGCTGC CTCCAAGAGG AACCTCTGAT 4440  
 10 TTATTTTGTG TGAATATAT GTGAAAGGAT ATGAATCTGA GAGATGCTGT AGACATCTGT 4500  
 CCTACACTTG AGATGATTTT CAAGCCTCTC TGGCCTTTG AGTTAAGTCT ATCTGGTATT 4560  
 AAAATGCCAAG GACCTTTTGC TGCCCTAAATC CACTCTGCAG GAAATAGGCC CAACCAACAG 4620  
 ATGAGAATTA GGCCTGGAT GAGTAGCGCT ATAGTTACTG TCCTGTGAT TAATTTCTGC 4680  
 CATTTTCATG CCATAAAGA GACCAACCAT ATCATGCACA CAATTAGATT TCTCACACTC 4740  
 15 TAACTGTATA TTTGTATGAT ATTTTAAAT CTCCTAAATG CTGGGCAATG GCTATTAACA 4800  
 ATTAATTTGCT TTGCACTGGC CTCTGTATGA AATGTTAACA ATGCCTATTG TAATATAGAA 4860  
 AAAAACATTG TTTGCTACTG TTTGGGCTGA ATGATGTAA ATAGGTTTCT AAAAAGTCAG 4920  
 ATGTTTGAGC AGTGCCCTAC AAATCAGTAA TTTTCGGGTG GGAGAGTTTC TTTACATTGC 4980  
 CGTGGCATCT TAAAGCTAT CTTCATGTAA ATGACTGTGA CTAGGCCTAC TGGGGATCAG 5040  
 20 AGTTCCCAAG AAAGGAAACC TTTTCTGTGA TCTGGATTCA AATTTATTTC CAATGTTTCA 5100  
 AGCGGGAAAC ATGACTCTTT ATTTCTGTGA AATCTAACAT TATTACTTTT CCTCTTAGAA 5160  
 GAATATTGTA TTTGTAGATG TTTGTGAGC TGGTAACATC GTTGCAACCA CTGCAATATC 5220  
 TTCGTAGTA ATCTGTATA TACTTTGTAT ACAAGTACTG GTAAGATTGT TATTAAATGT 5280  
 AGCTTCAGTA ATTAATATG TATAGCAAAG TAGTACTTCT TCTGTATAT TTAATATGTA 5340  
 25 TTAAGCCAC AGTATATTTT ATTTCAATGT AATTAACTG TTAACCTTAT CAAAGAGAAA 5400  
 ACATCTCATC ATGCTTATTG TCCAAAGTTA CCTGGAATCA AATAAAAAAT CTAGATTACC 5460  
 ATGAAGAACA TA

Seq ID NO: 238 Protein sequence  
 Protein Accession #: NP\_057167.1

30 1 11 21 31 41 51  
 MKSILDGLAD TTFERTITD L YVGSNDIQY EDIKGDMASK LGVFPQKFLP TSFRGSPFQE 60  
 35 KMTAGDNQPL VPADQVNITE FYNKSLSSEK ENEENIQCGE NFMDECFMV LNPQQQLAIA 120  
 VLSLTGTFV VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF YSFIDFHFV 180  
 HRKDSRNVL FKLGGVTASL TASVGSFLPT AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240  
 WTIAIAIAVL PLLGWNCEKL QVSCDIFPH IDETYLMFWI GVTSVLLLFV YAYMYILWK 300  
 AHSIAVRMIQ RGTKSIIH TSEDGKVQVT RDQARMDIR LAKTLVLILV LIIICWGPLL 360  
 40 AIMVYDVFGK MNKLIKTVFA FCSMLCLLNS TVNPIIYALR SKDLRHAFRS MPSPCEGTAQ 420  
 PLDMSMGDS DCLHGHANNA SVHRAEESCI KSTVKIAKVT MSVSTDTSAB AL

Seq ID NO: 239 DNA sequence  
 Nucleic Acid Accession #: NM\_033181.1  
 Coding sequence: 17..1252

45 1 11 21 31 41 51  
 ATGAAGTCGA TCCTAGATGG CCTTGCAGAT ACCACCTTCC GCACCATCAC CACTGACCTC 60  
 50 CTGTACGTGG GCTCAATGA CATTAGTAC GAAGACATCA AAGGAGAATG AGGAGAATC 120  
 CCAAGTGGG GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCGTAACC CCAGCCAGCA 180  
 CTGGGCCATT GCACTCTCTG CCTCAAGCT GGGCAACCTC ACGGTCTCTG AGAACCTCCT 240  
 GGTGCTGTGC GTCATCTCC ACTCCCGCAG CCTCCGCTGC AGGCCCTCCT ACCACTTCAT 300  
 CGGCACGCTG GCGGTGGCAG ACCTCCTGGG GAGTGTCAAT TTTGCTACA GCTTCATTGA 360  
 55 CTCCACGTG TTCCACGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT 420  
 CACGGCTCC TTCACTGCTT CGTGGGCGAG CCGTGTCTC ACAGCCATCG ACAGGTATAC 480  
 ATCCATTAC AGGCCCTCGG CCTATAAGAG GATTGTCAAC AGGCCCAAG CCGTGGTGGC 540  
 GTTTTGCCGT ATGTGGACCA TAGCCATTGT GATCGCGTGT CTGCCCTCCT TGGGCTGGAA 600  
 CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT 660  
 60 GATGTTCTGG ATCGGGGTCA CCAGCGTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA 720  
 TATTCTCTGG AAGGCTCACA GCCAAGCGGT CGCATGATT CAGCGTGCCA CCCAGAAGAG 780  
 CATCATCATC CACACGCTG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG 840  
 CATGACATCT AGGTAGCCCA AGACCTCGGT CCTGATCCTG GTGGTGTGA TCACTGCTG 900  
 GGGCCCTCTG CTGCAATCA TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTAA 960  
 65 GACGGTGTGT GCATTCTGCA GTATGCTCTG CCGCTGAAC TCCACCCTGA ACCCATCAT 1020  
 CTATGCTCTG AGGAGTAAGG ACCTGCGACA CGCTTTCGGG AGCATGTTTC CCTCTGTGTA 1080  
 AGGCATCGG CAGCCTCTG ATAACAGCAT GGGGGAATCG GACTGCTGTC ACAAACAGCG 1140  
 AAACATGCA GCCAGTGTTC ACAGGGCCGC AGAAGCTGTC ATCAAGAGCA CGGTCAAGAT 1200  
 TGCCAAGGTA ACCATGCTG TGTCCACAGA CAGTCTGCC GAGGCTCTGT GA

70 Seq ID NO: 240 Protein sequence  
 Protein Accession #: NP\_149421.1

75 1 11 21 31 41 51  
 MALQIPSPAP SPLTSTWAO MTFSTKTSKE NEENIQCGEN FMDIECFMV LNPQQQLAIAV 60  
 LSLTLGTFV LLENLLVLCV LHSRSLRCR SYHFIGSLAV ADLLGSVIFV YSFIDFHFV 120  
 RDSRNVL FKLGGVTASFT ASVGSFLTA IDRYISIHRP LAYKRIVTRP KAVVAFCLMW 180  
 TTAIVAVLP LLGWNCEKLQ SVCSDFPHI DETYLMFWIG VTSVLLLFV YAYMYILWKA 240  
 80 HSHAVRMIQR GTQKSIIHT SEDGKVQVTR PDQARMDIR AKTLVLILV LIIICWGPLLA 300  
 IMVYDVFGKM NKLIKTVFAP CSMCLLNS TVNPIIYALRS KDLRHAFRSM PPSCEGTAQ 360  
 LDNSMGDSDC LHHGHANNA SVHRAEESCIK STVKIAKVTM SVSTDTSABEA L

Seq ID NO: 241 DNA sequence  
 Nucleic Acid Accession #: NM\_003596.1

Coding sequence: 82..1194

```

1      11      21      31      41      51
5      |      |      |      |      |
      GTAGACTGTC CATGGCCTGA ACATTTTCGG AAAATCATTT TGAGCAAAAT ATCTGTTTAA 60
      TAACAAGATA ACCACATCAA GATGGTTGGA AAGCTGAAGC AGAACTTACT ATTGGCATGT 120
      CTGGTGATTA GTTCTGTGAC TGTGTTTTAC CTGGGCCAGC ATGCCATGGA ATGCCATCAC 180
      CGGATAGAGG AACGTAGCCA GCCAGTCAAA TTGGAGAGCA CAAGGACCAC TGTGAGAACT 240
      GGCCCTGGACC TCAAAGCCAA CAAAACCTTT GCCTATCACA AAGATATGCC TTTAATATTT 300
      ATTGGRGGTG TGCTCGGAG TGGAAACCACA CTCATGAGGG CCATGCTGGA CGCACATCCT 360
      GACATTGCGT GTGGAGAGGA AACCAGGGTC ATTCCCGGAA TCCTGGCCCT GAAGCAGATG 420
      TGGTCACGGT CAAGTAAAGA GAAGATCCGC CTGGATGAGG CTGGTGTTC TGATGAAGTG 480
      CTGGATTCTG CCATGCAAGC CTCTTACTA GAAATTATCG TTAAGCATGG GGAGCCAGCC 540
      CCTTATTATG GTAATAAAGA TCCTTTTGCC CTGAAATCTT TAACTTACCT TTCTAGGTTA 600
      TTCCCAATG CCAAATTTCT CTGATGGTC CGAGATGGCC GGGCATCAGT ACATTCAATG 660
      ATTTCTCGAA AAGTTACTAT AGCTGGATTG GATCTGAACA GCTATAGGGA CTGTTTGACA 720
      AAGTGAATC GTGCTATAGA GACCATGTAT AACCATGTGA TGGAGGTGG TTTAAAAAAG 780
      TGCATGTTGG TTCACTATGA ACAACTGTGC TTACATCCTG AACGGTGGAT GAGAACACTC 840
      TTAAAGTTCC TCACGATTCC ATGGAACCA TCAGTATTGC ACCATGAAGA GATGATTGGG 900
      AAAGCTGGGG GAGTGTCTCT GTCAAAAGTG GAGAGATCTA CAGACCAAGT AATCAAGCCA 960
      GTCAATGTAG GAGCTCTATC AAAATGGGTT GGAAGATAC CGCCAGATGT TTTACAAGAC 1020
      ATGGCAGTGA TTGCTCCTAT GCTTGCCAGG CTGGATATG ACCCATATGC CAACCCACCT 1080
      AACTACGAAA AACTGATGCC CAAAATTATT GAAACACTC GAAGGGTCTA TAAGGGAGAA 1140
      TTCCAACTAC CTGACTTTCT TAAAGAAAAA CCACAGACTG AGCAAGTGA GTAGCAGAAC 1200
      CAGGAGCCTC TTCCATACAT GAGGAAAGAT TGCTGCCTTT TCAGCAGAAG GGAATTTCCT 1260
      AGGATTGGCT GTCCCTGCC AAGCTTGGTG GAGCGTCTGC ACCTTGGCTG CGCGCCTGT 1320
      GCATTGCGA GTTCTCTCCC ACTGAGAGGA TGGAGGTGTC CGCACAGCTT TGGGCCCTCGT 1380
      GAGGATCTG CTTCTCTGAG AAGAGCTCT TGATCCCGAT TTCATGCACA GCCCTGCAGT 1440
      AAGGAGCCCA GAAGAAACAT GTGTTTCTCT TTAAGTCTC TCTTGTCTC TTTTCTTACA 1500
      TTATGACGTT TGTTTTCAAG GAGAGGTTT AAAAATGGGA TCCTGTAAAG AGACTTGGGC 1560
      AGTCTCCTTT TGAATAGGT TGTCTGTACA TGTCTTAATG TTTTGTAGAA CACGTGTGCC 1620
      TGTTTAAGTG TATTGATGTG AATAATATTA AATATCTATA TTATTTAATT CATTGTATTG 1680
      TTTCTGAGAA GTTGGGAAAT TACCATTATA CATTTACAAC CTAATGACTT TTGTATTTTA 1740
      TTTTCAAAA TAAAGCTTT CAATGTGA

```

Seq ID NO: 242 Protein sequence  
Protein Accession #: NP\_003587.1

```

1      11      21      31      41      51
40     |      |      |      |      |
      MVGKLKQNL LACLVISSVT VFYLGQHAME CHHRIERSQ PVKLESTRIT VRTGLDLKAN 60
      KTFAYHKDMP LIIFGVPRPS GTILMRAML AHPDIROGEE TRVIPRILAL KQMWSSRSKE 120
      KRLDEAGVT DEVLDSAMQA FLLEIVKHG EPAPYLCNKD PFALKSLTYL SRLFPNAKFL 180
      LMVRDGRASV HSMISRKVTI AGFDLNSYRD CLTKWNRAIE TMYNQMEVG YKQMLVHVE 240
      QLVLFPERWM RTLLKFLQIP WNHSLVHHEE MIGKAGGSVL SKVERSTDQV IKPFNVGALS 300
      KHWGKIPPDV LQDMAVIAPM LAKLGYDPYA NPPNYGKPDF KIIENTRRVY KGEFQLPDFL 360
      KEKPQTEQVE

```

Seq ID NO: 243 DNA sequence  
Nucleic Acid Accession #: NM\_001492.3  
Coding sequence: 1395..2513

```

1      11      21      31      41      51
55     |      |      |      |      |
      ACGCGGGGG CGCGGCTCGG TCGGCTACCG CGGGCGGGCG CAGGCGAGCG GCACGGGGG 60
      CGAGCGGGGG GTATGGCGGC GGCGGGGGCC GCGCGGGGGC CGACGGGGCC CGAGCCCATG 120
      CGGAGCTACG CGCAGCTAGT GCAGCGCGGC TGGGGCAGCG CGCTGGGGCC GGCGGGGGG 180
      TGCACGGACT CGCGCTGGGG GCTGGCGCGT CGCGGCTTGG CTGAGCACCG GCACCTGGCG 240
      CGCGCGGAGC TGTGCTGCTG GCGCTCGGCG GCGCTGGGCT GGAACGCGCT CGGCTCGCGG 300
      GCCACTGGCG GCCTCTTTGG GCCCTTGGCG AAGCGGTGCT GCTTCCAGCC CAGAGATGCC 360
      GCCAGATGCG CGGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGCAGCTG GAGCTACAGT 420
      GCCTACCTGC TGTITGGCAC GCACTACCCC TTCTTCCATG ACCCACCATC TGTCTTCTAC 480
      GACTGGACGC CGGGCATGGC AGTGCCACGG GACATTGCAG CGGCTACCT GCTCCAGGGA 540
      AGCTTCTATG GCCACTCCAT CTAAGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600
      GTGGTCAATG TGCTCCACCA CGTGGTCACT CTCATCTCTA TGTCTCTCTC CTAAGCTCTC 660
      CGGTACCACA ATGTGGGCAT CCTTGTGCTC TTCCTGCAAG ATATCAGTGA CGTGCACTT 720
      GAGTTACCCA AGCTCAACAT TTAATTCAAG TCCCGCGGCG GCTCTACCA TGGCTGCAT 780
      GCCTTGGCAG CAGACTTGGG CTGCCTCAGC TTGGGCTTCA GCTGGTTCTG GTTCCGCTC 840
      TACTGTTTCC CGCTCAAGGT CCTGTATGCC ACCAGTCACT GCAGTCTGG CAAGGTGCT 900
      GACATCCCTT TCTACTTCTT CTCAATGGG CTCCTGCTGC TGCTCACCTT TATGAACCTC 960
      TACTGTTTCC TGTACATCGT GCGGTTTGCA GCCAAGSTGT TGACAGGCCA GGTGACAGAG 1020
      CTGAAGGACC TGGGGAGTA TGACACAGCC GAGGCCAGGA GCTGAAGCC CAGCAAGCC 1080
      GAGAAGCCAC TGAGGAACGG CCTGGTGAAG GACAAGCGCT TCTGAACCCC TGGGCCCGCG 1140
      CCCGCTGGAC CGGCGCCAC CCAGAAATACC CGGCGCACGC TCOCCTGCTT TGGCGCGCCC 1200
      TCCACCCCTG CCAACTCTGC TCCTCTAGGG CGCGCGCCAC CTCCTCTGGG ACCCGCGCCC 1260
      CTCATCTGCG CTCATTTCCT CGGCCACGCC CCCAGGAGCC CCGTCCCTCT CGGGACACC 1320
      GGCCCGCGCC TCAGCCCATC GGTCCCGGGC CGCGCGGAGC CCGTGGCACT CTCTGGTCAT 1380
      GGCTTGGGAG GAAGATGCCA CGCGCGCAGC AAGTCCCTG CGGCGACACC CTCCTCTCTC 1440
      TCTTGGCCCT GCTGCTGCCC TCGCTGCCCC TGACCCGCGC CCGCTGCCCC CCAGGCCAGC 1500
      CGCGCGCTCG GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGGTGGC CCCAGGCTCC 1560
      GGCCTGTTCC CCGGTCATG TGGCGCTGT TTGACGCGG GACCCCGAG GAGACAGGT 1620
      CTGGCTCGCG CGGAGCGTCC CCAGGGGTCA CCTGCAACC GTGCCACGTG GAGGAGCTGG 1680
      GGGTGCCTGG AACCATATCC CGGCACATCC CGGACCGCGG TGCGCCACCC CGGCGCTCGG 1740
      AGCTGTCTCT GCGCGCGGG CATTCGCCCT AGTGGACAGT CGTCTTCGAC CTGTGGCTG 1800

```

5 TGAACCCGCG TGAGCGCCCG AGCCGGGCGC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860  
 CGGCAGCCCG GGAGGGGCGG TGGGAGCTGA GCGTGGGCGA AGCGGGCCAG GCGCGGGCGG 1920  
 CGGACCCCGG GCGGGTGTCT CTCGCCAGT TGGTGCCGCG CTGGGGGCGG CCAGTGCGCG 1980  
 CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG GCGGCGCAGC CTCGCGCTGG 2040  
 CGCTGGCGCT ACGCCCGCGG GCCCTGCGG CCGTGGCGCG CTGGCCGAG GCCTCGCTGC 2100  
 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTGGC CCGGCGCGG CGCGACGCGG 2160  
 AACCGGTGT GGGCGGGCGG CCGGGGGCGG CTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220  
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGCCTTCCTG GCCAACTACT 2280  
 10 GCCAGGTCA GTGCGCGCTG CCGTTCGCGC TGTGCGGGTC CGGGGGGCGG CCGGCGCTCA 2340  
 ACCAGCTGT GCTGCGCGCG CTCATGCACG CGGCGCGCCC GGGAGCCGCC GACCTGCCCT 2400  
 GCTGGGTGCC CGCGCGCTG TCGCCATCT CCGTGTCTT CTTTGACAA AGCGACAAAG 2460  
 TGGTGTGCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGCTGCCCG TAACCCGGGG 2520  
 CGGCGAGGA CGCGGGCCCA ACAATAAATG CCGGTGGTCT TGCTC

15 Seq ID NO: 244 Protein sequence  
 Protein Accession #: NP\_001483.2

20 1 11 21 31 41 51  
 MPPPPQGGPCG HLLLLLLALL LPSLPLTRAP VPPGPAAALL QALGLRDEPQ GAPRLRPVPP 60  
 VMWRLFRRRD PQETRSRRR TSPGVTLQPC HVEELGVAGN IVRHIFDRGA PTRASEPVSA 120  
 AGHCPEWTVV FDLSAVEPAE RPSRARLELR FAAAAAAPE GWEELSVQA QGAGADPGP 180  
 VLLRQLVPAL GPPVRAELLG AAWARNASWP RSLRLALALR PRAPACARL AEASLLLVTL 240  
 25 DPLRLCHPLAR PRDAEPVLG GPGGACRAR RLVVSFREVW WHRWIAPRG FLANYCQGGC 300  
 ALPVALSGSG GRPALNHAUL RALMHAAAPG AADLPCCVPA RLSPISVLFF DNSDNVVLRLQ 360  
 YEDMVVDECG CR

30 Seq ID NO: 245 DNA sequence  
 Nucleic Acid Accession #: NM\_021267.1  
 Coding sequence: 17..1125

35 1 11 21 31 41 51  
 ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCACGGCGGG 60  
 CGAGCGGGCG GTATGGCGCG GCGGGGGCGG CCGGCGGGCG CGACGGGGCG CGAGCCCATG 120  
 CGGAGCTACG CGCAGCTAGT GCAGCGCGCG TGGGCGAGCG CGCTGGCGCG GCGCGGGCGG 180  
 TGCAAGGACT GCGGCTGGGG GCTGGCGGCT GCGGCGCTGG CTGAGCAGCG GCACCTGGCG 240  
 CGCGCGAGC TGTCTGTCTG GCGCTCGCG CGCTGGGCT GGACCGCGCT GCGCTCGCGG 300  
 40 GCGACTGCGC GCTCTTTTCG GCCCTGCGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360  
 GCGAAGATGC CCGAGAGCGG TTGGAAGTTT CTCTTCTACC TGGGCGAGCT GAGCTACAGT 420  
 GCGTACCTGC TGTTTGGCAC GACTACCCG TTCTTCCATG ACCCACCATC TGTCTTCTAC 480  
 GACTGGAGCG CGGCGATGGC AGTGCCACGG GACATTGCAG CCGCCTACCT GCTCCAGGGA 540  
 AGCTTCTATG GCGACTTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600  
 45 GTGTCATGCG TGCTCCACCA CGTGGTCACT CTCATCTCA TCGTCTCCTC CTACGCTTTC 660  
 CGGTACCACA ATGTGGGCGT CTTTGTGCTC TTCTTCCAGC ATATCAGTGA CGTGACAGCT 720  
 GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCCGCGGCG GCTCTTACCA TCGGCTGCAT 780  
 GCGTGGGAGC CAGACTTGGG CTGCGCTCAG TTGCGCTTCA GCTGGTTCGT GTTCCGCTTC 840  
 50 TACTGTTTCC GCTCAAGGT CCGTATGCG ACCAGTCACT GCAGTCTGGG CACGGTGCCT 900  
 GACATCCCTT TCTACTTCTT CTTCATGCG CTCTGCTGCG TGCTCACCTT TATGAACCTC 960  
 TACTGTTTCC TGTACATCGT GCGGTTTGCA GCCAAGGTGT TGACAGGCCA GGTGCACGAG 1020  
 CTGAAGGACC TGCGGGAGTA TGACACAGCC GAGGCCAGCA GCCTGAAGCC CAGCAAGGCC 1080  
 GAGAGCCAC TGAGGAACCG CCGGTGTAAG GACAAGCGCT TCTGAACCCC TCGGCGGGCG 1140  
 CCGCGTGGAC CGCGCCCCAC CCGGAATACC CCGGCCAAGC TCCCGTCTCT TGGCGCGGCC 1200  
 55 TCCACCCCTT CCAACTCTGC TCCTCTAGGG CCGCGGCCAC CTCCTCTGGG ACCCGCGCCC 1260  
 CTGATCTGCG CTCATTCTCC GGGCCAGGCC CCGCAGGACC CCGTCCCTCT CCGGGACACC 1320  
 GCGCGCGGCC CTAGCCCATC GGTCCCGGGC CGCGCGGAGC CTGCGCACT CTCTGGTCACT 1380  
 CGCGTGGGAG GAGATGCCA CCGCGCGAGC AAGGTCCCTG GCGCCACCAC CTCTCTCTCC 1440  
 60 TCTGCGCTCT GCTGCTGCCC TCGCTGCCCC TGACCGCGCG CCGGCTGCCC CAGGCGCCAG 1500  
 CGCGCCCTCT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGCTGCC CCGAGGCTCC 1560  
 GCGCGGTTCC CCGGCTCATG TGGGCGCTGT TTCGACGCGG GGACCCCGAG GAGACAGGCT 1620  
 CTGGCTCGCG GCGGACGTCC CCAGGGGTCA CCTGCAACCC GTGCCAGTG GAGGAGCTGG 1680  
 GGGTCCGCGG AAACATCGTG CGCCACATCC CGGACCGCGG TGCGCCACCC CCGGCTCTCG 1740  
 65 AGCTGTCTC GCGCGCGGGG CATTGCCCTG AGTGGACAGT GGTCTTGGAC CTGTGCGCTG 1800  
 TGGAAACCGG TGAGCGCCCG AGCGGGGCGG GCGTGGAGCT GCGTTTCGCG GCGGCGGGCG 1860  
 CGGCAGCCCG GGAGGGGCGG TGGGAGCTGA GCGTGGGCGA AGCGGGCCAG GCGCGGGCGG 1920  
 CGGACCCCGG GCGGTGTCTG CTCGCCAGT TGGTGCCGCG CCGGGGGCGG CCAGTGCGCG 1980  
 CGGAGCTGCT GGGCGCGGCT TGGGCTCGCA ACGCCTCATG GCGCGCAGC CTCGCGCTGG 2040  
 70 CGCTGGCGCT ACGCCCGCGG GCCCTGCGG CCGTGGCGCG CCGTGGCGAG GCCTGCTGCG 2100  
 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTGGC CCGGCGCGG CGCGACGCGG 2160  
 AACCGGTGT GGGCGGGCGG CCGGGGGCGG CTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220  
 TCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGGCGCGG CGCTTCTCTG GCCAACTACT 2280  
 GCGAGGTGTA GTGCGCGCTG CCGGTGCGCG TGTGCGGGTC CGGGGGGCGG CCGGCGCTCA 2340  
 ACCAGCTGT GCTGCGCGCG CTCATGCACG CGGCGCGCCC GGGAGCGGCC GACCTGCCCT 2400  
 75 GCTGCGTGCC CGCGCGCTG TCGCCATCT CCGTGTCTT CTTTGACAA AGCGACAAAG 2460  
 TGGTGTGCGG GCAGTATGAG GACATGGTGG TGGACGAGTG CGCTGCCCG TAACCCGGGG

80 Seq ID NO: 246 Protein sequence  
 Protein Accession #: NP\_067090.1

1 11 21 31 41 51  
 MAAAGPAAGP TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60  
 LLLALGALGW TLRSAATAR LFRPLAKRCC LQPRDAAKMP ESANKFLFYL GSWSYSAYLL 120  
 FGTDPYPPFD PPSVFYDWTG GMAVPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180

LHHVVTLLI VSSYAFRYHN VGILVLFHLD ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240  
DLGCLSPFGS WFWFLRYWFP LKVLVATSHC SLRTVPDIPF YFFFNALLLL LTLNLYWFL 300  
YIVAFAAKVL TQGVHELKDL REYDTAEAS LKPSKAEKPL RNGLVKDKRF

5

Seq ID NO: 247 DNA sequence  
Nucleic Acid Accession #: NM\_002081.1  
Coding sequence: 222..1898

10 1 11 21 31 41 51  
GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCGCGCGCC CGCCGCGCGC 60  
GGCTTTTGTT GTCTCCGCCT CCTCGGCGCG CGCGCGCTCT GGACCGGAG CGCGCGCGC 120  
CGGAGCCTTG GCTCTGCCCT TCGCGGGCGG GAACTGCSCA GGACCCGCC AGGATCCGAG 180  
AGAGGCGCGG GCGGGTGGCC GGGGGCGCGG CCGGCCCGCC CATGGAGCTC CGGCGCCGAG 240  
15 CTTGGTGGCT GCTATGTGCG GCCGACGCGC TGGTCCGCTG CGCCCGCGGG GACCCGCGCA 300  
GCAAGAGCCG CAGCTCGCGC GAGGTCCGCC AGATCTACGG AGCCCAAGGGC TTCAGCTGTA 360  
GCCACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420  
CCTGTCTGAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480  
CCGCGCTCCG GGACAGCAGC CGGTCTCTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540  
20 TGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACCTGCGAG GCCACCTTCC 600  
CCGCGCGCTT CCGAGAGCTG TACACGCGAG ACGCGAGGGC CTTCCGGGAC CTGTACTCAG 660  
AGCTGCGCCT TACTACCGC GGTGCCAACC TGCACCTGGA GGAGACGCTG GCGGAGTTCT 720  
GGGCGCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCAACC CCAGCTGCTG CTGCTGATG 780  
25 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGGCGCTGCG GCCCTTCGGG GAGGCGCGCA 840  
GAGAGCTGCG CCTCGGGGCC ACCCGTGCCT TCGTGGCTGC TCGTCTCTTT GTGCAAGGCC 900  
TGGCGTGGG CAGCAGGCTG GTCCGGAAG TGGCTCAGGT CCCCCTGGGC CGGAGTGTCT 960  
CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTACTGCTCT GGGAGTCCCC GCGCCAGGCG 1020  
CCTGCCCTGA CTATTGCGA AATGTGCTCA AGGCTGCTCT TGCCAACCG GCGACCTGG 1080  
30 ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGTCTCAT CACCGACAAG TTCTGGGGTA 1140  
CATCGGCTGT GGAGAGTGTG ATCGGCGAGG TGCAACGCTG GCTGGCGGAG GCCATCAACG 1200  
CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCTAT CCAGGGCTCG GGAACCCCA 1260  
AGGTCAACCC CCAGGGCCCT GGGCTGAGG AGAAGCGGCG CCGGGGCAAG CTGCCCCGCG 1320  
GGGAGAGGCC ACCTTCAGGC ACGCTGAGGA AGCTGCTCTC TGAAGCCAAG GCCAGCTCC 1380  
35 GCGACGTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGCACTGAG AAGATGGCCC 1440  
TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG 1500  
AGGTCAATGG TGAAGGCTGT GCCAACGAGA TCAACAAACC CGAGGTGGAG GTGGACATCA 1560  
CCAAGCCGGA CATGACATC CGGACGAGA TCATGCACTG GAGATCATG ACCAACCGGC 1620  
TGCGCAGCGC CTACACGCGC AACGACGTGG ACTTCCAGGA CGCAGTGAC GACGCGAGG 1680  
40 GCTCGGGCAG CGGTGATGGC TGTCTGGATG ACCTCTGGCG CCGGAAGGTC AGCAGGAAGA 1740  
GCTCCAGCTC CCGGACGCCC TTGACCCATG CCCCCTCAGG CTTGTCTGAG CAGGAAGGAC 1800  
AGAAGACCTC GAGTCCGAGG TGCCCCCAGC CCGGACCTT CTTCTGCCCC CTCTCTCTCT 1860  
TCCTGGCCCT TACAGTAGCC AGGCCCCGGT GCGGTAACT GCGCCAGGCG CCGAGGGA 1920  
GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGAG ATATTTAATT CACCTCAGCC 1980  
45 TGGAGAGGCC TGGGGTGGGA CAGGGAGGGC CGGCGCTCT GAGCAGGGGC AGGCGCAGAG 2040  
GTCCACGCCC CAGGCTGGC CTGCGCTGCC TTCTGCGCTT TTAATTTTGT ATGAGTCTCT 2100  
CAGGTCACTG CAGGAGCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCA 2160  
TCCGCTGCGC TAGCCCTCCC CCGAGCTCCC TGACCGCGCG CAGAAGCAGC CCTCGAGGC 2220  
CTACAGAGGA GGCTCAAGG CAACCGCTG GAGCCACAG CGAGCCTGTG CTTCTCTCCC 2280  
50 CGCTCTCTCC CACTGGGACT CCGAGCAGAG CCCACGAGCC AGCCCTGGCC CACCCCCAG 2340  
CCTCCAGAGA AGCCCCGAC GGGCTGTCTG GGTGTCCGCG ATCCAGGGTC TGCCAGAGCC 2400  
TCTGAGATGA TGTGATGAG CTTCCCTCA CGGCAAGGCT CAGAGCCCGG CCCCACCTCC 2460  
CTGCGCCCTT GAGGGGCCCG AGCGTCTGCA GGTGACGCG TGAGACAGCA CCACTGCTGA 2520  
GGAGTCTGAG GACTGTCTCT CCACAGACC TGCACTGAGG GGCCCTCCAT GCGCAGATGA 2580  
55 GGGGCCACTG ACCCACCTGC GCTTCTGCTG GAGGAGGGGA AGCTGGGGCC AAAGGCCAG 2640  
GGAGGAGCGG TGGGCTCTGC CAATGTGGGC TGCCCCCTCG ACACAGGGCT CAGAGGGCAG 2700  
CGCTTGTGG GGTCCAGGGC TGTGGAGGA CCGGAGGGC TGAGGAGCAG CCAGGACCGG 2760  
CCTGTCTCCA TCTCACCAGA GATCAGGAAC CAGGGCTCTC CTGTTACCGG TGACACAGGT 2820  
CAGGGCTCAG AGTGACCTCT GGCTGTACC TGCTACAGG GATGCTGGTG GCTGGTGA 2880  
60 CCGGCACTG CACACGGGAA TGCTAGGTC CTTTCCGAC CCAGCCAGCT GCACTGCAGG 2940  
GCACGGGAGC CTGGATAGTT AAGGGCTTTT CCAACATGC ATCCATTATC TGACACTTCC 3000  
TGTCTTGTG CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTCCGAGGC CCGCAGGGCC 3060  
CAGCTTGGAG CCTGGTGACC TCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120  
CTGAGCGGCC CTTCTTCCC TCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180  
65 TGTGTGTGTG GGAAGGGGTC CTGAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCGAGTG 3240  
TCTGAACCG ACTGACCTTG AGGAGGCGCG TTAGTGTCTG TTTGCTTTTC ATCACCCTCC 3300  
CGCAGAGTGG ACGGAGGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360  
CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCAACACAG CCAAGTCCAC CCCATAATAA 3420  
CCTGCGCAGT CCGAGGGTGG GCTGGGGACT CTGGCACAGT GATGCGGGGC GCCAGGACAG 3480  
70 CAGCACTCCC GCTGCACACA GACGGCTTAG GGGTGGGCT CAGACCCAC CCTACGCTCA 3540  
TCTCTGGAAG GGGCAGCCCT GAGTGGTCA TGGTCAGGGC AGTGCCCAAG CCTGCTGTGT 3600  
CCTTCTCCA CAAGTCCCC CCAACGCTCA GTGTCAGCGG GTGACGTGTG TCTTTTGG 3660  
TCCTGTATG AATAAAGGC TGGAAACCTA AA

75

Seq ID NO: 248 Protein sequence  
Protein Accession #: NP\_002072.1

80

1 11 21 31 41 51  
MELRARGWVL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSQVP QAEISGEHLR 60  
ICPQGYTCTT SEMEENLANR SHALELTALR DSSRVIAQML ATQLRSFDDH FQHLNDNSR 120  
TLQATFPFAG GELYTNARA FRDLYSELRL YRGNALHLE ETLAEFWARL LERLFQLHP 180  
QLLLPDYDLD CLGQAEALR PFGEAPRELRL LRATRAVFAA RSFVQGLGVA SDVVRKVAQV 240  
PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI 300  
TDKFWGTSGV ESVGSVHTW LAEAINALQD NRDRTLAKVI QCGGNPKVNP QGPGPEEKRR 360

RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA 420  
 RGRYLPEVMG DGLANQINNP EVEVDITKPD MTIRQIMQL KIMTNRLRSA YNGNDVDFQD 480  
 ASDDGSSEGS

5 Seq ID NO: 249 DNA sequence  
 Nucleic Acid Accession #: NM\_001492.3  
 Coding sequence: 8..1864

10 1 11 21 31 41 51  
 | | | | |  
 GAAGGCCATG GTCTCCCCAC GGATGTCCGG GCTCCTCTCC CAGACTGTGA TCCTAGCGCT 60  
 CATTTTCTTC CCCAGACAC GGCCTCGTGG CGTCTTCGAG CTGCAGATCC ACTCTTTCGG 120  
 GCGGGGTCCA GGCCTGGGG CCGCGGGTC CCGCTGCAGC GCGCGGCTCC CCGCGGCCT 180  
 15 CTTCTTCAGA GTCTGCCTGA AGCCTGGGCT CTGAGAGGAG GCCGCGAGT CCCCGTGCSC 240  
 CCTGGGGGCG GCGCTGAGTG CGCGCGGACC GGTCTACACC GAGCAGCCCG GAGCGCCCG 300  
 GCCTGATCTC CCACTGCCCC ACGGGCTCTT GCAGGTGCCC TTCCGGGACG CCGTGCCTGG 360  
 CACCTTCTCT TTATCATCG AACCTGGAG AGAGGAGTTA GGAGACCAGA TTGGAGGGCC 420  
 CGCTTGAGC CTGCTGGCGC GCGTGGCTGG CAGGCGGCGC TTGGCAGCCG GAGGCCCGTG 480  
 20 GGCCTGGGAC ATTGAGCGCG CAGGCGCTGG GGAGCTGCGC TTCTCGTACC GCGCGCGCTG 540  
 CGAGCGGCT GCGCTCGGGA CGCGTGCAC GCGCTCTGCG CGTCCGCGCA GCGCCCGCTC 600  
 GCGGTGCGGT CCGGGAAGTG GCGCTGCGC ACCGCTCGAG GACGAATGTG AGGCGCGCTG 660  
 GGTGTGCGGA GCAGGCTGCA GCGCTGAGCA TGGCTTCTGT GAACAGCCCG GTGAATGCGG 720  
 25 ATGCTAGAG GCGCTGAGTG GACCCCTCTG CACGCTCCCT GTCTCCACCA GCAGTGCCT 780  
 CAGCCCCAGG GCGCGCTCTT CTGCTACAC CGGATGCCTT GTCCCTGGGC CTGGGCCCTG 840  
 TGACGGGAAC CCGTGTGCCA ATGGAGGCGAG CTGTAGTGAG ACACCCAGGT CCTTTGAATG 900  
 CACCTGCGCG CCGGCTGCTT ACGGGCTGCG GTGTGAGGTG AGCGGGGTGA CATGTGCAGA 960  
 TGGACCTCTG TTCAACGCGG GCTTGTGTGT CCGGGGTGCA GACCTGACT CTGCTACAT 1020  
 30 CTGCTACGCG CCACTGCTGT TCCAAGGCTC CAACTGTGAG AAGAGGGTGG ACCGTGCGAT 1080  
 CCTGCAGCCA TGCCGAATG GCGGACTCTG CTGAGACCTG GGCCAGSCCC TGGCTGCGG 1140  
 CTGCGCGGCC GGTCTCGCGG GTCTCGCTG CGAGCACGAC CTGGAGACT GCGCGGGCGG 1200  
 CGCTTGCCTG CCGCGGCGCA CGTGTGTGGA GCGCGCGCGC GCGCACGCTG GCTCTGCGC 1260  
 GCTGGGCTTC GCGCGCGCGC ACTGCCGCGA GCGCGCGGAC CCGTGCCTCG CCGCGCCCTG 1320  
 TGCTACGCG GCGCGCTGCT ACGCCACTT CTCCGCTCTG GTCTGCGCTT GCGCTCCCGG 1380  
 35 CTACATGGGA GCGCGGTGTG AGTTCCAGT GCACCCGAC GCGCGAAGCG CCTTGCCCGC 1440  
 GGCCCGCGCG GGCCTCAGCG CCGGGGACCC TCAGCGCTAC CTTTTCCTC CCGCTCTGGG 1500  
 ACTGCTCGTG CCGCGGGCGG TGGCGGCGC TCGCTCTTG CTGGTCCAG TGGCGCGCG 1560  
 TGGCACTCC CAGGATGCTG GGTCTCGCTT GCTGGCTGGG ACCCCGAGC CGTCAGTCCA 1620  
 40 CGCATCCCG GATGCACTCA ACAACCTAAG GACGAGGAG GGTTCGGGG ATGTCOGAG 1680  
 CTCGTCGTA GATTGAATC GCGCTGAAGA TGTAGACCCT CAAGGGATT ATGTATATC 1740  
 TGCTCTTCC ATCTACGCTC GGGAGGTAGC GAGCCCTCTT TTCCCGCGC TACACACTGG 1800  
 GCGCGCTGG CAGAGGCGAG ACCTGCTTTT TCCTACCTT TCCTGATTG TGTCCGTGAA 1860  
 ATGAATTGG TAGAGTCTCT GGAAGGTTT AAGCCCATTT TCAGTCTAA CTTACTTTCA

45 Seq ID NO: 250 Protein sequence  
 Protein Accession #: NP\_058637.1

1 11 21 31 41 51  
 | | | | |  
 50 MVSPRMSGLL SQTIVILALIP LPQTRPAGVF ELQIHSFPG PGPGAPRSPC SARLPCRLFF 60  
 RVCLKPGLSE EAAESPCLAG AALSARGPVY TEQPGAPAPD LPLPDGLIQV PFRDAWPGTF 120  
 SFIIRTWREE LGQIGGPAW SLLARVAGRR RLAAAGFWAR DIQRAGAWEL RPSYRACEP 180  
 PAVGTACTRL CRPSRAPSRC GPGLRPAAPL EDECEAPLVC RAGCSPEHGF CEQPGCECRL 240  
 EGWGTGLCTV PVTSSCLSP RGPSSATTGC LVPGPBGCDG NPCANGGSCS ETPRSFECTC 300  
 55 PRGFYGLRCE VSGVTCADGP CFNGSLCVGG ADPDSAYICH CPPGFQGSNC EKRVDRCSLQ 360  
 PCNRGSLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGTCVEGG GAHRCSCALG 420  
 FGGRDCRERA DPCAARPCAH GGRCYAHFSG LVCACAPGYM GARCEFPVHP DGASALPAAP 480  
 PGLRPGDPQR YLLFPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTPEFSVHAL 540  
 60 PDALNLRTO EGGSGDPSSS VDWNRPEDVD PQGIYVISAP SIYAREVATP LFPPPLHTGRA 600  
 GQRQHLLFPY PSSILSVK

Seq ID NO: 251 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

65 1 11 21 31 41 51  
 | | | | |  
 GAAATATAAC CATTGCAATT AGAAAATATC CAAAATAGCC TGTATCTTC CACGTGGCCT 60  
 AGATTATTGA CAATCCCAAA TATACAATTT TTCCTTAAA GTAGTACAA TTCCTTTGTA 120  
 GCTTCAATTC CTTATATGAC TTCAGACTGG AGAAGCCTGT TAAACCACTG TTAGTTTCAG 180  
 70 TTAGAAAGTC TGAGAGACTT TATACATAAA TTCTCAATTT GGCTGCTGTA CACGTGCCAG 240  
 AGTTTACTA CTGTAGTGAC CGTTGAGAAG ACCCTTGTTT ATTTACATTT GAAGCACTGT 300  
 TTGTGCAAA CACCTTTTAT TGTAAAGTGC CTGTATTCCT TTCATTACT TCATGTCCAG 360  
 GGGTGCTATT TACCTAGAAC CATTGTCTAC TACAATTAAC ATTTACATTA CAAAGTGTGT 420  
 75 GGTTTCTTTT TCAAGGAGG TTCAATTAAG GCAATAAGAT GTTGTCTGGA GAAACCTATT 480  
 GTTACTGAA AGCACTCAAT GAAGTCAAAT TACTGAAGCT TTTGCTACA TCTTGTCTT 540  
 TTATGTAAT ATGTTAAATA TAACATCTAA GGAAAATAA CAATATTATA ATTATGTGTT 600  
 TGCCATTGTC ATATCAAACT TGCTTTGTAT CATACTAATG TTACTAATCT TATCATCA 660  
 TAAAAATACA TTTCAATGTT AAAAAAATA AAAAAAATA

80 Seq ID NO: 252 DNA sequence  
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 AGGTACTGCC AGAAAGGATC AGGACCTGGA GTCTGGCAAG AGGAAGACAG AGGCCTGTGT 60

5 GGGGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC 120  
 TAGATAACCG AAAGTAAAAA CTCTTCAAG ATCGCCGGGG AGCGTGTGAG AATGAAAGAC 180  
 TACAGCCGAG AGACAGTAAA AACAGAAAAG GTCAGGAATA CTTATTGAAT CTAACCTTGT 240  
 TTTTGTGTTG TTTTTCCTCT TATGATTAAG GGTGGGATGA GAGAAAATTA AATGACACAC 300  
 ACATGCTAAA ATATCAAGGT TCCAGATATG TCTTGAGAGG GGTGTGTGCA GCTGCAARGG 360  
 AGAAGTGTAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTTCTATT TTAAGGCAAA 420  
 AGTTATATCA GGGATTTTTT TCTTAGAAAG GTGTTGCAGA GATGCTGGT ACCTAGTTTA 480  
 AAAATGATTC CATAATATGT AGACTTGGGC AGTTCCTTTG GGAGGCACCT CCCTCTCAAA 540  
 ATTTGAAGAT TGTGCTTGGG AATTACTTTA CATGTATTGG GGTGTATGTT CAATTGTGAC 600  
 10 GAAATTAGAC TTTCAGAAAA GTTTATACTG GAAGGTTAAT AATTGTATAT TACTGAGGAC 660  
 TTAGAGCTAG CAGGCAAAAT GAAAAAARG CAGGGGCTGA TTTTATTCTT 720  
 TCTATTCAAA ATACAAGGAC AGATGCTTCT CTGTTCCTAG AGGGTTTCTT TGAGGAAGCT 780  
 ACTGAAGCAG AAAGACATGA TGGAGACGAG ATCGCCTCCC CTCTGTGCAA AGTGTAAAAA 840  
 AAATGTTCTG TCTTACTCTG CGCCTAGCAT TGGAAATGAA AGTGACATTT ACGCCACAAC 900  
 15 CCACGTGTGC GCCTCCTCTC TTTTGTGTTA AGGATGATCA GGTCTATCCA GGAACACAGT 960  
 CTGGCATCCC AAACGTAAAT AATTAGGACG TATATAGACC TGACAAAAAT GGAAAGGGGG 1020  
 TGGGGAATCT GAGGGTCTGT CTGCTCTAAT TGATTCCTCT AAACGGAAATG CAGGAGATGT 1080  
 GAACGGCAGC ACGCTCCGAT TCCCACGCTC GGGGGCAAGT GATAAAGCGG GCGCGGGCAG 1140  
 CCTATGACAG ACAGCCCTGT TGGGGGTGGG GGGTATGAAA AAAACATCAA GTGCACACAC 1200  
 20 CATACTCATC TCCATCGCTT AAGAAAGTAA AGGCATTTC CACCCACAGC CATCTGCAGC 1260  
 TTCCCAATTT GCAGCACCAA CTGGTCTGTA GCTGCTACAT AGTCTGCTTC TGTTAATTTT 1320  
 TTAACCACTG TTAAATCTGG CCATAATTA GTTTGGCTTT CTTCGTGTTT TGAGATTCTT 1380  
 AGAATTCAAG CAAAGCTAGT AGAAAGCAAT TCCAAGAAAG TCCCATGACT CCCTGCCCTT 1440  
 AATGTCAAAA TCTCAGTCCA TGAGATTATG GCCTGTGAC CACATTTTGT CTTTGTGTTT 1500  
 25 GGGTGGGCAA ATGTGTATAG AGATAAATA CATATCTCTA TATAACAGTC GTTATTATAA 1560  
 TTTCTAGAGG CTTTTCCTCT CTTAACATGA TACATCTAGG AACTTGGTCT AATGTGTGTA 1620  
 GTAGATATAC ACTAGAATAA AAATATAAAA GTCAATAGCC TGTAAGAAAT TGATTATGAT 1680  
 AACAAATGTA TAAAGAGTTT GTTTTGAAT AGTCTCAGCT AGATGGGTCT AAATAGCCAT 1740  
 30 TTTAATGTAA TCTAAATAA AACTATGCC TAGCAGAAAC TTTGGGCTTT TGGAGGTCCC 1800  
 CATTGTGCCC TTTTCATAAA AGTCCTTAAG TTTTCCATAT GTACCAACGC AAACATTTGT 1860  
 ATAGGCATTG ACACAGAAAT ATAAACATTG CAATTAGAAA ATATCCAAAA TAGCCTGTGA 1920  
 TCTTCCAGCT GGCCTAGATT ATTGACAATC CCAATATATC AATTTTCTT TAAAGTAGT 1980  
 ACAATTTCTT TTGTAGCTTC AATTCTTAT ATGACTTCAG ACTGGAGAAG CCTGTAAAC 2040  
 35 CACTGTTAGT TCCAGTTAGA AAGTCTGAGA GACTTTATAC ATAAATTCTC AATTGTGCTG 2100  
 CTGTACAGCT GCCAGAGTTT TACTACTGTA GTGACCGTTG AGAAGACCTT TGTATTATTA 2160  
 CATTGTAAGC ACTGTTTGTG CAAACAACCT TTTATTGTTA AGTGCCTGTA TTCCTTTTAT 2220  
 TTACTTCACT TCCAGGGGTG CTATTACCTT AGAACCATTG TCTACTACAA TTAACATTTA 2280  
 CATTACAAAG TGTGTGTTT TCTTTTCAA GGAGGTTCAA TTAAGGCAAT AAGATGTTTG 2340  
 40 CTGGAGAAAC CTATTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC 2400  
 TTACATCTTG GTCTTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA 2460  
 TTATAATTAT GTGTTTGCCA TTGTATATC AAACCTGCTT TGTATCATAC TAATGTTACA 2520  
 TAACTTATCG ATCAATAAAA ATACATTCA ATGTT

Seq ID NO: 253 DNA sequence

Nucleic Acid Accession #: NM\_001650.2

Coding sequence: 40.1011

1 11 21 31 41 51  
 50 GGGGCAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCACAGCA 60  
 AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCCTTCAAA 120  
 GGGGTCTGGA CTCAGCTTCT CTGGAAGGCA GTCACAGCGG AATTCTTGCC CATGCTTATT 180  
 TTTGTTCTCC TCGCCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240  
 55 GTCGACATGG TTCTATCTC CTTTGTCTT GGAATCAGCA TTGCAACCAT GGTGCGAGTC 300  
 TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCACC 360  
 AGGAAGATCA GCATGCGCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420  
 ATTGGAGCAG GAATCCTCTA TCTGGTCACA CTCCCAAGTG TGGTGGGAGG CTTGGGAGTC 480  
 ACCATGGTTC ATGGAATATC TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540  
 60 TTTCAATTGG TGTTACTAT CTTTGCAGC TGTGATTCCA AACGGACTGA TGTACTGGC 600  
 TCAATAGCTT TAGCAATTGG ATTTCTGTGT GCAATTGGAC ATTTATTGTC AATCAATTAT 660  
 ACTGGTGCCA GCATGAATCC CGCCCGATCC TTGGACCTG CAGTTATCAT GGGAAATTGG 720  
 GAAACCAATT GGATATATTG GTTGGGCCC ATCATAGGAG CTGTCTCTGC TGTGGCCCTT 780  
 TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840  
 65 AAAGCTGCCC AGCAACAATA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900  
 GAGACGAGTG ACCTGATTTT AAAACCTGGA GTGGTGCAATG TGAATGACGT TGACCGGGGA 960  
 GAGGAGAAGA AGGGGAAGA CCAATCTGGA GAGGTATTGT CTTAGTATG ACTAGAAGAT 1020  
 CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCTCTAG ATTTCTCTCC ACCCATTAAG 1080  
 GAAACAGATT TGTATAAAT TAGAAATGTG CAGGTTTGTG GTTTCATGTC ATATTACTCA 1140  
 70 GTCTAAACAA TAAATATTTC ATAAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200  
 TCCAAATCTA AAAAAGAAAA TATTTTAAAG ATGTTCTTAA GCAATATAT ACCTATTTTA 1260  
 TCTAGTTACC TTTCATTAAAC AACCAATTTT AACCGTGTGT CAAGATTGAG TTAAGTCTTG 1320  
 CCTGACAGAA CTCAAAGACA CGTCTATCAG CTATTCTCT CTCTACTGGA ATATTGGTAT 1380  
 AGTCAATTCT TATTGAATA TTTATTCTAT TAAACTGAGT TTAACAATGG C

Seq ID NO: 254 Protein sequence

Protein Accession #: NP\_001641.1

1 11 21 31 41 51  
 80 MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG 60  
 GTEKPLPVDW VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120  
 AQCLGAIIGA GLYLVTTPPS VVGLGVMTVM HGNLTAGHGL LVELIITPQL VFTIFASCD 180  
 KRTDVTGSIA LAIGFSVAIG HLFAINYTGA SMNPARSFGP AVIMGNWENH WIYWGPIIG 240  
 AVLAGGLLEY VFCPDVEFKR RFKEAFSKAA QQTGSGYMEV EDNRSQVETD DLILKPGVVH 300

VIDVDRGEEK KGKQDSGEVL SSV

Seq ID NO: 255 DNA sequence  
 Nucleic Acid Accession #: U26742.1  
 Coding sequence: 325..1449

1 11 21 31 41 51  
 | | | | |  
 5 CAGGAAACCC TGGTACTGGC AGCAGCCAGC CTCTGCTGTG CCCACATGAC CCACAACTCT 60  
 10 GGCAGCGGAC CCGGCACCTC CAACATTATT AAATAATAAG AAAGCGGCTC CTACTCCAGG 120  
 CTCAAACCTC CTGCGAGACC AATGGACACC TTCTAAGAGT TTGGCGAGTC AGTGACTGAA 180  
 GCGCCCGTCC ATTCCAAGAT AAATAGGATT TACCAATCCT TGGATGAAGT GCTTGGGAAG 240  
 TCTTTAAGTG CCATAATCAA CTGCCATTTC AAAGAATATA GATGGTTTGT AAAAGTTCAT 300  
 15 GCTGTCCCTT CATTGAATTT TAGAATGATT GAAGATAGTG GGAAGAGAGG AAATACCATG 360  
 GCAGAAAGAA GACAGCTGTT TGCAGAGATG AGGGCTCAAG ATCTGGATCG CATCCGACTC 420  
 TCCACCTGCA TAAGCAGCATG CAAGCTTAGG TTTGTTTCTA AGAAATGCAA TTTGCACCTG 480  
 GTGGACATAT GGAATGTCTAT AGAAGCATTG CGGGAAATAT CTCTGAACAA CCTGGACCCA 540  
 AACACTGAAC TCAACGTGTC CCGCTTAGAG GCTGTGCTCT CCACTATTTT TTACCGACTC 600  
 20 AACAAACGGA TGCCAAACAC TCACCAAAATC CATGTGGAGC AGTCCATCAG CCTCCTCCTT 660  
 AACTTCTCTG TTGACGCTTT TGATCCGGAA GGCCATGGTA AAATTTTCAGT ATTTGCTGTC 720  
 AAAATGGCTT TAAGCAGCATG GTGTGGAGGG AAGATCATGG ACAAATTAAG ATATATTTTC 780  
 TCAATGATTT CTGACTCCAG TGGGGTGTAT GTTTATGGAC GATATGACCA ATTCCTTCGG 840  
 GAAGTTCTCA AACTACCCAC GGCAGTTTTC GAAGTCCCTT CATTGGTTA CACAGAACAG 900  
 25 TCAGCCAGAT CTGTTTCTTC CCAACAGAAA AAAGTCAAGT TAAATGGTTT CTTGACACAG 960  
 CTTATGTGAG ATCCTCCCCC GCAGTGTCTG GTCTGGTTGC CTCTTCTGCA TCGACTAGCA 1020  
 AATGTGGAAA ATGTCTTCCA TCCGGTTGAG TGTTCCTACT GCCACAGTGA GAGTATGATG 1080  
 GGATTTGCGT ACCGATGCCA ACAGTGTCTC AATTACCAAG TCTGTCAAGG CTGCTTCCTG 1140  
 AGGGGACATG CCGGTGGTTC TCATAGCAAC CAGCACCAAA TGAAGAGATA CAOGTCATGG 1200  
 30 AAATCACCTG CTRAGAAGCT GACTAATGCA TTAAGCAAGT CCCTGAGCTG TGCTTCCAGC 1260  
 CGTGAACCTT TGACCCCATC GTTCCAGATC CAGCCTGAGA AGCCACTCAA CTTGGCTCAC 1320  
 ATCGTTGATA CTTGGCTTCC CAGACCTGTA ACCAGCATGA ACGACACCTT GTTCTCCAC 1380  
 TCTGTTCCCT CCTCAGGAAG TCCTTTTATT ACCAGGAGCT CGGACGGTGC TTTTGGTGGG 1440  
 35 TGCGTCTAGA TGGATAACAT GACTTCTTCT ACCCTAAAT ATTCTATATA TACTTTGAGC 1500  
 TGTTCGGTT CCTCCAGGGT GCATGGTACC CATTAACCCA AAATATGATT ATTTCCCTTT 1560  
 TTTCCCATTT TCAGTCATTT TGGAAATGTT TCTGTGAACC ACAGTTGGGT TGTTTAAAGC 1620  
 TCACATTCTT TCTGTCAACC ACAGAGATTG GCTTACGGTT TCTGTTTGA GGGTGTCTTT 1680  
 CAATAAGCT. GTGTACATA AATGTCC

Seq ID NO: 256 Protein sequence  
 Protein Accession #: AAC50424.1

1 11 21 31 41 51  
 | | | | |  
 45 MIEDSGKRG N TMAERRQLFA EMRAQDLDR I RLSTYRTACK LRFVQKKCNL HLVDIWNVIE 60  
 ALRENALN L DPNTLNLVSR LEAVLSTIFY QLNKRMPPTH QIHVEQSISL LNFLLAAFD 120  
 PEGHGKISV F AVKMLATL C GKKIMDKLRY IFSMISDSSG VMVYGRYDQF LREVLKLPAT 180  
 VPEGPSFGY T EQSARSCFSQ QKKVTLNGFL DTLMSDPPQ CLVWLP LLHR LANVENVFEP 240  
 VECSYCHSE S MMGFRYRCQQ CHNYQLQDC FWRGHAGGSH SNQHQMKEYT SWKSPAKKLT 300  
 50 NALSKSLSC A SSREPLHPMF PDQPEKPLNL AHIVDTWPPR PVTSMNDILF SHSVPSGSGP 360  
 FITRSSDGA F GGCY

Seq ID NO: 257 DNA sequence  
 Nucleic Acid Accession #: NM\_004172.1  
 Coding sequence: 179..1807

1 11 21 31 41 51  
 | | | | |  
 55 GCGGATTGTT GCTCCGTGTG ACCTGCTGGG GAATTCACCT CGTACTGCT TGATATCTTC 60  
 CACCCCTTAC AAAATCAGAA AAGTTGTGTT TTCTAATACC AAAGAGGAGG TTTGGCTTTC 120  
 60 TGTGGGTGAT TCCAGACAC TGAAGTGCAA AGAAGAGACC CTCTAGAAA AGTAAATAT 180  
 GACTAAAGC AATGAGAAAG AGCCCAAGAT GGGGGCAGG ATGGAGAGAT TCCAGCAGGG 240  
 AGTCCGTAAA CGCACACTTT TGGCCAAGAA GAAAGTGCA GAACTATCAA AGGAGGATGT 300  
 TAAAGTTAC CTGTTTCGGA ATGCTTTTGT GCTGCTACA GTCACCGCTG TCATTGTGGG 360  
 65 TACAATCCTT GGATTTACCC TCCGACCATA CAGAATGAGC TACCGGGAAG TCAAGTACTT 420  
 CTCCTTCTCT GGGGAACCTT TGATGAGGAT GTTACAGATG CTGGTCTTAC CACTTATCAT 480  
 CTCAGTCTT GTACAGGAA TGGCGGCGCT AGATAGTAAG GCATCAGGGA AGATGGGAAT 540  
 GCGAGCTGTA GTCTATTATA TGACTACCAC CATCATGTCT GTGGTGATTG GCATATCAT 600  
 70 TGTATCATC ATCCATCCTG GGAAGGGCAC AAAGGAAAAC ATGCACAGAG AAGGCAAAAT 660  
 TGTACGAGTG ACAGCTGCAG ATGCCCTTCT GGACTTGATC AGGAACATGT TCCCTCCAAA 720  
 TCTGTAGAAA GCCTGCTTTA AACAGTTTAA AACCAACTAT GAGAAGAGAA GCTTTAAAGT 780  
 GGCATCCAG GCAACAGAAA CGCTTGTTGG TGCTGTGATA AACAAATGTT CTGAGGCCAT 840  
 75 GGAGACTCTT ACCCGAATCA CAGAGGAGCT GGTCCAGATT CCAGGATCTG TGAATGGAGT 900  
 CAATGCCCTG GGTCTAGTTG TCTTCTCCAT GTGCTTGGT TTTGTGATTG GAAACATGAA 960  
 GGAACAGGGG CAGGCCCTGA GAGAGTTCTT TGATTCTCTT AACGAAGCCA TCATGAGACT 1020  
 GGTAGCAGTA ATAATGTGTT ATGCCCCCGT GGGTATTCTT TTCCTGATTG CTGGGAAGAT 1080  
 TGTGGAGCTT GAAGACATGG GTGTGATTGG GGGGACGCTT GCCATGTACA CCGTACTGCT 1140  
 CATGTGTGGC TTAATCATTC ACGCAGTCAT CGTCTTGCCA CTCCTCTACT TCTTGGTAA 1200  
 80 ACGGAAAAAC CCTTGGGTTT TTATTGAGG GTTGTGCAA GCACTCATCA CCGCTCTGGG 1260  
 GACCTCTTCA AGTTCTGCCA CCTTACCCAT CACCTTCAAG TGCCCTGGAAG AGAACATGG 1320  
 CGTGGACAGG CCGGTCACCA GATTGTGCT CCCCGTAGGA GCCACATTA ACATGGATGG 1380  
 GACTGCCCTT TATGAGGCTT TGGCTGCCAT TTTCAATGCT CAAGTTAACA ACTTTGAAGT 1440  
 GAACTTCGGA CAAATATTAT CAATCAGCAT CACAGCCACA GCTGCCAGTA TTGGGGCAGC 1500  
 TGGAAATCTT CAGGCGGGCC GTGTCACTAT GGTCAATGTT CTGACATCTG TCGGCTGCC 1560  
 CACTGACGAC ATCAGCTCA TCATCGCGT GGACTGTGTC CTGATCGCC TCCGACCAC 1620



5 CACCAACGTA CTGGGAGACT CCCTGGGAGC TGGGATTGTG GAGCATTGT CACGACATGA 1680  
 ACTGAGAAC AGAGATTGTT AAATGGGTAA CTCAGTGATT GAAGAGAAATG AAATGAAGAA 1740  
 ACCATATCAA CTGATTGCAC AGGACAATGA AACTGAGAAA CCCATCGACA GTGAAACCAA 1800  
 GATGTAGACT AACATAAAGA AACACTTTCT TGAGCACCAG GTGTTAAAAA CCATTATAAA 1860  
 ATCTTTCCAT CTCATTACAG CTCATTGCTT CCAGCAAGCC CGTCATCTTC CCTTTCTCTC 1920  
 CTCTGATAA GACTGGAAAA TAGTCCTCCA AAACACAAGG GAGGATTTTG GGTGGCCAAA 1980  
 GTGTACAATT TTCATCCCA AATTGAAATT TTAAATCAT TTCATGTTAG TCTTACCGAA 2040  
 TAAGGTACCA AGATCACAAA TAGTGTGAT CAGATCTAC AAGTTTATGT GGCACACAAT 2100  
 10 TCCTATAAAT GTGATTTTTT TATATAAGTT AAAGAGACAA ATAGTAGGCT AAAAACATTT 2160  
 TAAATCAAC TTTTGAATTT TAAAAATCTT TCAGAAATACA ATTCAGTTTT AGTTTCAAAA 2220  
 TGTTAAACAC TTGAATTACA ACCGGTTATC AGTTGGACAG TAAGATTTTA TCCCTTCTC 2280  
 TTCTGACTGG TATACCTATT TCATTAGTAG CTAGGTGCAC ATATACATCT AGCAGAGCTG 2340  
 TGAGGACAGA CAGAAGGCAA AGTTTCCATG TGGCTTGAG CAAGTCCCAT CTCACCTCTA 2400  
 15 GGCTCAGTG TCCTCATCTA TAAATGAGG GACTTCCCTA GAAGTCTTCA TGGTCTCTTC 2460  
 CAGCCAGAG ATCTGTGATG GTCATGAAAG CACCTGCCCT CTGTTTCCCC TCAGAACACC 2520  
 CTGTACCATC CTGAGGACAG GAGGCCCTCA GAAAGACAC TTCAATGGGA GTGAACATTT 2580  
 CTAACAAAG ACAGGATGGC TGTGTGTGGT GGTCAACAGG TCCTGTGAGC AAAGTGCAGG 2640  
 TTATGCAAGT CCCCAGGCG GAGGCCATTG CAGGAGTGGG ATTATTCTC AACTCTTTG 2700  
 20 CCCAGTTTAT CCCAATGGGG GAAGTATTCC CTCTTTCTCT ACTCTGGGAA GAATGTCTCC 2760  
 TGCCACTCCT CACTGATAGA TAGACTTCGA AAACAGATGA GAAGACTAGC AGCTAGCAAG 2820  
 GGTGCTTGTG TGCAGACTGT GGAACACTAA AGAGCTAGGA AAGAGTTGAG CACAGGCAAC 2880  
 ATTACAAACA AAGGATTGTA AAACACCAAG AGTACAGGTC TTCTTAAAGG AAGAATAAAA 2940  
 AAGAAGAGGT TCATTTTTCT GGCTTTTTCT TTCACCTGAA ACATTTTTCT TCGAGTCCAA 3000  
 25 AATCATTCCC CCCGTGAAGT CTGCTTACCA AAACATAAGA CGACTTATAT ATTTGAAAGA 3060  
 AGTCAAAATG ATGAGCTCTC TAAATAGAAG CCATGAGTTG AGTGGGTATT TCTTATTGTA 3120  
 AAGTGTTTTT CTTTAATCAA AAGTCCCTAG AATGAGGGAA ACAAATATT TATTGTGTTT 3180  
 GGAATCCAC TTATCAATC ATTCAAACT TTCAGCTGGA GTGGGGTTTG CTTTGTGTTT 3240  
 GTTTGTGTCC ATAAGAGAAA TGGTAGAAGA TGAATCAGTA TGAAGACAT GTCAATGAGG 3300  
 30 TTATGAGAAA AAAACAGCAG GGGCATTAGT TTCAGGCAAG GCAGCTCCCA GGTITAGAGA 3360  
 TTAATTTTTA CCCCTAAGG AATATCCAGT CAAAGACGCT GAGTGGGAGC TGTGAGGCAG 3420  
 TAGCAGCTGT GTTTGAGTTT CTGGCTGAAA ATGGTGAAGA ATGGACTTAA TTATGCTAAC 3480  
 AAACGAAAA ATCTAGACAT AGATCCTCTG ATATACAATT AGAGATATT TATATAGAC 3540  
 35 CCCAAGCATT CTGTGCATAA AAGTTAACAT TAGGCTGTGG TGCAGTAACC ATTATATGTC 3600  
 GAGGCTCTAT TCGGAATAA CACTACAAAT GTTAAAGTAC GTGGCTGTCC TCTTAAGACA 3660  
 CTAGTAGAGC AAAGACTTAA TCATATCAAC TTAATTTCTG TACACAATAT GTGTTTTTAA 3720  
 ATATACTAAC CATTTCTTAT GGAAAGGTCC TGTGGGAGC CCATCCTCTC GCCAAGCCAT 3780  
 CACAGGCTCT GCATACACAT GCACTCAGTG TGGACTGGGA AGCATTACTT TGTAGATGTA 3840  
 TTTTCAATAA AGAAAAAAT AGTTTACAT T

Seq ID NO: 258 Protein sequence  
 Protein Accession #: NP\_004163.1

45 1 11 21 31 41 51  
 | | | | |  
 MTKSNGEPEK MGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAP VLLTVTAVIV 60  
 GTILGFTLRP YRMSYREVKY FSFPGELLMR MLQMLVLP LI ISSLVTGMAA LDSKASGKMG 120  
 MRVAVVYMTT TIIAVVIGII IVIIHPGKG TKENMBREK IVRVTAADAF LDLIRNMFPP 180  
 NLVEACFKQF KTYNEKRSEK VPIQANETLV GAVINNVSEA METLTRITEE LVPVPGSVNG 240  
 50 VNALGLVFPF MCFGVIGNM KEQGQALREF FDSLNEAIMR LVAVIMYAP VGILFLIAGK 300  
 IVEMEDMGVI GQGLAMVTVT VIVGLLIHAV IVLPPLLYFLV TRKNPNWVFIG GLIQLALITL 360  
 TSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IFIAQVNNFE 420  
 LNFQGIITIS ITATAASIGA AGIPQAGLVT MVIVLTSVGL PTDDITLIIA VDWFLDRLRT 480  
 TTNVLGDSLG AGIVEHLRSH ELKNRDVEMG NSVIEENEMK KPYQLIAQDN ETEKPIDSET 540  
 KM

Seq ID NO: 259 DNA sequence  
 Nucleic Acid Accession #: NM\_021948.1  
 Coding sequence: 48..2783

60 1 11 21 31 41 51  
 | | | | |  
 TGTGGCAGTG CCTGCGTACC CAACCCAGC CCTGGGTAGC CTGCAGCATG GCCAGCTGT 60  
 TCCTGCCCTT GCTGSCAGCC CTGGTCTGCG CCCAGGCTCC TGCAGCTTTA GCAGATGTTT 120  
 TGGAAAGGAGA CAGCTCAGAG GACCGCGCTT TTCGCTGGG CATCGCGGCG GACGCGCCAC 180  
 65 TGCAGGCGGT GCTCGGCGGC GCCCTCACCA TCCCTTGCCA CGTCCACTAC CTGCGGCCAC 240  
 CGCGGAGCGC CCGGGCTGTG CTGGGCTCTC CGCGGTCAA GTGGACTTTC CTGTCCCGGG 300  
 GCGGGAGGCG AGAGGTGCTG GTGGCGCGGG GAGTGGCGGT CAAGGTGAAC GAGGCGCTACC 360  
 GGTTCGCGGT GCGACTGCTT CGGTACCCAG CGTGGCTCAC CGAAGTCTCC CTGGGCTGTA 420  
 GCGAGCTGCG CCCCAACGAC TCAGGTATCT ATCGCTGTGA GGTCCAGCAC GGCATCGATG 480  
 70 ACAGCAGCGA CGCTGTGGAG GTCAAGGTCA AAGGGGTGCT CTTTCTCTAC CGAGAGGGCT 540  
 CTGCGCGCTA TGCTTTCTCC TTTTCTGGGG CCCAGGAGGC CTGTGCCCGC ATTGGAGGCC 600  
 ACATCGCCAC CCGGAGCAG CTCTATGCCG CCTACCTTGG GGGCTATGAG CAATGTGATG 660  
 CTGGCTGGCT GTCGGATCAG ACCGTGAGGT ATCCCATCCA GACCCACAGA GAGGCTGTT 720  
 ACGGAGACAT GGATGGCTTC CCCGGGGTCC GGAACATAGG TGTGTTGAGC CCGGATGACC 780  
 75 TCTATGATGT GTACTGTTAT GCTGAAGACC TAAATGGAGA ATTGTTCTGT GGTGACCCCTC 840  
 CAGAGAAGCT GACATTGGAG GAAGCACGGG CGTACTGCCA GGAGCGGGGT GCAGAGATTG 900  
 CCACCAGCGG CCAACTGTAT GCAGCCTGGG ATGGTGGCCT GGACCACTGC AGCCAGGGGT 960  
 GGCTAGCTGA TGGCAGTGTG CGCTACCCCA TCGTCACACC CAGCCAGGCG TGTGGTGGGG 1020  
 80 GCTTGCCTGG TGTCAAGACT CTCTTCTCTT TCCCAACCA GACTGGCTTC CCCAATAAGC 1080  
 ACAGCCGCTT CAACGTCTAC TGCTTCCGAG ACTCGGCCCA GCCTTCTGCC ATCCCTGAGG 1140  
 CCTCCACCC AGCCTCCAAC CCAGCCTCTG ATGACTAGA GGCTATCGTC ACAGTGACAG 1200  
 AGACCCCTGA GGAATCTGAG CTGCCTCAGG AAGCCACAGA GAGTGAATCC CGTGGGGCCA 1260  
 TCTACTCCAT CCCATCATG GAGGACGAG GAGGTGGAAG CTCCACTCCA GAAGACCCAG 1320  
 CAGAGGCCCT TAGGACGCTC CTAGAATTGG AAACACAATC CATGGTACCG CCCACGGGGT 1380

5	TCTCAGAAGA	GGAAGGTAAG	GCATTGGAGG	AAGAAGAGAA	ATATGAAGAT	GAAGAAGAGA	1440
	AAGAGGAGGA	AGAAGAAGAG	GAGGAGGTGG	AGGATGAGGC	TCTGTGGGCA	TGGCCACGCG	1500
	AGCTCAGCAG	CCCGGGCCCT	GAGGCTCTCT	TCCCCACTGA	GCCAGCAGCC	CAGGAGGAGT	1560
	CACTCTCCCA	GGCGCCAGCA	AGGCGAGTCC	TGCAGCCTGG	TGCATCACCA	CTTCTGTATG	1620
	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
	CTCCAGGGA	GAGGAACCTA	GCATCCCAT	CACCTTCCAC	TCTGGTTGAG	GCAAGAGAGG	1740
	TGGGGGAGGC	AACTGGTGGT	CCTGAGCTAT	CTGGGGTCCC	TCGAGGAGAG	AGCGAGGAGA	1800
	CAGGAAGCTC	CGAGGGTGCC	CCTTCCCTGC	TTCAGCCAC	ACGGGCCCCCT	GAGGGTACCA	1860
10	GGGAGCTGGA	GGCCCCCTCT	GAAGATAATT	CTGGAAGAAC	TGCCCCAGCA	GGGACCTCAG	1920
	TGCAGGCCCA	CCAGTGTCTG	CCCACTGACA	GCGCCAGCCG	AGGTGGAGTG	GCGTGTGTC	1980
	CCGATCAGG	TGACTGTGTC	CCCAGCCCCCT	GCCACAATGG	TGGGACATGC	TTGGAGGAGG	2040
	AGGAAGGGGT	CCGCTGCCTA	TGCTGCCTG	GCTATGGGGG	GGACCTGTGC	GATGTTGGCC	2100
	TCGCTTCTG	CAACCCCGGC	TGGGACGCTT	TCCAGGGGCG	CTGCTACAAG	CACTTTTCOA	2160
	CACGAAGGAG	CTGGGAGGAG	GCAGAGACCC	AGTGCCGGAT	GTAACGGCGG	CATCTGGCCA	2220
15	GCATCAGCAC	ACCCAGGAA	CAGGACTTCA	TCAACAACCG	GTACCGGAG	TACCACTGGA	2280
	TCGGACTCAA	CGACAGGACC	ATCGAAGGCG	ACTTCTTGTG	GTCGGATGGC	GTCCCCCTGC	2340
	TCATAGAGAA	CTGGAACCTT	GGGCAGCCTG	ACAGCTACTT	CCTGTCTGGA	GAGAACTGGG	2400
	TGTCATGCTG	TGGCATGAT	CAGGGACAAT	GGAGTGAOGT	GCCCTGCAAC	TACCACTGTG	2460
20	CCTACACCTG	CAAGATGGGG	CTGGTGTCTT	GTGGGCGGCC	ACCGGAGCTG	CCCTGTGGCT	2520
	AAGTGTTCGG	CGGCCACGCG	CTGCGCTATG	AGGTGGACAC	TGTGCTTCGG	TACCGGTGCC	2580
	GGGAAGGACT	GGCCACGCGC	AATCTGCCCG	TGATCCGATG	CCAAGAGAAC	GGTGGTTGGG	2640
	AGGCCCCCCA	GATCTCCTGT	GTGCCAGAA	GACCTGCCCG	AGCTCTGCAC	CCAGAGGAGG	2700
	ACCCAGAGGG	ACGTACAGGG	AGGCTACTGG	GACGCTGAA	GGCGCTGTTG	ATCCCCCCTT	2760
25	CCAGCCCCAT	GCCAGGTCCC	TAGGGGGCAA	GGCCTTGAAC	ACTGCCGGCC	ACAGCACTGC	2820
	CCTGTCACCC	AAATTTTCCC	TCACACCTCG	CGCTCACCCAC	AGGAAGTGAC	AACATGAC	

Seq ID NO: 260 Protein sequence  
Protein Accession #: NP\_068767.1

30	1	11	21	31	41	51	
	MAQLFLPLLA	ALVLAQAPAA	LADVLEGDS	EDRAFRVRIA	GDAPLQGVLG	GALTIPCHVH	60
	YLPPPPRRRA	VLGSPRVKWT	FLSRGREAEV	LVARGVRVKV	NEAYRFRVAL	PAYPASLTDV	120
35	SLALSELRFN	DSGIYRCEVQ	HGIDSSDAV	EVKVKGVVFL	YREGSARYAF	SFSGAQEACA	180
	RIGAHIAATPE	QLYAAYLGGY	EQCDAGWLS	QTVRYPIQTP	REACYGDMDG	FFGVRYNGVV	240
	DPDDLVDVVC	YADDLNGLF	LGDPPKLT	EEARAYCQER	GAEIATTGQL	YAAWDGGLDH	300
	CSPGWLADGS	VRYPIVTPSQ	RCGGGLPGVK	TLFLFPNQTG	FPNKHRSFNV	YCFRDSAQPS	360
	AIPEASNPA	NPASDGLLEAI	VTVTETLEEL	QLPQEATESE	SRGAIYSIPI	MEDGGGSSST	420
40	PEDPAPAPPT	LLEFETQSMV	PPTGFSEEEG	KALEEEEEKYE	DEEEKEEBEE	EEVEDEALW	480
	AWPSELSSPG	PEASLPTBPA	AQEEESLSQAP	ARAVLQPGAS	PLPDGSEBAS	RPRVHGFPPT	540
	ETLPTPRERN	LASPSSTLIV	EAREVGEATG	GPESLGVPRG	ESEETGSSEG	APSLLPATRA	600
	PEGTRELEAP	SDNSNGRTAP	AGTSVQAQPV	LPTDSASRGG	VAVVPASGDC	VPSPCNNGYT	660
	CLBEEEGVRC	LCPLPGYGGDL	CDVGLRFCNP	GWDAPQAGCY	KHFSTRRSWE	EAETQCRMV	720
45	AHLASISTPE	BQDFINNRYR	EYQWIGLNDR	TIEGDFLWSD	GVPLLYENWN	PQGPDSYFLS	780
	GENCVPMVWH	DQSQWSDVPC	NYHLSYTKRM	GLVSCGPPE	LPLAQVFGRR	RLRYEVDTVL	840
	RYRCREGLAQ	RNLPLIRQCE	NGRWEAPQIS	CVPRRPARAL	HPEDPEGRQ	GRLLGRWKAL	900
	LIPSPSPMPG	P					

Seq ID NO: 261 DNA sequence  
Nucleic Acid Accession #: NM\_004386.1  
Coding sequence: 2..3967

55	1	11	21	31	41	51	
	GATGGGGGCC	CGTTTGTCT	GGGCCTTGGG	CCTTTTGATG	CTGCAGATGC	TGCTCTTGT	60
	GGCTGGGGAA	CAGGGCACAC	AGGATATCAC	CGATGCCAGC	GAAAGGGGGC	TCCACATGCA	120
	GAAGCTGGGG	TCTGGGTCTG	TGCAGGCTGC	GCTGGCGGAG	CTGTTGGCCC	TGCCCTGTCT	180
	CTTTACCCCT	CAGCCACGCG	CAAGCGCAGC	CCGAGATGCC	CCTCGGATAA	AGTGGACCAA	240
60	GGTGGGACT	GGTGGGGGCC	AGCGACAGGA	CTTGCCCATC	CTGTTGGCCA	AGGACAATGT	300
	CGTGAAGGTG	GCCAAAGCT	GGCAGGGACG	AGTGTCACTG	CCTTCTTACC	CCCGCGCGCG	360
	AGCCACGCGC	AGCTACTTTC	TGGGGCCACT	GAGGGCCAGT	GACTCTGGGC	TGTACCGCTG	420
	CCAGGTGGTG	AGGGGCATCG	AGGATGAGCA	GGACCTGGTG	CCCTTGGAGG	TGACAGGTGT	480
	TGTGTTCCAC	TACCGATCAG	CCCGGGACCG	CTATGCACCTG	ACCTTCCGCTG	AGGCCACGGA	540
65	GGCTCGCGT	CTCAGCTCAG	CCATCATTCG	AGCCCTCGG	CATCTACAGG	CTGCCCTTGA	600
	GGATGGCTTT	GACAACTGTG	ATGCTGGCTG	GCTCTCTGAC	GGCACTGTTC	GGTATCCTAT	660
	CACCCAGTCC	CGTCTGGT	GCTATGGCGA	CGTAGCAGC	CTTCCAGGGG	TTCCGAGCTA	720
	TGGGAGGCGC	AACCCACAGG	AACTCTACGA	TGTGTATTGC	TTTGCCTGGG	AGCTGGGGGG	780
	CGAGGTCTTC	TACGTGGGCC	CGGCCCGCGC	CCTGACACTG	GCGCGCGCGC	GTGCACAGTG	840
70	CCGCGCCAG	GGTGGCGGCG	TGGCCTCGGT	GGGACAGCTG	CACCTGGCCT	GGCATGAGGG	900
	CCTGGACCCAG	TGCGAACCGG	GCTGGCTGGC	CGAOGGCAGC	GTGCGCTACC	CGATCCAGAC	960
	GCGCGCGCGG	CGCTGCGGGG	GCCACAGCCC	GGGCGTGCGC	ACCGTCTACC	GCTTCCGTAA	1020
	CCGACCGCGC	TTCCCCCTAC	CCGCGGAGCG	CTTCCAGCGC	TACTGCTTCC	GAGCTCATCA	1080
	CCCCAGCTCA	CAACATGGAG	ACCTAGAGAC	CCCATCTCTT	GGGGATGAGG	GGGAGATTCT	1140
75	GTACAGCAGG	GGGCCCCCAG	TTAGAGAACT	GGAGCCCACT	CTGGAAGAGG	AAGAGGTGGT	1200
	CACCCCTGAC	TTCCAGGAGC	CTCTGGTGTG	CAGTGGGAA	GAAGAACCCT	TGATTTTGA	1260
	GGAGAAGCAG	GAGTCTCAAC	AGACCCTCAG	CCCTACCCCT	GGGACCCCCA	TGCTGGCCTC	1320
	ATGGCCCACT	GGGGAAGTGT	GGCTAAGCAC	GGTGGCCCCC	AGCCCTAGGG	ACATGGGGGC	1380
80	AGGCAGTCA	GCAAGTTTCA	ACACGGAGGT	GGCCCCAACT	GACCCTATGC	CTAGGAGAAG	1440
	GGGCGCTTC	AAAGGGTTGA	ATGGGCGCTA	CTTCCAGCAG	CAGGAACCGG	AGCCGGGGCT	1500
	GCAAGGGGGG	ATGGAGGAGC	GCGCCAGGCC	CCCCACCTCA	GAGGCTGCAG	TGAACCAAT	1560
	GGAGCCTCCG	TTGGCCATGG	CAGTCACAGA	GATGTTGGGC	AGTGCCAGAG	GCCGGAGCCC	1620
	CTGGGCTGAT	CTGACCAATG	AGGTGGATAT	GCCTGGAGCT	GGTTCCTGCT	GTGGCAAGAG	1680
	CTCCCCAGAG	CCCTGGCTGT	GGCCCCCTAC	CATGGTCCCA	CCAGCATCT	CAGGCCACAG	1740
	CAGGGCCCTG	GTCCTGGAGC	TAGAGAAAGC	CGAGGGCCCC	AGTGCCAGGC	CAGCCACCCC	1800

5 AGACCTGTTT TGGTCCCCCT TGGAGGCCAC TGTCTCAGCT CCCAGCCCTG CCCCCTGGGA 1860  
 GGCACTTCCT GTGGCCACCT CCCAGATGCT CCCTATGATG GCCATGCTGC GTGGTCCCAA 1920  
 AGAGTGGATG CTACACACAC CCACCCCAT CTCCACCGAG GCCAATAGAG TTGAGGCACA 1980  
 TGGTGGAGCC ACGGCACCGG CTCCACCTCT CCCTGTGCA GAGACCAAGG TGTATTCCCT 2040  
 10 GCCTCTCTCT TTGACCCCAA CAGGACAGGG TGGAGAGGCC ATGCCACAA CACCTGAGTC 2100  
 CCCCAGGGCA GACTTCAGAG AACTTGGGGA GACCAGCCCT GCTCAGGTCA ACAAGCTGA 2160  
 GCACTCCAGC TCACGCCCAT GGCTTCTGT AAACAGGAAT GTGGCTGTAG GTTTGTGCCC 2220  
 CACTGAGACT GCCACTGAGC CAACGGGCCT CAGGGGTATC CCGGGTCTG AGTCTGGGGT 2280  
 15 CTTCGACACA GCAGAAAGCC CCACTTCTGG CTTCGAGGCC ACTGTAGATG AGGTGCAGGA 2340  
 CCCCCTGGCC TGACTGTACA GCAAAGGGCT GGATGCAAGT TCCCCATCTG CCCCCTGGG 2400  
 GAGCCCTGGA GTTCTCTTGG TACCCAAAGT CACCCCAAT TTGGAGCCTT GGGTGTCTAC 2460  
 AGATGAAGGA CCCACTGTGA ATCCCATGGA TTCCACAGTC ACGCCGGCCC CCAGTGTATG 2520  
 TAGTGGAAAT TGGGAACCTG GATCCCAAGT GTTTGAAGAA GCCGAAAGCA CCACCTTGAG 2580  
 20 CCCTCAGGTG GCCTGGATA CAAGCATTTG GACGCCCTC ACGACCCCTG AGCAGGGGGA 2640  
 CAAGGTGGGA GTTCCAGCCA TGCTTACACT GGGCTCCTCA AGCTCCCAAC CCCACCCAGA 2700  
 GCCAGAGGAT CAGGTGGAGA CCCAGGGAAC ATCAGGAGCT TCAGTGCCTC CGCATCAGAG 2760  
 CAGTCCCTTA GGGAAACCGG CTGTTCTCTC TGGGACACCG ACTGCAGCCA GTGTGGGGCA 2820  
 GTCTGCTCA GTTTCCTCAG GGGAGCCTAC GGTACCGTGG GACCCCTCCA GCAOCCCTGT 2880  
 25 GCCTGTCAAC CTGGGCATAG AGGACTTGA ACTGGAGGTC CTGGCAGGGA GCCCGGGTGT 2940  
 AGAGAGCTTC TGGGAGGAGG TGGCAAGTGG AGAGGAGCCA GCCCTGCCAG GGAACCCATAT 3000  
 GAATGCAGGT GCGGAGGAGG TGCACTCAGA TCCCTGTGAG AACCAACCTT GTCTTCATGG 3060  
 AGGAGCATGT AATGCCAATG GCACCATGTA TGGCTGTAGC TGTGATCAGG GCTTCGCCGG 3120  
 GGAGAACTGT GAGATTGACA TTGATGACTG CCTCTGCAGC CCCTGTGAGA ATGGAGGCAC 3180  
 30 CTGTATTGAT GAGGTCAATG GCTTTGTCTG CCTTTGCTC CCCAGCTATG GGGGCGAGCT 3240  
 TTGTGAGAAA GACACCGAGG GCTGTGACCG CGCTGGCAT AAGTTCCAGG GCCACTGTTA 3300  
 CGCTATTTTT GCCCACCGGA GGCATGGGA AGATGCGGAG AAGGACTGCC GCCCGCGCTC 3360  
 CGGCCACCTG ACCAGCGTCC ACTCACCGGA GGAACACAGC TTCAATTAATA GCTTTGGGCA 3420  
 TGAAAAACAG TGGATCGGCC TGAACGACAG GATCGTGGAG AGAGATTTC AGTGGACGGA 3480  
 35 CAACACCGGG CTGCAATTGG AGAACTGGCG AGAGAACCCG CCGGACAATT TCTTCGCGGG 3540  
 TGGCGAGGAC TGCTGTGTGA TGGTGGCGCA TGAAGCGGG CGCTGGAAAG ATGTCCCTCG 3600  
 CAACTACAAC CTACCCCTATG TCTGCAAGAA GGGCAGAGTG CTCTGTGGTC CCCCCTCCGG 3660  
 AGTGGAGAAT GCCTCACTCA TCGGTGCCCC CAAGGCCAAG AACATGTCC ATGCCACTGT 3720  
 AAGGTACCAG TGCAATGAAG GATTTGCCCA GCACCATGTG GTCACCATTC GATGCGGAG 3780  
 40 CAATGGCAAG TGGGACAGGC CCCAAATGT CTGCACCAA CCCAGAGCTT CACATCGGAT 3840  
 GCGGGGACAC CACCACCACC ACCAACACCA CCACACGAT CACCACCACA AATCCCGCAA 3900  
 GGAGCGCAGA AAACACAGA AACACCAAC GGAGGACTGG GAGAAGGAG AAGGGAATTT 3960  
 TTGCTGAAGA ACCAGAAAAA AGAAAGCACA ACACCTTTCC CATGCCCTCT CTGGAGCCTT 4020  
 CGCCTGGGAG GAGTATCGCC AGAGAGAAAC AAGAGAGTCC AGAAGTCCCT GAACCCCAAA 4080  
 45 CTGTTCTGCG AAAAAAATA TTCTTTGAA CAAAGGTCTT CTTTCTCTT TTTTACATAC 4140  
 ACAAGATCTT CTGTGCAGGT GGAGCCAGGT GTCTGAAAAG TTTCTTCTG TCTGGCTGAA 4200  
 CTCTGGGAGT GTGTCCGAGC TGAGGGAAGC ACAAGTAGCA AAGCTCATTG GTCTGGTCTC 4260  
 TTGTTTGCCA GGCTGATTGA AGCAGGCTT GATGAGGGTG CATGAGTGTA TGTGTGCAAT 4320  
 CACATGAGTA AATTGCTTTT CACACAGAAA ATTFCAGACT AGTCAATGTT GGCTGAATTC 4380  
 50 CTAAATCCAG GAAGAAGCCT GGACGTAGGG TCATTAGCTT TGGGAATAGA AGGCTACACA 4440  
 GAAGCACACT GTTTTGAAC TTGACAACAG CTCTCCCTTT ACCCTGGACT TCAGCCCAAG 4500  
 TTCCGTCTTT GGTCTGGTG GATAAACACA CAGTGTGGAG ATCCCACTGA CTGCATTTTA 4560  
 GGGATGTTTT TAGGACAACC TCCTCCATG CCTTCAGAGT TAGGAGTGAG AATGATCAAA 4620  
 GCAATATGTA GGTGATGGAG GGAGAGTGTA TTGCTAAACC TTCCAGGTCT AGTCCAGGCG 4680  
 55 TGAGATTGGG TGGTCTGCA TGTGTGATGA ATCTCTTCA CACAATAGA CGAGAGGATA 4740  
 TTAGGGCTA GATGAGCCCA GATTTCTTCC CCTCCATCT CTCAGGAGA CAAAGAACCT 4800  
 CCTTCTGGGA CCAAGGAGGT GCTGCCAAGT TTTCTAGCCC AGTGACATA CCCAGTCTT 4860  
 AAGCAGACAT TGGTAGTGCC CCTGCCCTGG GTCCCACTCC TGCCCCACCC CACCTTGTG 4920  
 CCTGGCATT GCTGGTGGT CTAGAAACAC TTAACACTTG AAGTAGTGAC ACCTACCTGC 4980  
 60 GGTCAATTTG TAGAGAGATG CTCAGTGTTA AACTGAAAC ACACAAACAC ACACACACAC 5040  
 ACATTTTTCT CTGTAGATT TTAATTTTTT AAGTGGGAAA GAACTCACCT TGCCTTCTC 5100  
 CCCCAAATGT GCAACTGTGA AAAGGTCTCT CCACACCAGG GGCAGGATC CAGTTCCTC 5160  
 ATCTCTGCA GGAAGATGCC ACAGCTTTTC CTCCATGTCT GTTACTCACT TTCAGCAGTC 5220  
 CGGGTAAAT CTGTGATCA GGGTTAAAAA AGCACCGTGG AGAATGGCCC TCTTCAGGAA 5280  
 65 AGAAAAATA GCAATGAAT GGTCCACCTA GGGGTTCAGT AAGAAAGAA ATGTGTTAAC 5340  
 TGAGCCTGAA TCCCTCTGCG GAAGTAATAA TGACCATGGA CACTAAGAA GTAGACACCA 5400  
 TGCTAAAGAC TTACATACAA TCTCCTTGAA TCTTCTCAAT AGCCCATGTA CTTAGAAACT 5460  
 GTTACTTTCC CATTTTACAC ACAGTGAAGC TGAGGCTCAG ATATAAAGGA AAGGTACTGG 5520  
 CTTGAAGTCA CAACACGAGC AGGAGTAAGG ATTTGGAATA AGGATTGGT CCGTGTCTT 5580  
 70 GGACCAATCT TACTCTGCG CTCTGCTTAC ACTTCTCTC CATCACCAA TCTTACTTCC 5640  
 AAATCCAGAA GTACAGACCA ACTCCCATCT TGGTCTGAC CCAATCCCTG CTCTGACTC 5700  
 TGGAGAGGAG ATTGAATAT AATTGCACCC TCATACACAT TTAGGAAATG GTTAAGAAGT 5760  
 GTAAACTGAA CCGTTATCCT TGTCTTCAAT CTCTCTCTC GTAGACATCT ATCTTATTAT 5820  
 GGTATTATT CAGAAAACCC AGGGATACAG GTTTGTCTTC TTACTTTGAT AACTTCTCT 5880  
 75 AGTTTAAAT AATAATAATA ACACATCTTT GGTCACTAT GTACACAAA AATTTTCTT 5940  
 TGTTTGCGGG GGGCTGGGGA TGCAAGTTT TTTGGGGGGT CTGGGTTTAT GCTCCCTGCC 6000  
 CTTGAGCCCC TCAGCGGTTT GCCCTGCCCC CACCTCGGCT CCAATGGTGG AGGGGCTCT 6060  
 GGTCTTTTCT AAAGTGGGCG GTTTGTCTTT TGATCTTTCC CTTTGGATG TGGCTGTGTG 6120  
 TCTGCGTGTG CCAATGTGCT GGCAACGATA TGAGTGTGTG TGGCTGTGAA CGGCTTGGG 6180  
 80 TCTGCTGCT TTTGCTGTGA GCTGCAGTGT TCTGAGGGTC TGTGGTATCT GACACTGTGG 6240  
 ACATTAATGT ACTTCTTGGA CATTTTAATA AATTTTTTAA CAGTTCAAA AAAAAAAA 6300  
 AAAAAAAA

Seq ID NO: 262 Protein sequence  
 Protein Accession #: NP\_004377.1

1 11 21 31 41 51  
 | | | | |  
 MGAPFVNALG LLMLQMLLFV AGEQGTQDIT DASERGLHMQ KLGSGSVQAA LAELVALPCL 60

5	FTLQPRPSAA RDAPRIKWK VRTASGQRQD LPILVAKDNV VRVAKSWQGR VSLPSYPRRR 120
	ANATLLGLPL RASDSGLYRC QVVRGIEDEQ DLVPLEVTGV VFHYRSARDR YALTFAEAQE 180
	ACRLSSAILA APRLHQAAFE DGFNDADAGW LSDRTVRYPI TQSRPGCYGD RSSLPGVRSY 240
	GRRNPOELVD VYCFARELGG EVFYVGPARR LTLAGARAQC RRQGAALASV GQLHLAWHEG 300
	LDQCDPFWLA DGSVRYPIQT PRRCGPGAP GVRTVYRFAN RTGFPSPAER FDAYCFRAHH 360
	PTSQHGDLLET PSSGDEGEIL SAEGPPVREL EPTLEEEVV TPDFQEPLVS SGEETLILE 420
	EKQESQQLTS PTPGDPMLAS WPTGEVWLST VAPSPSDMGA GTAASSHTEV APTDPMRRRR 480
	GRFKGLNGRY FQOQEPFGL QGGMEASAQF PTSEAAVNQM EPPLAMAVTE MLGSGQSRSP 540
10	WADLTNEVDM PGAGSAGGKS SPEPWLWPT MVPPSISGHS RAPVLELEKA EGPSARPATP 600
	DLFWSPLEAT VSAPSPAPWE AFPVATSPDL PMMAMLRGPK EWMPLHPTPI STEANRVEAH 660
	GEATATAPPS PAETATVYSL PLSLTPTGQG GEAMPTTPES PRADFRETGE TSPAQVNKAE 720
	HSSSSPWPSV NNRNVAGFVP TETATEPTGL RGIPGSESV FDTAESPTSG LQATVDEVQD 780
	PWPSVYSKGL DASSPSAPLG SPGVFLVPKV TPNLEPWWAT DEGPTVNPMD STVTAPAPSDA 840
15	SGIWEPSQV FEEAESTTSL PQVALDTSIV TPLTLEQGD KVGVPAMSTL GSSSSQPHPE 900
	PEDQVETQGT SGASVPPHQS SPLGKPAVPP GIPTAASVGE SASVSSGEPT VFWDPSSSTLL 960
	PVTLGIEDFE LEVLAGSPGV ESFWEVAVSG EEPALPGTGM NAGAEVHSD PCENNPLCHG 1020
	GTQNGMTMY GCSCDQGFAG ENCEIDIDDC LCSPCENGST CIDEVNGFVC LCLPSYGGSF 1080
	CEKDTGCDR GWHKFGQHCY RYFAHRRRAWE DAEKDCRRRS GHLSVHSPE EHSFINSFGH 1140
20	ENTWIGLNDR IVERDFQWTD NTGLQFENWR ENQPDNFFAG GEDCVVMVAH ESGRWNDVPC 1200
	NYNLPVCKK GTVLCGPPPA VENASLIGAR KAKNNVHATV RYQCNQFPAQ HHVVTICRS 1260
	NGKWRDPQIV CTKPRRSHRM RGHHHHHQHH HQHHHHSRK ERRKHKHPT EDWEKDEGNF 1320
	C

25 Seq ID NO: 263 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 7..2085

	1	11	21	31	41	51	
30	GCCGCGATGG	CCAGCACCAG	GAGTATCGAG	CTGGAGCACT	TTGAGGAACG	GGACAAAAGG	60
	CCCGGCGCGG	GGTGCOCGAG	AGGGGCCCCC	AGCTCCTCCG	GGGGCAGCAG	CAGCTCGGGC	120
	CCCAAGGGGA	ACGGGCTCAT	CCCCAGTCCG	GCGCACAGTG	CCCACTGCAG	CTTCTACCGC	180
	ACGCGGACCC	TGCAGGCCCT	CAGCTCGGAG	AAGAAGGCCA	AGAAGGCGCG	CTTCTACCGG	240
	AACGGGGACC	GCTACTTCAA	GGGCCTGGTG	TTTGCCATCT	CCAGCGACCG	CTTCCGGTCC	300
35	TTCCGATGCG	TCCTCATAGA	GCTCACCCGC	TCCCTGTCCG	ACAACGTGAA	CCTGCCCCAG	360
	GGTGTCCGCA	CTATCTACAC	CATCGACGCG	AGCCGGAAGG	TCACCAAGCT	GGACGAGCTG	420
	CTGGAAGGTG	AGAGTTAAGT	GTGTGCATCC	AATGAACCAT	TTCTGTAAGT	CGATTACACC	480
	AAAAATATTA	AAATTGGAAA	GTCTGTGAAC	ATCAAGGGTG	GGACATCCCG	AGCGCTGGCT	540
40	GCTGCCTCCT	CTGTGAAGAAG	TGAAGTAAAA	GAAAGTAAAG	ATTTCATCAA	ACCCAAGTTA	600
	GTGACTGTGA	TTGCAAGTGG	AGTGAAGCCT	AGAAAAGCCG	TGCGGATCCT	TCTGAATAAA	660
	AAGACTGCTC	ATTCTCTTGA	ACAAGTCTTA	ACAGATATCA	CCGAAGCCAT	TAAACNAGCC	720
	TCAGGAGTGG	TCAAGAGGCT	CTGCACCCCT	GATGGAAAGC	AGGTGAGAGT	TAGCTGTGTG	780
	CATCTGTCAG	ACTTTTTTGG	TGATGACGAT	GTTTTTATTG	CATGTGGACC	AGAAAAATT	840
45	CGTTATGCCC	AAGATGACTT	TGTCCTGGAT	CATAGTGAAT	GTGCTGTCTT	GAAGTCATCT	900
	TATTCCTCGT	CCTCAGCTGT	TAAGTATTCT	GGATCCAAAA	GCCCTGGGCC	CTCTCGACGC	960
	AGCCAGATT	TTGCTCATGG	CAGATCTTCT	TCCAATGTAA	ACGGTGACCC	TGAGCTTGAC	1020
	CGTTGCATAA	GTCTGTAAGG	TGTGAATGGA	AACAGATGCT	CTGAATCATC	AATCTTCTCT	1080
	GAGAAATACA	AAATTGGAAA	GGTCATTGGT	GATGGCAATT	TTGAGTAGT	CAAAGAGTGT	1140
50	ATAGACAGGT	CCACTGGAAA	GGAGTTTGCC	CTAAAGATTA	TAGACAAAGC	CAAATGTTGT	1200
	GGAAAGGAAC	ACCTGATTGA	GAATGAAGTG	TCAATACTGC	GCCGAGTGAA	ACATCCCAAT	1260
	ATCATTATGC	TGCTCGAGGA	GATGGAAACA	GCAACTGAGC	TCTTCTGGGT	GATGGAAATT	1320
	GTCAAAGGTG	GAGATCTCTT	TGATGCAATT	ACTTGTGCGA	CCAAAGTACAC	TGAGAGAGAT	1380
	GGCAGTGGCA	TGGTGTACAA	CTTAGCCAAT	GCCCTCAGGT	ATCTCCATGG	CCTCAGCATC	1440
55	GTGCACAGAG	ACATCAAACC	AGAGAATCTC	TTGGTGTGTG	AATATCCTGA	TGGAACCAAG	1500
	TCTTTGAAC	TGGGAGACTT	TGGGCTTGCG	ACTGTGGTAG	AAGGCCCTTT	ATACACAGTC	1560
	TGTGGCACAC	CCACTATGTG	GGCTCCARAA	ATCAITGCTG	AAACTGGGTA	TGGCCTGAAG	1620
	GTGGACATTT	GGGAGCTGGG	TGTGATCACA	TACATACTTC	TCTGTGGATT	CCCAACATT	1680
	CGAAGTGAGA	ACAATCTCCA	GGAAGATCTC	TTCCAGCCAG	TCTTGGCTGG	GAAGCTGGAG	1740
60	TTTCCGGCCC	CCTACTGGGA	TAACATCACG	GACTCTGCCA	AGGAATTAAT	CAGTCAAATG	1800
	CTTCAGGTAA	ATGTTGAAGC	TCGGTGTACC	GCGGACAAA	TCCTGAGTCA	CCCTTGGGTG	1860
	TCAGATGATG	CCTCCACGGA	GAATAACATG	CAAGCTGAGG	TGACAGGTAA	ACTAAAACAG	1920
	CACCTTAATA	ATGCGCTCCC	CAACAGAAAC	AGCACTACCA	CCGGGGTCTC	CGTCATCATG	1980
	GTGAGTGGAA	GGCGGCAGGT	CTGGCCTGAC	TGCGGAGCCG	GCCTTGAAGT	TTTTGAATTA	2040
65	GGTAGCCGGG	AGCTGCCCTC	ACATGGAAGT	TGGTGCCTTC	CGTAGTCCTA	TTTCATATGA	2100
	AGATTGGCTT	GGCATGTGGA	GGGCACTCAT	TCGGCAACTC	CCAGGCTTTG	GGCACTGTGT	2160
	GGAGGGGCTT	GTGTAGGGAC	CAGCAGGCCT	GGTGTGAGGG	GTCCAGGCGT	CAAGGAGCTC	2220
	CTGGCTGGGC	CCTCTGGGCA	GCTGCTTCCA	CTCTTGTCTC	TGCCCTTCTA	TCTAGAGAGA	2280
	CTCCCAAGCC	CTGGAGGGGT	GTGTTGTGTT	AGGAATTAA	TCCCTGCCTA	CCCAAGGCC	2340
70	TCAGAAATAG	ATTATTAGAG	ATGTGAATTA	TTCTTTGAGA	CTTGGGATAA	GAAACAGCCA	2400
	AAGCTAAACA	TATTTCAAGT	TTAAAAATC	AGTGTGTTAT	AAAACACAGT	TTGGGGCTTT	2460
	TAAAGGTACA	TAAATCAAGGA	AAAAAATATA	TATTCATTTT	TCAGGTTTGG	TAACATTTTA	2520
	TGAGATGTCA	GTGACAAAGA	TGGCCTTAT	TTTTTCAGCC	TTTTCTTCTT	CCAAAAATGT	2580
	TCCTTAAGGAG	ACTCTCTTAA	ATACATAAAC	ACAACAAATT	AAATGAAAAA	GTGACATGAG	2640
75	AGTAAATGAA	TCAAAAGGAA	AAAACATTGA	ACCAGAGGTG	AGGGCAGCAC	ACCCGACGCA	2700
	GCTGTCCAGG	CCTGAGCCAA	TGCAACCCCTG	GGCGGGAAGG	CCAGCTCACC	GTGAGCAGGT	2760
	AGAAAGCCAG	CAGCCACCCA	GGCAGGGACC	TGTTTCTCC	CCACACACTC	CCAGGAGCAG	2820
	GGAAACAGGG	TGGAGTGGCC	TTTCCACAG	CTGGAGTTGG	CTGCAGCAGC	TTTCCGATCA	2880
	GACCTGCCAA	GTCTGAGTTT	CACATCTGGG	CCCCCGGTGA	CCCACTGAG	CCCACTGAG	2940
80	TCCTGACAGC	TAAGGATGGG	CCACCTCCAC	AGCTCCGTCA	CTGCTACTTG	GGACAGGCCT	3000
	CTCATCTCT	GGGAAGGTCC	TCCTTGTTC	CTACCCAACT	AGAAGGGAAA	CAGTGGCATA	3060
	TTCTCATGGT	ACATGGTTGT	CTGAAAGCCT	TACCTAGGAA	GAGCGAGGGT	CTAGATAGAA	3120
	GCTATAAGGA	AGCCACACAC	ATAACCCACA	TCCCCACACC	CCCAACATCC	CCCACTCTCC	3180
	CCACACCCCC	CACACCCCCC	ACATCCCCAC	CATAATTACC	CCCACCTCCA	AATATCTCAT	

Seq ID NO: 264 Protein sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
5							
	MASTRSIELE	HFEERDKRPR	PGSRRGAPSS	SGSSSSSGPK	GNGLIPSPAH	SAHCSFYRTR	60
	TLQALSSEKK	AKKARFYRNG	DRYFKGLVFA	ISSDRFRSFD	ALLIELTRSL	SDNVNLPQGV	120
	RTIYIDGSR	KVTSLEDELLE	GESYVCASNE	PFRKVDYTKN	INPNWSVNIK	GGTSRALAAA	180
	SSVKSEVKES	KDFIKPKLVT	VIRSGVKPRK	AVRILLNKKT	AHSFEQVLTD	ITEAIKXASG	240
10	VVKRLCTLDG	KQVRVTCVHL	PDFFGDDDFV	IACGPEKFRY	AQDDFVLDHS	ECRVLKSSYS	300
	RSSAVKYSGS	KSPGFSRRSQ	ISAHGRSSSN	VNGGPELDR	ISPEGVNNGR	CSESSTLLEK	360
	YKIGKVIGDG	NFAVVKECID	RSTGKEFALK	IIDKAKCGK	EHLIENEVSI	LRRVKHPNII	420
	MLVEEMETAT	ELFLVMELVK	GGDLFDAITS	STKYTERDGS	AMVYNLANAL	RYLHGLSIVH	480
	RDIKPENLLV	CEYPDGTKSL	KLGDFGLATV	VEGPLYTVCG	TPTYVAPXII	AETGYCLKVD	540
15	IWAAGVITYI	LICGPPPPFRS	ENNLQEDLFD	QILAGKLEFP	APYWDNITDS	AKELISQMLQ	600
	VNVEARCTAG	QLSHPPWVSD	DASQENNMQA	EVTGKLKQHF	NNALPKQNST	TTGVSVIMVS	660
	GRRQVWPCDG	AGLEVFEELGS	RELPSHGSWC	LP			

Seq ID NO: 265 DNA sequence  
Nucleic Acid Accession #: AB020684.1  
Coding sequence: 1..1744

	1	11	21	31	41	51	
25							
	CCCCCTTGTC	ATTAATACAT	TAAAAAGATT	CAATCTTTAC	CCTGAGGTAA	TTTGGCCAG	60
	TTGGTACCGG	ATTTATACCA	AAATAATGGA	CTTGATTGGT	AITCAAACCA	AGATATGTTG	120
	GACCGTTACC	AGAGGAGAA	GACTCAGTCC	TATTGAAAGC	TGTGAAGGAT	TGGGAGATCC	180
	TGCTTGCTTT	TATGTTGCTG	TAATTTTTAT	TTTAAATGGA	CTAATGATGG	CATTATTCTT	240
	CATATATGGC	ACATATTTAA	GTGGCAGCCG	ATTAGGAGGC	CTGGTTACAG	TGTTGTGCTT	300
30	CTTTTTCAT	CATGGAGAGT	GTACCGGTGT	AATGTGGACA	CCACCTCTCC	GTGAAAGCTT	360
	CTCATATCCA	TTTCTTGTTT	TTCCAGATGT	GCTAGTGACT	CATATTCTCA	GGGCTACAAA	420
	ACTTTATAGA	GGAGCTGTGA	TGCACTCTCG	CATTTCCTAT	GTATTTTCTA	TGCTTCTCTG	480
	GCAGTTTGCT	CAGTTTGATC	TTCTTACTCA	GATTGCATCA	TTATTTGCTG	TATATGTTGT	540
	CGGGTACATT	GATATATGTA	AATTACGGAA	GATCATTTAT	ATACACATGA	TTTCTCTTGC	600
35	ACTTTGTTTT	GTTTTGATGT	TTGGGAACTC	AATGTTATTA	ACTTCTTATT	ATGCTTCTTC	660
	TTTGTAATTT	ATTGGGGTGA	TTCTGGCAAT	GAAACACAT	TTCTGAAAA	TAAATGTATC	720
	TGAACCTAGT	TTATGGGTTA	TTCAAGGATG	TTTTTGTTTA	TTTGGAACTG	TCATACCTAA	780
	ATACCTTGAC	TCATAAAATT	TTGGTATTGC	AGATGACGCT	CATATTGGCA	ACTTACTAAC	840
	ATCAAAATTC	TTTAGTTATA	AGGATTTTGA	TACTTTATTG	TATACCTGTG	CAGCGAGATT	900
40	TGACTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	ACATTATTGC	TTCCAGTTGT	960
	TCTTGTAGTG	TTGTTTGCTA	TTGTTAGAAA	GATTATTAGT	GATATGTGGG	GTGCTTAGC	1020
	TAAACACACG	ACACATGTAA	GAAAAACACCA	GTTTGATCAT	GGAGAGCTGG	TTTACCATGC	1080
	ATTGCACTTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	ATGAGACTAA	AACCTTCTCT	1140
	GACACCACAC	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	AGACAGCTAT	TTGGATGGCT	1200
45	CTTTTGCAAA	GTACATCTCG	GTGCTATTGT	GTTTGCTATA	TTAGCAGCAA	TGTCAATACA	1260
	AGGTTGACGA	AACTGTCAAA	CCCAAGTGGAA	TATGTAGGG	GAGTTCAGCA	ATTTGCCCAA	1320
	AGAAGAACTT	ATAGAATGGA	TCAAATATAG	TACTAAACCA	GATGCACTGT	TTGGGGGTGC	1380
	CATGCCCACT	ATGGCAAGTG	TTAAGCTCTC	TGCACCTGG	CCCATTTGTA	ATCATCCACA	1440
50	TTATGAAGAC	GCAGGCTTGA	GAGCCAGAAC	AAAAATAGTA	TACTCAATGT	ATAGTCGGAA	1500
	AGCAGCCGAA	GAAGTGAAGC	GAGAACTGAT	AAAGTTAARA	GTGAACATAT	ACATTCTAGA	1560
	AGAGTCACTG	TGTGTAAGAA	GATCEAAGCC	TGGTTGCAGT	ATGCCCTGAA	TTTGGGATGT	1620
	AGAAGATCTC	GCCAAATGCTG	GGAAACTCCT	CTTATGTATC	CTCTTGTTGA	AGGATTCCAA	1680
	ACCTCACTTC	ACCACGTGAT	TCCAGAACAG	TGTTTACAAA	GTCCTAGAAG	TGTAAAGA	1740
55	ATGACTGCTA	CATGACCTGC	TGCCTACGGA	GAACATACAT	TGTAATGTTT	TTAATGTTTT	1800
	GCTAAGTCAT	GTGTGTGTCA	TATCCCAAAA	ACTTTTATAG	GTAAGTGTTT	TCAATAGAAA	1860
	AACTGTTTAT	TTGTTCAATT	TGAATGTCTT	TCTAATTATA	AAAATGACTT	ACACCTTTAT	1920
	CAATTGGTTA	CTATTTCAAT	GCACCCCTTA	AAATTGTCTA	TGCAAAATGAG	TATATGCTTG	1980
	TACTTCTGCT	TAAATTTTGT	GCTAAAGTGA	GCAAGCTAC	CTGTATAAAG	AAAACACAGT	2040
60	GGTTTGTGAC	AAGGATGACA	TGAAAAATACA	GGACAATTCT	GACAAATGTAG	GGGCTGATTT	2100
	TATAGTGTA	GAACATTTAA	TGCCCTTTCG	TTCTTTTTC	TGCCCTTTCG	TCTTGTCTTT	2160
	TGGACATTTT	AGTGATTGTA	AGTTCTTCGG	TCATGTCAGC	CCCTGTCACT	AACCTGAGTT	2220
	ACAGTAGATG	GGGCAGACAT	GGAGTGTTCG	CTATATAAAA	CTATCTGTTT	GTTTTACTTC	2280
	CTTGTGCGCT	TTTTGTCTCT	TGTTCTCTTG	TAAATGAAGC	TTTTCTCTGC	CATTATTAAT	2340
65	CCAAACTCTT	GGACCTTGTG	GTTAGGAAAT	TCCCTTAACT	TCCAGCCATA	TGGCATTATC	2400
	GTGTCTCTTT	CTCTCTCTCT	CTTGCTCTCT	CTCTCTCTCT	CTTCCCATTA	TTTTCTGTCA	2460
	AATAAGTACT	GTTTACTCAT	TTAGTTGCTT	ATCAAGTACT	TATCTTGGT	TTTAAAAAAA	2520
	ATTAATGGTA	ACTGTATTTT	TCTCATTTTT	AGCATTATTC	AAATGTTTAT	ATTTTAAATC	2580
	CTTTAAACCA	CTTTAAAGTT	TTTTCATGTT	TAATTATAGT	TTTAAAGAAA	ACTATTTTGA	2640
70	ACAACCCCAA	ATATAGTGCA	TCTAGAAACT	AATGTATATT	TGATTAGACA	TCATTATATG	2700
	TGGAACAGTA	GACTGTAGTA	CATGGTAATT	TTTCTTTTAC	TATTAAGATA	CAATAAAACA	2760
	TGACTAATTT	TGCTGTCAAA	AATGTAAAGA	ATAATGATAA	ATGGAGTTTT	TTATATTTTA	2820
	CTTTTAAGAT	TGCCGTGCTT	TAATAAGACA	AAGCCTTAAG	CCTTATGTGA	TAATTTTGGT	2880
	TCTAAAAACC	ATCATTTTCA	TATAAGGAAT	AAGTATATTT	CGTCTCTCTC	TTTAGTTTTT	2940
75	TTCTTCTTAT	TTATTTTAT	TTTGAATAAT	TTCTACACCT	TCTTTGAATT	CCTTGTATGA	3000
	ATTTTGTGTT	CTTGAAGTTT	AATTTGTGTG	AAATGAGATT	CTTCAAAACG	ATGAAACCTC	3060
	ATAGCTACTG	GAAAGAGTTT	TAGGGTTTTA	AATCTAAGC	AAAGOGTGAC	TATGGCTGAC	3120
	AGACTACACA	TTTAATATA	CAGCTTCTCT	TTCTTAAACA	CAGGCAGATT	AACTCATG	3180
	TGGATTGTCT	TCAGACCTT	AGTCTCAGG	CAAGGTTTCT	GGTGCCCACT	CCTGGAAGCC	3240
	GCTGTTCCTT	TTCTACCTTC	TTACCAAGGC	CCAAGGGCAG	GCTTGGTCCC	GGGGAAGCAG	3300
80	CAGCTTGCTG	ACATAAGTCA	GCTGCAAGG	CTCAGGAGTG	TGCCCTCAGA	GAAGCACCGC	3360
	CCCCAGTCT	TGTGCCAGCG	CCTAGAGCCG	CAGCTCCAG	GGATGCTCTT	TCCTGTGAGG	3420
	CAGCCCAAGG	GAGGAGCTCT	GGCAGCGTTC	TTCAGATTG	TGGCCACTGT	TTCTCATTTG	3480
	CTGGTTGACT	TTTTTATTTT	CITAGGCTTT	TGCTAGTTTT	AGAAATAGG	GAAGCACCGC	3540
	TGATTTTGTG	GATTAAGAGC	AACATTTGAG	CGATGATGCA	CAACAGTCCA	GGAAATAGG	3600

5 CGGTGGACAC TTGAGGCTGA GSATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC 3660  
 TCGTTATCTG TGATTGTGTC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA 3720  
 ATTTTAAAAA ATTATACITT TACATTTATT TTATATTTTT CTCACCCCCA GTAATTTCCCT 3780  
 TCCAAGAGAG TTACATGTGA ATAAGTAGAA ATTCTGTATA GGAAGAAAGC ATTAAGAAATA 3840  
 CTATTATAAC TGCTTCATTT GCTGGGAACC ATTAAAGTA ATATAAATTA GCTTTTTCCA 3900  
 GAAGGATCCT TTTGTAGCAG TGTTTATGAA TGTAAACCCC AGCAAAATAT GGCTATATAT 3960  
 TAGGGGAGCC AGTTGGAGC AGAGGCTGA AGGTCCTGTC TATGCAGCCG TGGCCACAGC 4020  
 TCGCAGCCCA AGCACTGTGG AGCATCCACA CCTTGATGGS CAATGCAGAT TGGTAGCAGG 4080  
 TTCCATAGGC GTACAAAACA GTATTAAAGC TCAGTGTTTT GCATATTGTT AGCATTATCA 4140  
 10 AATATTTTTG CTTTGTATG AGGAAAGTAA GGATGGGCAA AGAAGCGATC AAAATAGCTA 4200  
 TTGCTACAAC ATTTTCGAAA ACAAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT 4260  
 AAAATGCTT GGCAGAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAA 4320  
 GAAAGTATG ATCAGGAATA AAGTGATATT GCATAGGAGT ATTGTATTTT TATGAATTTT 4380  
 15 ATGCCAGTTG TTTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 266 Protein sequence  
 Protein Accession #: BAA74900.1

20 1 11 21 31 41 51  
 | | | | | |  
 PLVINTLKRP NLYPEVILAS WYRIYTKIMD LIGIQTKICW TVTRGEGLSP IESCEGLGDP 60  
 ACFFVAVIFI LNLGMLALFF IYGYLSGSR LGGLVTVLCP FENHGECTRV MWTPLRESF 120  
 SYFFLVLMQL LVTHILRATK LYRGLIALC ISNVFFMLPW QPAQFVLLTQ IASLFAVYVV 180  
 25 GYIDICKLRK IYIYHMSLA LCFVLMFGNS MLLTSYYASS LVIWIGILAM KPHFLKINVS 240  
 ELSLWVIQGC FWFPGTVILK YLTSKIFGIA DDAHIGNLLT SKFFSYKDFD TLLYTCAAEF 300  
 DFMKETPLR YLTKLLFPV LVVFVAIVRK IISDMWGLA KQQTHVRKHQ PDHGELVYHA 360  
 LQLLAYTALG ILMRLKFLP TPHCMVMASL ICSRLFGWL FCKVHPGAIV FAILAAMSIQ 420  
 GSAANLQTNW IVGEFNLQP EELIEWIKYS TKPDAVFAGA MPTMASVKLS ALRPIVNHPI 480  
 30 YEDAGLRART KIVYSMSYRK AAEVVKRELI KLVNYIYLE ESWCVRRSKP GCSMP EIWDV 540  
 EDPANAGKTP LCNLLVKDSK PHFTTVFQNS VYKLEVUVKE

Seq ID NO: 267 DNA sequence  
 Nucleic Acid Accession #: U26744.1  
 Coding sequence: 59..1600

35 1 11 21 31 41 51  
 | | | | | |  
 CTTCAAAGAA TATAGATGGT TTTGAAAAGT TCATGCTGTC CCTTCATTGA ATTTTAGAAT 60  
 GATTGAGAT AGTGGGAAAA GAGGAAATAC CATGGCAGAA AGAAGACAGC TGTTCGAGA 120  
 40 GATGAGGGCT CAGATCTGG ATCGCATCCG ACTCTCCACC TACAGAACAG CATGCAAGCT 180  
 TAGGTTTGT CAGAAGAAAT GCAATTTGCA CCTGGTGGAC ATATGGAATG TCATAGAAGC 240  
 ATTGGCGGAA AATGCTCTGA ACAACCTGGA CCAAAACACT GAACCTCAAG TGTCCCGCTT 300  
 AGAGGCTGTG CTCTCCACTA TTTTATACCA GCTCAACAAA CGGATGCCAA CCACTCACCA 360  
 AATCCATGTG GAGCAGTCCA TCAGCCTCCT CCTTAACTTC CTGCTTCGAC CGTTTGATCC 420  
 45 GGAAGGCCAT GGTAAAAATT CAGTATTGTC TGTCAAAATG GCTTTAGCCA CATTTGTGTT 480  
 AGGGAAGATC ATGACAAAT TAAGATATAT TTTCTCAATG ATTTCTGACT CCACTGGGGT 540  
 GATGGTTTAT GGACGATATG ACCAATTCCT TCGGGAAGTT CTCAAACACT CCAACGGAAGT 600  
 TTTGGAGCTG CTCTCATTG GTTACACAGA ACAGTCAGCC AGATCCTGTT TCTCCCAACA 660  
 50 GAAAAAAGTG ACGTAAATG GTTCTTGGGA CAGCCTATG TCAGATCCTC CCGCCGAGTG 720  
 TCTGGCTCGT TGGCTCTTC TGCATCGACT AGCAAAATGT GAAAATGTCT TCCATCCGTT 780  
 TGAGTGTTC TACTGCCACA GTGAGAGTAT GATGGGATTT CGCTACCGAT GCCAACAGTG 840  
 TCACAATTAC CAGCTCTGTC AGGACTGCTT CTGGAGGGGA CATGCCGGTG GTTCTCATAG 900  
 CAACCCAGCA CAATGAAAG AGTACAGTTC ATGGAATCA CCTGCTAAGA AGCTGACTAA 960  
 55 TGCATTAACT AAGTCCCTGA GCTGTGCTTC CAGCCGTGAA CCTTTCACCC CCATGTTCCC 1020  
 AGATCAGCTC GAGAAGCCAC TCACTTGGC TCACATCGTT GATACCTGGC CTCCAGAGCC 1080  
 TGTAAACGAG ATGAACGACA CCGTGTCTC CCACTCTGTT CCCTCCTCAG GAAGTCCCTT 1140  
 TATTACCAGT AGCATGCTTG AGAGTTCAAA CCGGCTTGAT GAAGAACACA GGCTAATTGC 1200  
 CAGGTATGCG GCAAGGCTGG CAGCAGAGTC CTCTTGTCT CAGCCACCTC AGCAGAGAAG 1260  
 60 TGCTCTGAC ATCTCTTCA CCATCGATGC GAATAAGCAG CAAAGGCAGC TGATTGCTGA 1320  
 GCTAGAAAC AAGAACAGAG AAATCTTACA GGAGATCCAG AGACTTCGCG TAGAGCATGA 1380  
 ACAAGCTTCT CAGCCACGCG CAGAGAAGGC ACAGCAAAC CCCACCCTGC TGGCAGAACT 1440  
 CCGGCTCCTC AGACAGCGCA AAGATGAGCT GGAACAGAGA ATGTCTGTCT TCCAGGAGAG 1500  
 COGGAGAGAG CTAATGCTCC AGTTGGAGGG TCTCATGAAG CTACTAAAGG AAGAAGAACT 1560  
 65 GAAGCAGGGA TTAAGTTATG TCCTCTACTG CAGGCTTAA CTAAACAGTG AGGGGCTGCG 1620  
 GACCTGCGG TTTTCTCAT GCTTTTGCTC TAATGTATG TCATGCTTCA GTTTGGAAG 1680  
 AGAAAAAGT CATACTARTT TGCTTCTTTT TCAATGTAGT GCTTGAATG AGATATATAA 1740  
 ATTTAGCATT TTTTATAACT ATCACTACTA TCCACATCAA AAGAAGAACT ATGACATCTT 1800  
 70 TTAGAAAAGG GAACGAATG TCATTATTG GAAACATTTT AGATCCCCAG AGGTATAAGT 1860  
 TTCAAACAGC TCTTAGCTTT TCAAGTTGTT GATCAGACCC TTCTCTTAAC AGAGAGATAC 1920  
 CACAGTCACT ATGATACCC TGAGGTTTAT GTCATCCCAA AACCACAGC ACTCAGAGC 1980  
 TAACCTCTAC ACCCACTCAC ACTGTGAGTA TTCAGTTCGG TTTCAATTTA CTGAAAACCT 2040  
 GTGAAACCTC TTTTATAAAA AATCAGGCAA TTAATCCCT TTTTCATACA CAATTATTGA 2100  
 CCCTGTGTT CCAATGGCTCA CCAAAATGTG CTCAATTTTG TGAGAGAAAG ACTGTACTCC 2160  
 75 ATAACTGACT ATTCAGTCC CATCTTTTGT GCTCTCCCC AAGCAGAAAT CCTTACTGTT 2220  
 GGTGACACT AATCTCTTTT TAAAAAGTAA CTCTCAGCTT TTTCTTAGC ACCAGAGCCT 2280  
 TTCGGCTCCG GGAGACGAGA GGTTCATTAC ATACTTTTTT TTTTCTTGG AAATAGGGGC 2340  
 ATTGTGACTT TATAGCTTAA ACTGGAGCTG TCTGAACCTG TGGTCAGGCT CAAGAGCCAG 2400  
 CAGGGGGAGC AGCAAACTC

Seq ID NO: 268 Protein sequence  
 Protein Accession #: AAC50426.1

1 11 21 31 41 51  
 | | | | | |

MIEDSGKRGN TMAERQFLFA EMRAQDLDR IRLSTYRTACK LRFVQKKCNL HLVDIWNVIE 60  
 ALRENALNNL DPNTLENVSR LEAVLSTIFY QLNKRMPTTH QIHVEQSISL LNFLLAALFD 120  
 PEGHGKISVF AVKMALATLC GGKIMDKLRY IFSMISDSSG VMVGRYDQF LREVLKLPTE 180  
 VLEGPSFGYT EQSARSCFSQ QKQVTLNGFL DTLMSDPPPQ CLVWLPLLHR LANVENVFHP 240  
 VECSYCHSES MMGFYRCQQ CHNYQLCQDC FWRGHAGGSH SNQHQKEYT SWKSPAKKLT 300  
 NALSKSLSCA SSREPLHPMF PDQPEKPLNL AHIVDTWPPR PVTSMNDTLF SHSVPSGSP 360  
 FITRSMLESS NRDDEEHLRI ARYAARLAAE SSSSQPPQR SAPDISFTID ANKQQRQLIA 420  
 ELENKNREIL QEIQRLRLEH EQASOPTPEK AQQNPTLLAE LRLLRQRKDE LEQRMSALQE 480  
 SRRELMVQLE GLMKLLKEEE LKQGVSVVPY CRS

Seq ID NO: 269 DNA sequence  
 Nucleic Acid Accession #: NM\_001276.1  
 Coding sequence: 127..1278

1 11 21 31 41 51  
 AGTGGAGTGG GACAGGTATA TAAAGGAAGT ACAGGGCCTG GGAAGAGGC CTGTCTAGG 60  
 TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCCTGCCCTG CTCTGCTGCA 120  
 GCCAGAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGTG GTCACAGTGC 180  
 TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240  
 GGGAGCTGCT TCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300  
 GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGG ATGATGTGAC GCTCTACGGC 360  
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTG TGTGGGAGGA 420  
 TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480  
 TTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540  
 TGGCTCTACC CTGGACGGAG AGACAAAACAG CATTTTACCA CCTAATCAA GGAATGAAG 600  
 GCGCAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG 660  
 TCTGCGGGGA AGGTCAACAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG 720  
 GATTTCATTA GCATCATGAC CTACGATTTT CATGAGGAGC GGCCTGGGAC CACAGGCCAT 780  
 CACAGTCCCC TGTTCCGAGG TCAGGAGGAT GCAAGTCTCT ACAGATTCAG CAACACTGAC 840  
 TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC 900  
 CCCACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTGG AGCCCCAATC 960  
 TCAGGACCGG GAATTCAGG CCGGTTCAAC AAGGAGGCGG GGACCCCTGC CTACTATGAG 1020  
 ATCTGTGACT TCCTCCGCGG AGCCACAGTC CATAGAACC TCAGCCAGCA GGTCCCCTAT 1080  
 GCCACCAAGG GCAACCAAGT GGTAGGATAC GACGACCAGG AAGCGCTCAA AAGCAAGGTG 1140  
 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200  
 TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260  
 GCACTCGTGA CAACGTAGCC CTCTGTCTG CACACAGCAC GGGGGCCAAAG GATGCCCCGT 1320  
 CCCCCTCTGG CTCACGCTGG CCGGGAGCCT GATCACTGCG CCTGCTGAGT CCCAGGCTGA 1380  
 GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTGAGCTCA 1440  
 GCCTCGTGG GCAGAGAGGT AGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500  
 GACTCGGGAT TAGTACACAC TTGTGTATGA TTAATGGAAA TGTTTACAGA TCCCAAGGCC 1560  
 TGGCAAGGTC ATTTCTTCAA CTCCTGCCCC CTTAGCCCTC CTTATCAAAG GACACCAATT 1620  
 TGGCAAGCTC TATCACAAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680  
 TACCCCTGCG AAGCCAGCT TGAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740  
 ACTTCCCTCT CTAATTTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAACT AGTGTGTTGG 1800  
 CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCGCCCATC 1860  
 TCTTCTGGGT TCCTCTCTCT GAGCCTTGGG ACCCGTGAGC TTGCAGAGAT GAAGGCCGCG 1920  
 ATGTT

Seq ID NO: 270 Protein sequence  
 Protein Accession #: NP\_001267.1

1 11 21 31 41 51  
 MGVKASQTGF VVLVLQCCS AYKLVCIYTS WSQYREGDGS CFPDALDRFL CTHIIYSPAN 60  
 ISNDHIDTWE WNDVLYGML NTLKNRNPNI KTLSSVGGWN FGSQRFKRIA SNTQSRRTPI 120  
 KSVPPFLRTH GTDGLDLAWL YPGRDRKQHF TTLIKEMKAE FIKERQPGKK QLLLSAALSA 180  
 GKVITIDSYD IAKISQHLDF ISIMTYDFHG AWRGTTGHHH PLFRGQEDAS PDRFSNTDYA 240  
 VGYMLRLGAP ASKLVMGIPT FGRSPTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC 300  
 DFLRGATVHR TLGQQVPYAT KGNQWVGYYD QESVSKSVQY LKDRQLAGAM VWALDLDDFQ 360  
 GSFCQDLRF PLTNAIKDAL AAT

Seq ID NO: 271 DNA sequence  
 Nucleic Acid Accession #: NM\_006474.1  
 Coding sequence: 181..669

1 11 21 31 41 51  
 GCTGCCTAGG GTCTGGAAG CTCGGGCACC CTCCTCTCC GGGGCTCCTG CTCACCCCC 60  
 TCCGGCCCCC CCACCGTCCG GCTCCTCCAG GCTGGGCTG TGGCCGCGST GCTTTTAAT 120  
 TTCCCCAGC TCAGAACTCT GCTGCTCGGC CCCAGGAGA GCAACAACTC AACGGGAACG 180  
 ATGTGGAAGG TGTGAGCTCT GCTCTCGTT TTGGGAAGCG CGTGGCTCTG GGTCTCGCA 240  
 GAAGGAGCCA GCACAGGCCA GCCAAGAT GACACTGAGA CTACAGTTT GGAAGGCGGC 300  
 GTTGCATGCG CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAAGGA AGACCGCTAT 360  
 AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTCGCATC 420  
 GAGGATCTGC CAATCTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480  
 GCCTCAAAGC TGGCCACCAG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540  
 GTTGAGAAAG ATGTTTGTG AACAGTACC CTGTTTGAA TCATAGTTG GGTCTTACTA 600  
 GCCATCGGTT TCATTGGTGG AATCATGCTT GTGTTATGCG GAAAAATGTC GGGAGGTAC 660  
 TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720  
 TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCTG GGAACATTG 780  
 GGGGCCCATH CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840

TCACCAGATT TGGTTCTTAA ACTTT

Seq ID NO: 272 Protein sequence  
Protein Accession #: NP\_006465.1

5  
1 11 21 31 41 51  
| | | | |  
MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDY 60  
10 KSLGLTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVDGDTQTT 120  
VEKDLSTVT LVGIIVGVLL AIGFIGGIIV VVMRKMSGRY SP

Seq ID NO: 273 DNA sequence  
Nucleic Acid Accession #: CAT cluster

15  
1 11 21 31 41 51  
| | | | |  
GCGGCCGCCA GCTTGCAAAG CCGAAGTCTG GCCGCGCTCT TCGACTOGCT GCGCCACGTC 60  
CCCGGGGGTG CCGAGCCGGC GGGGGGTGAG GTGGCTGCGC CGCGCGCCGG GCTAGGAGGT 120  
20 GCGGCCACTG GGGCGCGGG AGGGGACGTG GCAGGCCCGG CGGGGGCCAC GCGGATCCCA 180  
GGGGCCAGGA AGGTCCCGCT GCGGGCACGC AATCTGCCTC CGTCCTTCTT CACCGAGCCG 240  
TCCCGGGCAG CGGCGCGCGG GTGTGGCCCG TCGGGGCGGG ACCTGAGCTT GGGCGACCTG 300  
GAGAAGGGCG CGGAGGCCGT GAGTTCTTT GAGCTGCTGG GCGCCGACTA CGGCGCCGGC 360  
ACGGAGGCGG CAGTCTTGTG TGCCGCGGAG CCTCTCGACG TGTTCGCCCG CGGAGCCTCC 420  
GTACTGCGGG GACCCCGGGA GCTGGAGCCC GGCCTCTTTG AGCCGCGGCC GGCAGTGGTG 480  
25 GGAAACCTAC TGTATCCCGA GCCCTGGAGC GTCCCGGGCT GCTCCCGGAC CAAAAGAGC 540  
CCCTGACTG CCCTCCCGGG CGGGTTGACC TTGAACGAGC CCTTGAGCCC CCTGTACCCC 600  
GCGCTGCGA ATTTCTCCCG GCGGGGAGGA CGGGCGGGC CATTGGCTT CTTTGGCCCC 660  
CTTCTTCCA GACTGCGCTT TGC

Seq ID NO: 274 DNA sequence  
Nucleic Acid Accession #: Eos sequence

35  
1 11 21 31 41 51  
| | | | |  
CAAAGAGGCC GGGCTCCAGC TCCGGGGGTC CCGCAGTAC GGAGGCTCCG GCGGGGAACA 60  
CGTCGAGAGG CTCGGCGGCA AGCAAGACTG CCGCTCCGT GCGGCGCCGG TAGTCGGGCC 120  
CCAGCAGCTC AAAGAACTCC ACGGCTCCG CCGCTTCTC CAGGTGCGCC AAGCTCAGT 180  
CGGGCCCGA CGGGCCACAC CCGCGCGCGC CTGCGCGGGA CGGCTCCGTG AAGAAGGAGC 240  
40 GAGGCAGATT GGTGCCCCG AGCGGACCT TCTGGCCCC TGGGATCGCC GTGGCCCCCG 300  
CGGGCCCTGC CAGCTCCCTT CCGCGCCCC CAGTGCCCC ACCTCCTAGC CGGCGCGCCG 360  
CGCAGCCAC CTCACCCCC GCGGCTCGG CACCCCGGG GACGTGGCGC AGCGAGTCGA 420  
AGAGCGCGGC CAGACTTCGG CTTTCAAGC TGGCGCGCC

Seq ID NO: 275 DNA sequence  
Nucleic Acid Accession #: NM\_001118.1  
Coding sequence: 74..1651

50  
1 11 21 31 41 51  
| | | | |  
AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGAGGCC AGTGGTCTG 60  
GCCAAGAAGT GTCATGGCTG GTGTCTGTGA CGTTTCCCTG GCTGCTCACT GCGGGGCTG 120  
TCGCTGGGGC CGGGGCGAGC TCGCAGAAAG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180  
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG 240  
55 TGTCATGCTC GTGTGCTGTC ACGTTTCCCT GCGTCTCTC CTCTGCTGC CTATGGCCCC 300  
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCTCGG AGAAGATCCA 360  
GAGGGCCAAAT GAGCTGATGG GCTTCAATGA TTCTCTTCCA GGCTGTCTCG GGATGTGGGA 420  
CAACATCAGC TGTGTGAAGC CCGCCCATGT GGGTGAGATG GTCTCTGTCA GCTGCCCTGA 480  
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCAATT GAGAGTCTGA 540  
60 TTTTGTGAC AGTAACCTCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600  
GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTACTTTGAT GCCTGTGGGT TTGATGAATA 660  
TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACAGGCT 720  
TGCTACAGC ACATCCCTCG TCACCTCTAC CACTGCCATG GTCTCTCTT GTGCTTCCG 780  
GAAGCTGCAC TGCACAGCA ACTTCATCCA CATGAACCTG TTTGTGTGCT TCACTGTGAG 840  
65 GCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900  
CTTCATCTCC ACTGTGGAAT GTAAGGCGGT CATGGTTTTC TTCCACTACT GTGTGTGTC 960  
CAACTACTTC TGGCTGTTC TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT 1020  
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGTGGGGGA CCCCACCTGT 1080  
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140  
70 GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT 1200  
TAACCTTTGT CTTTATTATG GCATTATGCT CATCCTGTGT CAGAACTTC AGTCTCCAGA 1260  
CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT 1320  
CCCACTATTG GGAATCCACT ACACAGTATT TGCTTCTCC CCAGAGAATG TCAGCAAAAG 1380  
GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCCTTGTGG TGGCTGTTCT 1440  
75 CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAATGGGC GAAGCTGGAA 1500  
GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACCGACAC CGTCTCTGG CCAGCAGTGG 1560  
GGTGAATGGG GGCACCCAGC TCTCATCTCT GAGCAAGAGC AGCTCCCAA TCCGATGTCT 1620  
TGGCTCCCT GCTGACAATC TGGCAACTG AGCCATGCTC CCTT

Seq ID NO: 276 Protein sequence  
Protein Accession #: NP\_001109.1

80  
1 11 21 31 41 51  
| | | | |  
MAGVVHVS LA AHGACAPWGR GRLRKRAAC KSAAQRHIGA DLPLLSVGQ WCNPRSV MAG 60



VVHVSALALL LLPMAPMHS DCIFKKEQAM CLEKIQRANE LMGFNDSSPG CPGMMDNITC 120  
 WKPAHVGEML LVSCPELFRI FNPDQVWETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180  
 SEPPFHYFDM CGPDEYSEST GDQDYIYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC 240  
 TRNFHMLNLF VSMFLRAISV PIKDWILYAE QDSNHCFIST VECKAVMVVF HYCVVSNYFW 300  
 LFIEGLYLFET LLVETFFPER RYFYWYTIIG WGTPTVCVTV WATLRLYPDD TGCWDMNDST 360  
 ALWWVIKGFV VGSIMVNEVL FIGIIVILVQ KLQSPDMGNG ESSYILRLAR STLLLIPLFG 420  
 IHYTVFAFSP ENVSKRERLV FELGLGSPQG FVVAVLYCFL NGEVQAEIKR KWRSMKVNRY 480  
 FAVDFKRRHP SLASSGVNGG TQLSILSKSS SQIRMSGLPA DNLAT

Seq ID NO: 277 DNA sequence  
 Nucleic Acid Accession #: NM\_004000.1  
 Coding sequence: 36..1193

1 11 21 31 41 51  
 AGAAGAAGCT GGCCAAGGAT ATGGGAGCAA CCACCATGGA CCAGAAGTCT CTCTGGGCAG 60  
 GTGTAGTGGT CTGTGCTGCT CTCACGGGAG GATCTGCCTA CAAACTGGTT TGCTACTTTA 120  
 CCAACTGTGTC CCAGGACCGG CAGGAACCGA GAAAATTCAC CCCTGAGAAT ATTGACCCCT 180  
 TCCTATGCTC TCATCTCATC TATTCATTGG CCAGCATCGA AAACAACAAG GTTATCATCA 240  
 AGGACAAGAG TGAAGTGATG CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA 300  
 AACTGAAAAT TCTCTGTGCC ATTGGAGGGT ACCTGTTTGG TTCCAAAGGG TTCCACCCTA 360  
 TGGTGGATTG TTCTACATCA CGCTTGGAAAT TCATTAACTC CATAATCCTG TTTCTGAGGA 420  
 ACCATAACTT TGATGGACTG GATGTAAGCT GGATCTACCC AGATCAGAAA GAAAACACTC 480  
 ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTCA GAAGGACTTC ACAAATCCCA 540  
 CCAAGGAAG GCTTCTCTTG ACTGCGGGCG TATCTGCAGG GAGGCAATG ATTGATAACA 600  
 GCTATCAAGT TGAGAAACTG GCAAAAGATC TGGATTTCAT CAACCTCCTG TCCTTTGACT 660  
 TCCATGGGTC TTGGGAAAAG CCCCTTATCA CTGGCCACAA CAGCCCTCTG AGCAAGGGGT 720  
 GGCAAGCAGC AGGGCCAAGG TCCTACTACA ATGTGGAATA TGCTGTGGGG TACTGGATAC 780  
 ATAAGGGAAT GCCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA 840  
 CACTGGCCTC TGCAGAAACC ACCGTGGGGG CCCCTGCCTC TGGCCCTGGA GCTGCTGGAC 900  
 CCATCACAGA GTCTTCAGGC TTCCTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG 960  
 CCAAGATCAC GCGCCTCCAG GATCAGCAGG TTCCTACGCG AGTCAAGGGG AACCAGTGGG 1020  
 TGGGCTATGA TGATGTGAAG AGTATGGAGA CCAAGGTTCA GTTCTTAAAG AATTATAACC 1080  
 TGGGAGGAGC CATGATCTGG TCTATTGACA TGGATGACTT CACTGGCAAA TCCTGCAACC 1140  
 AGGGCCCTTA CCTCTTGTG CAAGCAGTCA AGAGAAGCCT TGGCTCCTTG TGAAGGATTA 1200  
 ACTTACAGAG AAGCAGGCAA GATGACCTTG CTGCTGGGG CCGCTCTCTT CCCAGGAATT 1260  
 CTCATGTGGG ATTCCTCTTG CCAGGCTGGC CTTTGGATCT CTCTTCCAAG CCTTTCCTGA 1320  
 CTTCTCTTGA GATCATAGAT TGGACCTGGT TTTGTTTTC TGCAGCTGTT GACTTGTGTC 1380  
 CCTGAAGTAC AATAAAAAAA ATTCATTTTG CTCCAGTA

Seq ID NO: 278 Protein sequence  
 Protein Accession #: NP\_003991.1

1 11 21 31 41 51  
 MDQKSLWAGV VVLLLIQGGG AYKLVCFYTN WSQDRQEPGK FTPENIDPFL CSHLIYSFAS 60  
 IENNKVIKD KSEVMYQTI NSLTKNPKL KILLSIGGYL PGSKGFHEMV DSSTSRLEFI 120  
 NSIILFLRNH NFDGLDVSWI YPDQKENTHF TVLIHELAEA FQKDFKSTK ERLLLTAGVS 180  
 AGRQMIDNSY QVEKLAKDLF FINLLSFDHF GSWEKPLITG HNSPLSKGWQ DRGPSSYYNV 240  
 EYAVGYWIHK GMPSEKVVMG IPTYGHSTFL ASAETTVGAP ASGPGAAGPI TESSGFLAYY 300  
 EICQFLKGAQ ITRLQDQQVP YAVKGNQWVG YDDVRSMETK VQFLKXNLNG GAMINSIDMD 360  
 DFTGKSCNQG PYPVLQAVKR SLGSL

Seq ID NO: 279 DNA sequence  
 Nucleic Acid Accession #: NM\_015166.1  
 Coding sequence: 116..1249

1 11 21 31 41 51  
 TGCTGGAAGT CCTCACCCA GAGACCAAGT CTCCCAACGG CAGAGCAGCG GGGGAGATAA 60  
 AGAACTGGTG ACAGTGGCT GTACATTGAG CACAGCTGTG GTGTCCCAA GTGCCATGAC 120  
 CCAGGAGCCA TTCAGAGAGG AGCTGGCCTA TGACCGGATG CCCACGCTGG AGCGGGGCGG 180  
 GCAAGACCCC GCCAGCTATG CCCAGACGCG GAAGCCGAGC GACCTGCAGC TGTGAAGAG 240  
 ACTGCCCCCC TGCTTCAGCC ACAAGACGTC GGTCTTCTCT GTGCTGATGG GGAGCTGCCT 300  
 CCTGGTGACC TCGGGGTTTT CGCTGTACCT GGGGAACGTC TTCCCGGCTG AGATGGGATTA 360  
 CTGCGCTGT GCTGCAGGCT CTGTCATCCC CTGGCAATT GTGAGCTTCA CGCTCTCCAG 420  
 GAGGAACGCC AATGTGATTC CCAACTTCA GATATGTTT GTTCCAGCT TTGCTGTGAC 480  
 CACTACGTGT TTAATTTGGT TTGGATGCAA ACTAGTCTGT AACCCATCAG CAATAAACAT 540  
 CAACTTCAAC CTCATCTGCG TGCTCCTGCT GGAGCTGCTC ATGGCGGCCA CGGTGATCAT 600  
 CGCTGCACGG TCCAGCGAGG AGGACTGCAA GAAAAAGAG GGCTCCATGT CTGACAGCGC 660  
 CAACATTCCT GACGAAGTGC CATTTCTGCG TCGGGTCTGT AAATCTTACT CAGTGTGCGA 720  
 GGTAAATCCA GGCACTCTCG CGCTCCTCGG GGGGATCATT GCCTGAACG TGGATGACTC 780  
 AGTTTCAGGC CACACCTCT CAGTGACGTT CTTTGTGATC CTAGTGGCCT GCTTTCACAG 840  
 TGCCATTGCC AGTCACTGTT CAGCAGAGTG TCCAGCAAG TGCTTGGTGG AGGTCTTGAT 900  
 TGCCATAAGC AGCCTCAGT CTCCGCTGCT GTTCAACGCG TCTGGATATC TGTCATTGAG 960  
 CATCATGAGA ATCGTGGAGA TGTTTAAGGA TTACCGGCCA GCCATAAAC CATCTACGGA 1020  
 TGTGCTGCTG CTGCTGCTGC TGCTAGTGCT CCGTCTGAG GCGGCTCA ACACGGGCAC 1080  
 CGCCATCCAG TGGTGGCTG TCAAGGTGAG TGCAAGGCTG CAGGCTGCAT CCTGGGACAC 1140  
 CCAGAACCGC CCGCAGGAGC GCCTGGCTGG GGAGGTGGCC AGGAGCCCCC TGAAGGAGTT 1200  
 CGACAAGGAG AAGAGCTGGA GAGCGTCTGT GGTGCAATG GCCCAGTGAC CCCAGACGCG 1260  
 GGAAACCGGG TGGCAGCGCC CAGCTGGGCC CCAAGCATGG AAACGACCAA CCCCTAATCG 1320  
 CCTGAGCTA CTGCTCTTAA CACCTCTTTT CCTTGTGTG AGGGCAAAAC AGGCTGCAGG 1380  
 TGGGGTTTTT ACTTCTTAGG GTAGTTTAAT TTTAAATAG GCCAATGTG GCTAGTCTGT 1440  
 GCCTCAGTGA GATCAGTCAG CTCGAGTGG CTCCGCTGTC GTACAGCAG GAGCATGGCC 1500

5  
10  
15  
20  
25  
30  
35

GCAACTTCCC AGGCGGAGGA AGGGCCCCCG GCTCGGCCTC TTGAGAGCCC CACCCCTGAA 1560  
CTGGCCCCAG CTCCTCTTCC TGCCCTCTCTC ATGGCTTGGG CTGGAGTGGG CTCTCTGGAC 1620  
CTGACACAGC TGTGGGTCCC TGGCTCTCCT GCCACTCTG ACCGGGCTTC CTCCTCCAC 1680  
GCTTAGGGTC TGTCCGGGT ACTCAGTCAG CCCAGTGGGA TCTTACCAC TTCCTGCAA 1740  
GGTGACCTG CCCAGGCTC AGGCTGCCCA GCGGCTCTTC CTGGACAGTG AGAGCAGGGC 1800  
TTGGGCGCTC TGTCTTGGCC CGGGAGCCGC AGGGGCCCCCT CCTCCAGAGC CTGGGCGCAA 1860  
GGGACACAGG CTGCGCGTGC TCTCCAGGT GAAATCCACA CCAGTCCACG CCGGGTCGCC 1920  
TGCCCTGTCT CCTACTTAG ACCCAGTCAT TCTAGAGGGA TCCACCGCCA CACTGGCCGG 1980  
CCACGTCCT GGTGTCTGTC ATGCCAGCT TGGAGTGCCA CGTGGCCGCT GCCACGTC 2040  
CGGCACTGT CATGCCAGC TTGGAGTGCC ACATGGCCGC TGCCACGTC CCGGGCACTG 2100  
TCATGCCAG CTGGAGTGC CAGTGGCGG CTGCTGTGAC AGGCAGTGT CTGGGGGTG 2160  
GGGCTGCATC CAAGGCTTTG TAAACCGGCT GGACCACTG TCCCTGGCCC CAGTGACCGG 2220  
GGGAAGCTGA GCCCTCCCT CTTGTGTTG CTCCATTAC TCAAAATGCA GGACAGATCA 2280  
GGTCAGAGCC CAGGAATTC CACAGTTCA CCCAGCGCCC TCTACCTCT AGCAAGTACT 2340  
TTGTCTTAG CCTCACTAG AAGGCCCCAG GGCAGCGTC TTCTCATCT CCGCTGTTT 2400  
GGGCTCTTAG GTCACAGCCC AGGCGGTAC TGCCACCTG CCAGGTGCA GGGACAGTTG 2460  
GGTGTGAGAA TAACATGCG TTTGGGTAG GCCATGCCA GGAGTGGGT TCCCTGCGTC 2520  
TCTCGTCCC GCGGGCGCT GGTCTCTCC AGCTGACGC AGTAAATCCA CAGTGAGTTG 2580  
GGGCACTGT GAACTGGAA TGCTGTACT TTGATAATTA CTTTCCAGCA GGTGTTTTCC 2640  
20 TTACAATGG TTTTGTCTT TTCTTCTGA TCTGAGAAGA CATGAACGT TTCTCTTAC 2700  
CGCGGTGGG TGTATTGACT GGTCCCCAT GGGCTGCTGG AAAGGCCCG AGATGCATCT 2760  
GTGGCTGGG GCCATCAAGA TCAAAGAAC AGGAGCGCTG GGAGATGCAG CTGGATGGG 2820  
CGGCTGCAG ACCCTCCAG GGGGTTTGG GACCTCCCA GGTTCCTCC TGCGGAACAG 2880  
GAGTACTCT GGTGCGAAG ATACCTTCAT GGTGTTGATG ACAAGTGGAA TCATTATTT 2940  
25 CAACCATGA AGGGGATGC AGGCAAGACA CCTTCCAGC TGCTCTAGA GGGGACAGC 3000  
CAGGCCCTCT CTCAGTCTC CGGAGCTCC GGAAGGACAG AGTCAGGGG CGGGCAACA 3060  
CTTTGGCCAC AGCCCCAAC AAGCGCCACC GTGGGAGAGG AGAGGCTGCT GTCACTGGTA 3120  
CGGATGACG PARVLKSYV GTCTGAGGC CACCCCCACC TCCCTGCAGC TTTGAGGCTG 3180  
GCGGGGTCTG CTCTGGGAA TGGGGTGGGA GCCACAGGGA CGACCGGGG CGGGCTGATG 3240  
30 TCTTCTTGG GGCAGACCG AGAGCTCAAG TTTGAGTCA AGAATTAGG ACTTGAACG 3300  
TTTTGTGGG CTTCAGCTT CTTATTTCT TATTTTAGAG CGCTTAAAA ATCCGAAAA 3360  
ATGGGTTTA AAGAACTGT CTCITTCAGT CTACATTTT GTTTAATACG CTGAGCAAT 3420  
AAGCGTGC TGCAGACGT G

Seq ID NO: 280 Protein sequence  
Protein Accession #: NP\_055981.1

40  
45

1 11 21 31 41 51  
MTQEPFREEL AYDRMPTLER GRQDPASYAP DAKPSDLQLS KRLPPCPFSHK TWVPSVLMGS 60  
CLLVTSGLSL YLGNVFAEM DYLRCAAGSC IPSAIVSFTV SRRNANVIPN FQILFVSTFA 120  
VTTCIWIWFG CKLVNPSAI NINPNLILL LLELLMAATV IIAARSEED CKKKKGSMSD 180  
SANILDEIVP PARVLKSYV VEVIAISAV LGGILALNVD DSVSGPHLSV TFFWILVACF 240  
PSAIAHVAA ECPKSKLVEV LIAISSLTSP LLFTASGYLS PSIMRIVEMF KDYPPIAKPS 300  
45 YDVLILLILL VLLIQAGLNT GTAIQCVRFK VSARIQASW DTQNGPQERL AGEVARSLPK 360  
EPDKEKAWRA VVVQMAQ

Seq ID NO: 281 DNA sequence  
Nucleic Acid Accession #: NM\_004518.1  
Coding sequence: 43..2577

55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
GCTGAGCCTG AGCCCGAGCC GGGGCGCCTC CGCCAGGCA CCATGGTGCA GAAGTCGCGC 60  
AAGCGCGCGG TATACCCCGG CCGAGCGGGG GAGAAGAAGC TGAAGTGGG CTTCGTGGGG 120  
CTGGACCCCG GCGGCGCCGA CTCACCCCGG GACGCGGCGC TGCTGATGCG CGGCTCGAG 180  
GCCCCCAAGC GCGGCGAGAT CCTCAGCAAA CCTCGCGGGG GCGGCGCGGG CGCGCGGAAG 240  
CCCCCAAGC GCAAGCCCTT CTACCGCAAG CTGAGAAATT TCCTCTACAA CGTGCTGGAG 300  
CGGCGCGCGG GCTGGGCTTC CATCTACCAC GCTACGTGT TCCTCTGCTT TTTCTCTGTC 360  
60 CTGCTGCTGT CTGTGTTTTC CACCATCAAG GAGTATGAGA AGAGCTCGGA GGGGGCCTTC 420  
TACATCTCTG AAATCGTGAC TATCGTGGTG TTTGGCGTGG AGTACTTCTG GCGGATCTGG 480  
GCCGCGAGCT GCTGCTGCGG GTACCGTGGC TGGAGGGGGG GGCTCAAGTT TGCCCGGAAA 540  
CGGTTCTGTG TGATTGACAT CATGGTGCTC ATCGCTCCA TTGCGGTGCT GGCOCGCGGC 600  
TCCAGGGGCA ACGTCTTTGC CACATCTGCG CTCGCGAGCC TGCGCTCTCT GCAGATTCTG 660  
65 CGGATGATCC GCATGGAGCC GCGGGGAGGC ACCTGGAAGC TGCTGGGCTC TGTGGTCTAT 720  
GCCACAGCA AGGAGCTGGT CACTGCTGG TACATCGGCT TCCTTTGTCT CATCTCGGCC 780  
TGTTTCTTGG TGTACTTGGC AGAGAGGGGG GAGAAGGACC ACTTTGACAC CTACGCGGAT 840  
GCATCTTGGT GGGGCGCTGAT CAGCTGACC ACCATTGGCT ACGGGGACAA GTACCCCCAG 900  
70 ACCTGGAAGC GCAGGCTCCT TGGCGCAACC TTCACCTCA TCGGTGTCTC CTCTCTCGG 960  
CTGCTGCGAG GCATCTGCT GTCTGGGTTT GCCTGAAGG TTCAGGAGCA GCACAGGCAG 1020  
AAGCACTTTG AGAAGAGGCG GAACCCGCGA GCAGGCTGTA TCCAGTCCGC CTGGAGATTG 1080  
TACGCCACCA ACCTCTCGCG CACAGACCTG CACTCCAGCT GGCAGTACTA CGAGCGAAGC 1140  
GTCAACGTCG CCATGTACAG ACTTATCCCC CCGCTGAACC AGCTGGAGCT GCTGAGGAAC 1200  
CTCAAGAGTA AATCTGAGT CGCTTTCAGG AAGGACCCCG CGCGGAGGCC GTCTCCAAGC 1260  
75 CAGAAGGTCA GTTTGAAGA TCGTGTCTTC TCCAGCCCCG GAGGCGTGGC TGCCAAGGGG 1320  
AAGGGGTCCC CGCAGGCCCA GACTGTGAGG CGGTCAACCA GCGCCGACCA GAGCCTCGAG 1380  
GACAGCCCCA GCAAGGTGCC CAAGAGCTGG AGCTTGGGG ACCGACGCGG GGCACGCCAG 1440  
GCTTTCCGCA TCAAGGGTGC CGGCTCACGG CAGAACTCAG AAGAAGCAAG CCTCCCGGA 1500  
GAGGACATTG TGGATGACAA GAGCTGCCCG TGCGAGTTTG TGACCGAGGA CCTGACCCCG 1560  
80 GGCTCAAGG TCAGCATCAG AGCCGTGTGT GTCATGCGGT TCCTGGTGTG CAAGCGGAAG 1620  
TTCAAGGAGA GCTTGCAGCC CTACGACGTG ATGGAAGTCA TCGAGCAGTA CTCAGCCGCG 1680  
CACTTGGACA TGCTGTCCCG AATTAAAGAG CTGCAGTCCA GAGTGGACCA GATCGTGGG 1740  
CGGGGCCAG CGATCAAGCA CAAGGACCGC ACCAAGGGCC CGGCGGAGGC GGAGCTGCC 1800  
GAGGACCCCA GCATGATGGG ACGGCTCGGG AAGGTGGAGA AGCAGGTCTT GTCCATGGAG 1860

5 AAGAAGCTGG ACTTCTGGT GAATATCTAC ATGCAGCGGA TGGGCATCCC CCCGACAGAG 1920  
 ACCGAGGCCT ACTTTGGGGC CAAAGAGCGG GAGCCGCGCG CGCCGTACCA CAGCCCGGAA 1980  
 GACAGCCGGG AGCATGTGGA CAGGCACGGC TGCAATTGTCA AGATCGTGCG CTCAGCAGC 2040  
 TCCACGGGCC AGAAGAACTT CTCGCGCGCC CGGCGCGCGC CCCCTGTCCA GTGTCGCGCC 2100  
 TCCACCTCCT GGCAGCCACA GAGCCACCCG CGCAGGGGCC ACGGCACCTC CCCCGTGGGG 2160  
 GACCAACGGCT CCCTGGTGG CATCCGCGCG CGCCCTGCCC ACGAGCGGTC GCTGTCCGCC 2220  
 TACGCGGGG GCAACCGCGC CAGCATGGAG TTCTGCGCGC AGGAGGACAC CCCGGCTGTC 2280  
 AGGCCCCCG AGGGGACCTT GCGGGACAGC GACACGTCCA TCTCATCCC GTCCGTGGAC 2340  
 10 CACGAGGAGC TGGAGCGTTC CTTACGCGGC TTCAGCATCT CCCAGTCCAA GGAGAACCTG 2400  
 GATGCTCTCA ACAGCTGCTA CGCGGCGGTG GCGCCTTGTG CCAAAGTCAG GCCCTACATT 2460  
 GCGGAGGGAG AGTCAGACAC CGACTCCGAC CTCTGTACCC CGTGCGGGCC CCCGCCACGC 2520  
 TCGGCCACCG GCGAGGGTCC CTTTGGTGAC GTGGGCTGGG CCGGGCCCA GAGTGAGGC 2580  
 GCGCCTGGSC CAGTGGACCC GCGCGCGGCC CTCTCAGCA CGGTGCTCC GAGGTTTGA 2640  
 15 GCGGGGAACC CTCTGGGGCC CTTTCTTAC AGTAACTGAG TGTGGCGGSA AGGCTGGGCC 2700  
 CTGGAGGGGC CCAATGTGGC TGAAGGATGG GGGCTCTGG CAGTGACCTT TTACAAAAGT 2760  
 TATTTTCCAA AGTCAGACAC CCAGGCGCTG TCGCCATTGA GGTGCTCCG CTGGGCTGTC 2820  
 TCTTCACCCC TCCCTGTGCT GGAGCCTGTC CCAAAAAGGT GCCAATGGG AGGCCTCGGA 2880  
 AGCCACTGTC CAGGCTCCCA CTGCTGTCT GCTCTGTTC CAAAGGCAGC GTGTGTGGCC 2940  
 20 TCGGGCCCTG CGGTGGCATG AAGCATCCCT TCTGGTGTGG GCATCGCTAC GTGTTTGGG 3000  
 GCGACGGTTC CACGCGGGT CCCCTGCTGT CTCCCTTGGG CTGGCTGAG CCTGGGGTCC 3060  
 ATGTCCCTTT GCGCTCCCT CATGGGCGAG GGAATCCATA CGCGGGCCCA CAGGCAGGGG 3120  
 TATGAGTGG TCCACCCCAA GCGAGCACA GCGCGGCCA CCGCTCCCG GTGCCCCAGT 3180  
 TCGCTCTCAG CTACCTGGAC TCCAGGACCC TGGAGAAGG AGACCTGGCA GTGGAGGGAG 3240  
 25 GCTGTGCTGT GTGTCCCTCT CAGGCTGTGA CCGCGCTGC TCTTTCTCC CCCGCCAGT 3300  
 GTGGCCCGCG CTGCTCTTTC CTCCCCACCC AGTATGGGCC CACTGTCTCT TTCTNCCCC 3360  
 CCAAGGTGT GCGCCACCT GTTCTTTCT CCCCTGCCA GGTGTGACCC CACTGTCTCT 3420  
 TTCTCTCTC CCAGTATGGC CCCACCTGCT CTTTCTCCC CCGAGGTGAG GCGCGCGCTG 3480  
 CTCTTCTCT CCAATGGAGC CGCTGAGGCG TGCGCACCTT GGCACAGGT GGGGCTCTGC 3540  
 30 AGGATGAGGA AGACAGGCCA ATCCCTTCCC TCCAGAAAG TGGCGGCCA GCAGGAGGA 3600  
 CTGAGGCCAG ACTCATGTCC AGCAAGGAAC GTGTGGTGTG TCCCTGGGA AGTCTCTGGG 3660  
 CCGCTGGGAAG AGGGAAGGTG CACGTCTCGG GATGTTGCG GGGCCCTGTT TTGGGAGACA 3720  
 AAGGGGTAGA GGGTCTGTCT TGGGCCCCCC CAGACTTAG CCGAGCAGT GCAGCCACCT 3780  
 ACTGCCCACT CTCAGAGAAG TGCAGCGGGA AGGAGGCTGG AGGTGGTGG GCGCTGCTC 3840  
 35 GGGTGTCTGC GTGAATGAGC GTGGCCAAG ACCAGTGCCA CCTCATGGCA AAGAGCTCCC 3900  
 GCAGTGTGTT TTAGAGTGCA CATCTACGT GCCCACTGGC ACACACACGT GCTCACATAC 3960  
 ANGTGNGT ACAGGNGTAC ACATGCANGC TTGCACACAT GCACACAGAC CACATAGCAC 4020  
 ACATGTGAC TGCACACACC TGTATAGACC ATGCACAGTA CACATACGTG CACATACATG 4080  
 40 CCGCATACA GGCATACACA TGCAGCTTA CATGTACA GTCACAGAT ACACACATGC 4140  
 ACACAGTGT AGCTCACACA CAGTATACAC ATACACAAG GCACAGACCA CACACAGCAC 4200  
 TAACACATGC ACACACAAAG TGCATAGGCC ACACAGCACA TGCACACAGG TGCACAGACC 4260  
 ACACACACACA CAGAGTGCA CAGAGCACAT TGCACACATG CACACACACA CCGGTGATG 4320  
 CACACTCTCT GCACTTCCAG CCTTGGAGCC CTTCTGTCT TGGTCTTCT CTTTACCCCT 4380  
 GCTGAGTGTA AGTGTGAGGT GAGGGGGCTA CAAGGAGTAA TTGTGGCTTT AGGGGTGGT 4440  
 45 GTGATGTGCG AATGTCAAGC GCGGTGCTGG GGTATCCGAC TGTCCGGCT CCGTGTCCGC 4500  
 AGTGGGACAG CGCCAGGACG AGCCAAATCAG GGTCTGTGCG TGCCCTTCCC CCCACAGCC 4560  
 TGGCAGCCAT CCAGAGGAGG GGCTCTACCA GATGCCAAG TGCCCGGTG TCTGTATGG 4620  
 TGTCCGGTGG GGTCTGTGTT TTGGTCTGCC CTGGAGGTGG CTGGGCCCTC CTGGGATGGG 4680  
 TGGCTCAGC TCGAATCCCA GCGCCAGCC CAGGCAGGTG CTGCTGCTG TTGTGGTTTC 4740  
 50 CTGGCCAGC TTCTCTTCT CCCTCTGCAT AAAATCACAG TCCGTGAGTC TTCCAGCTGC 4800  
 CACCAACGGT GGGACAGGCT GGGGAGGGG TCTTCCATG CCTCTGCAC ACAGCGCTCT 4860  
 GAGCAGGGCA GGTGCCAACA CCCCCAACG GAGACACGCT GCCCTCAGC GATGCCCTA 4920  
 CCTTTTGGG GCGCTCGTCT CAGGCCCCCC CTGGAGGCT GAAATCACCC CAGGCACGT 4980  
 GAGGGCTTCT CCAGGGGAGC ACCCTTTGAG CTGTGGTCT GATCACCCCA AGTCCCGCAC 5040  
 55 ACGAGGAGGA GGCACAGCCA GGGCGTGGG TTTAATGTTT GCGCCTTCGG GGCTGGAGGT 5100  
 CTCAGTGTCT CTAGATTCCA GACCTGCTG CAGAGAGAC CTGCTGCCG AGAGAAGGGG 5160  
 AGGAGGATG CAGCTGGGCT CGGTCCCCA CAGTCAGGGA CCCCCATAA GGACACCCC 5220  
 TTCTCTCTAG AAAGAGCTGG GCTCTCAGCT ATTTCTAGTT GCTTCCAGA AGCCGAGGAG 5280  
 CAGAGGAGC TGTGAGAGCT TTGCAGAAC GCGCTGTGC CCGCCCTCT GAGCTATGAA 5340  
 60 TGCCGTACAG AGCAGAGGCT GGGGCATTGG CAAGATCACA GGTGTATGCT GCACAGCCCC 5400  
 ATTGACACAA ACCCTCAAG CAGACGTGAG AGGGACGGTT CACAAAGCTT GACCTGCCG 5460  
 TGGAGGGTGC CCGGCAGAGG TGGCGTGAGA GGAACGGCTC ACGAGGCTTG GACCTGCTGT 5520  
 GGAGGGTGCC CAGCAGAGCT GGTGTGAGAG GAACGGCTCA CAGACCTTGG ACCTGGTGGA 5580  
 GGGTGCCGAG CAGACGTGCT GTGAGAGGGA CGGCTCACAG GGCTTGGACC GGAGAGAGAT 5640  
 65 GGCTCATGAG ACTTGGACCT GCGGTGGAGG GTGCCAGCA GACGTGGTAT GAGAGGGATG 5700  
 GCTCACAGG CTTGGACCTG GTGGAGGGTG CCGGCAGAC GTGTGAGAGG GACGGTTTAC 5760  
 AAGGCTTGGA CCGCCATGAG AGGGTGCCCA GCAGACGTGG TGTGAGAGGG ACAGCTCAG 5820  
 AGGCTTGGAC CTGCGGTGGA GGGTGCCAG CAGGGGGCTG AGCTCTGAGG GGTGGGTGCT 5880  
 CAGTGCAGG GTGCCCCAG TGTCTCTGA TCTGTCCGG TGCCCTCCCC AACCCCCACA 5940  
 70 CCAATGCAGA ACTCCAGGT CACATGCAG TATGTCCAG GCAATGGGGT GCGTGAAGA 6000  
 GGCCTGGTCA GGGCCTTTAG GGGCTGAGG ACGAATGGC CACTTGGGA GCTGTGTGG 6060  
 CTGTGCGGGG CAGCCATCTT GCATTTCCAC CCAGCGCGCA GTCTCACCT CGGCCCCAGC 6120  
 AAAGCGCTAA CAGCGCGGAG AGACAGCCAG GCGCGCTTCC TGAAGGATGT GGGATGGTGG 6180  
 ACTCCGGGCT CAGGGGAATA GCGAGTTCC TGTCTCCGG GAGACCTAGA GAAGCTGCAC 6240  
 75 ACCCAGGAGC TTTCCATGAC CCGGAGCAT GAGTGAATGG GGGGTTCCAG TTTGCTGAAC 6300  
 TTTGCTGTCT TGTAGGGTG GGGGCTGAGC GCCGACCCTG GGAGGAGTG ACACCGCAGG 6360  
 GGGAGGTTGT GGGCAACGGT GGAAGGAGAG AGACGGGAG GACCAATTG GAGTGGAGGG 6420  
 GCCTCTTCAG AGTTTAAAA GGGCTTTGT GGTGGAGTT GAGTGTGCTC TGGGCTTGA 6480  
 CACTGCGCT GGTGCCCTG GCTGGCGAG GAGACTGGCT CTGGCCAGGG CCGGCTCTG 6540  
 80 AGAGGTCCTC AGCTCTGAC TCTCGCCAG GCGCCAGCA GAGGGGCGG GTCCCGGGG 6600  
 CTACAGGCA GGCAGGTGCA CATGCCATC GCCACAGCC AACTCCGCTT GGGTTTACA 6660  
 AAGTCGTGCT CTTAATGCAT GTGGACAGGA ACTCCCTGAG GTCCGCCAT GCGCCCTGGC 6720  
 TGTGCCAGGT ACGACGCCCC TGGACCTGCG GAACAGGTGG GCGCGCGAG GGGCCAGG 6780  
 GACGGGCTCT AGAGACAGCG GCAGGCGAG AGGGGTCTCA CCGAGGGGTC TCGACTGAG 6840  
 GCGCCAGAG CTGGTGTGTC CGCTGGAGC CATCCCTCT CCGGGATCC ACACGGCCCA 6900

5 CGTGTGCCCG CCATGCCCCG GCCCCACGCC ATTGCAGTCT TCCATCCTCT GGCCGTGACG 6960  
 GTGGCTGCAG CTTCCTCCATT TGCGCCGTTG CCTCTGGCTG TCTGCACTTT TGTTCATGCT 7020  
 CCAAAGAACA TTTCATAATG CCTTCAGTAC CGACGTACAC TTCTGACCAT TTTGTATGTG 7080  
 TCCTTGTGCC GTAGTGACCA GGCCTTTTTT TGGTGGATGT GTTACCCCGC ACACCTCAAT 7140  
 CTCACCTTTG TGCACGCTCC ATTTTCTAGG GATAGACGCC CAGGGAATGA ACTCTAGTTT 7200  
 TCTAACAGAT TAGCTGAGAT ATTAACCTAC TCACACGGAC AGGTTGATGC CAGAGCCGTA 7260  
 AGAATGCGCC AGTGCGGGTT TGCGGGGGAC TTCGGGTGTG GGGTCCTGCG GCCGCGATGG 7320  
 CCGTGAAGG TTCTGGGGAT CCTGCTGCC ACGGGGACGA GTTCGGACGC CAGGTGGACC 7380  
 TGTGCACTCA GTAAACGCA GTGATTCAA AAAAAAAAAA

Seq ID NO: 282 Protein sequence  
 Protein Accession #: NP\_004509.1

15 1 11 21 31 41 51  
 MVQKSRNGGV YPGSPGKKL KVGPFVGLDPG APDSTRDGL LIAGSEAPKR GSILSKPRAG 60  
 GAGAGKPPKR NAFYRKLQNF LYNVLERPRG WAFIYHAYVF LLVFSCLVLS VFSTIKEYEK 120  
 SSEGALYILE IVTIIVFGVE YFVRIWAAGC CCYRGRWRGR LKFPARKPCV IDIMVLIASI 180  
 20 AVLAAQSQGN VFATSAIRSL RFLQILRMIR MDRRGGTWKL LGSVVYAHSK ELVTANYIGF 240  
 LCLILASFLV YLAEGENDH FDTYADALWW GLITLTITIGY GDKYPQTWNG RLLAATFTLI 300  
 GVSFFALPAG ILGSSFALKV QEHRQKHFE KRNPAAGLI QSAWRFYATN LSRTDLHSTW 360  
 QYYERTVTVP MYRLIPPLNQ LELLRLNLSK SGLAFRKDPF PEPSPSQKVS LKDRVFSSPR 420  
 GVAAGKGGSP QAQTVRRSPS ADQSLSDSPS KVPKSWSPGD RSRARQAFRI KGAASRQNSE 480  
 25 EASLPGEDIV DDKSCPCFV TEDLTPGLKV SIRAVCMRF LVSKRKFKES LRPYDVMQVI 540  
 EQYSAGHLDL LSRIKLSQSR VDQIVGRGPA ITDKDRTKGP AEAELEPEDS MMGRIGKVEK 600  
 QVLSMEKILD FLVNIYMQRM GIPPTETEAY FGAKPEPAP PYHSPEDSRE HVDRHGCIWK 660  
 IVRSSSTGQ KNFSAPPAAP PQQCPSTSW QPQSHPRQGH GTSFVGDHGS LVRIPPPPAH 720  
 ERSLSAYGGG NRASMEFLRQ EDTFGCRPPE GTLRSDTSI SIPVDHEEL ERSFSGFSIS 780  
 30 QSKENLDALN SCYAAPVPCA KVRPYIAEGE SDTDSLCTP CGPPPRSATG EGPFQDVGWA 840  
 GPRK

Seq ID NO: 2838 DNA sequence  
 Nucleic Acid Accession #: AF152496.1  
 Coding sequence: 1..2391

35 1 11 21 31 41 51  
 ATGGAGCGCG GAGGAGAGCG ATTCTTTAGA CAAAGGCAAG TCTTGCTTCT CTTGTTTTT 60  
 CTGGGAGGGT CTCTGGCTGG GTCCGAGTCA AGACGCTATT CTGTGGCTGA GGAAAAAGAG 120  
 40 AAGGGCTTTT TAATAGCCAA CCTAGCAAAG GATCTGGGAC TAAGGGTAGA GGAACCTGCC 180  
 GCGAGGGGGG CCCAAGTTGT GTCCAAAGGG AACAAACAGC ATTTTCAGCT CAGTCATCAG 240  
 ACAGGTGATT TGCTCTCGAA TGAGAAATG GACCGGGAGG AGCTATGCGG CCCACAGAA 300  
 CCATGCATAC TACATTTTCA GATATTACTG CAAACCCCTT TGAATTCTGT TACAAACGAG 360  
 CTCGATATCA TAGATGTAAA TGACCATCTT CCGGTATTCT TTGAAATGA AATGCATCTG 420  
 45 AAAATCCTAG AAAGCACTCT GCCAGGAACA GTAATTCCTT TGGGAAATGC TGAGGACTTG 480  
 GATGTGGGAA GAAACAGCCT CCAAACTAC ACTATCACT CGAATTCCTT CTTCCACGTA 540  
 CTCACTCGCA GTCTAGGGA CGGAAGGAAG TACCCGGAAC TAGTACTGGA TAAAGCGCTC 600  
 GATCGGGAGG AGCAGCCGGA ACTCAGCTTA ACCTCAGCG CGCTGGACGG CGGCTCTCCC 660  
 50 CCTCGGTCTG GGACAGCCCA GATAAACATC CAGGTCTTAG ATATAACGA CAATGCACCA 720  
 GAATTTGCAC AGCCGCTCTA TGAGGTTGCA GTTCTAGAGA ATACCCCGGT TAACCTCTGT 780  
 ATTGTCACTG TCTCGGCTTC TGACTTAGAT ACAGGAAGTT TTGGGACAAT ATCATATGCA 840  
 TTTTTTCATG CTTCTGAAGA AATTGCAAA ACTTTTCAGC TAAATCCAAT TACTGGTGAT 900  
 ATGCAACTGG TCAATATTGT GAATTTTGA GCGATTAAAT GTTATGAAGT CGACATCGAG 960  
 55 GCCAAGGATG GCGGAGGCTT ATCCGGAAG TCTACAGTCA TAGTCCAGGT GGTGTATGTC 1020  
 AACGACAAAC CACCGGAAGT GACCTTGCTT TCAGTAAACA GCCCTATTCC TGAGAACTCG 1080  
 GGAGAGACTG TACTGGCTGT TTTCACTGTT TCTGATCTAG ACTCTGGAGA CAACGGAAGA 1140  
 GTGATGTGTT CCATGAGAA CAATCTCCCC TTCTTCTCTA AACCATCTGT AGAGAAATTT 1200  
 TACACCCTAG TGTGAGAAGG CGCGCTGGAC AGAGAGACCA GATCCGAGTA CAACATTACC 1260  
 60 ATCACTATCA CTGACCTGGG GACACCCAGG CTGAAAACCA AGTACAACAT AACCGTGCTG 1320  
 GTCTCCGACG TCAATGACAA CGCCCCCGCC TTCACCCAAA TCTCTACAC CCTGTTCTGT 1380  
 CGCGAGAACG ACAGCCCCGC CCTGCACATC GGCAGTGTCA GCGCCACAGA CAGAGACTCA 1440  
 GGCACCAACG CCCAGTAAAC CTACTCGCTG CTGCGCCCCC AGGACCCGCA CCTGCCCTCT 1500  
 TCTTCCCTGG TCTCCATCAA CGCGGACAA GGCACCTGT TTGCCCTCAG GTGCTGGAC 1560  
 65 TACGAGGCCG TGCAGGCGTT CGAGTTCCGC GTGCGGCCCA CAGACCGTGG CTCCCGGGCT 1620  
 TTGAGCAGCG AGCGCTGGT GCGCGTGGT GTGCTGGAG CCAACGACAA CTCGCCCTTC 1680  
 GTGCTGTACC CGCTGCAGAA OGGCTCCGCG CCTGCAACG AGCTGGTGCC CCGGGCGGCT 1740  
 GAGCGGGGCT ACCTGGTGAC CAAGGTGGTG CCGGTGGAG GCGACTCGGG CCAGAAAGCC 1800  
 TGGCTGTGCT ACCAGCTGCT CAAGGCCACG GAGCCCGGGC TGTTCGGCGT GTGGGGCCAC 1860  
 70 AATGGGGAAG TGGCAGCGC CAGGCTGCTG AGCGAGGCGG ACGCGGCCAA GCACAGGCTG 1920  
 GTGGTGCTGG TCAAGGACAA TGGCGAGCCT CCGCGCTCGG CCACCGCCAC GCTGCATGTG 1980  
 CTCTGTGGG ACAGCTTCTC CCAGCCCTAC CTGCTCTCC CGGAGGCGGC ACGGCCCCAG 2040  
 GCCAGGCGCG ACTTGTCTAC CGTCTACCTG GTGGTGGCAT TGGCCTCGGT GTCTTCTGCTC 2100  
 TTCTCTTTT CGGTGCTCGT GTTGTGGCG GTGCGGCTGT GCAGGAGGAG CAGGGCGGCC 2160  
 75 TCGGTGGGTC CGTGTCTCGT GCCCGAGGCG CCTTTTCAG GGCAGATGGT GGCAGTGAGC 2220  
 GGCACCGGGA CCTGTGCCA GAGCTACAG TACGAGGTGT GTCTGACTCG AGGCTCCGGG 2280  
 ACAAATGAGT TCAAGTCTCT GAAGCCAATT ATCCCAACT TCGTTGCTCA GGGTGCAGAG 2340  
 AGGGTTAGCG AGGCAATCC CAGTTTCAGG AAGAGCTTTG AATTCAGTTA A

Seq ID NO: 284 Protein sequence  
 Protein Accession #: AAD43757.1

80 1 11 21 31 41 51  
 MEAGGERFLR QRQVLLLFVF LGGSLAGSES RRYSVAEKE KGFLIANLAK DIGLRVEELA 60

5 ARGAAVVSKEG NKQHFQLSHQ TGDLLNEKL DREELCGPTE PCILHFQILL QNPLOFVTNE 120  
 LRIIDVNDHS PVFFENEMHL KILESTLPST VIPLGNAEDL DVGRNSIQNY TITPNSHFHV 180  
 LTRSRDRGRK YPELVLDKAL DREEQPELSL TLTALDGGSP PRSGTAQINI QVLDINDNAP 240  
 10 EFAQPLYEVA VLENTPVNSV IIVTSASDLD TGSFGTISYA FFHASEEIRK TFOINPITGD 300  
 MQLVKYLNFE AINSYEDIE AKDGGGLSGK STVIVQVVDV NDNPELTLN SVNSPIPENS 360  
 GETVLAVFSV SLDSDGDNDR VMCSIENNLP FFLKPSVENF YTLVSEGLD RETRSEYNIT 420  
 ITITDLGTPR LTKYNTIVL VSDVNDNAPA FTQISYTLFV RENNSPALHI GSVSATDRDS 480  
 GTNAQVTVSL LPFQDPHLPL SSLVSINADN GHLPALRSLD YEALQAFEPF VGATDRGSPA 540  
 15 LSSEALVRVL VLDANDNSPF VLYPLQNGSA PCTELVPRAA EPGYLVTKV AVDGDGSGQA 600  
 WLSYQLLKAT EPLGFGVNAH NGEVTRARLL SERDAKHRL VVLVKDNGEP PRSATATLHV 660  
 LLVDGFSQPY LPLPEAAPAQ AQADLLTVYL VVALASVSSL FLPSVLLFVA VRLCRSRRAA 720  
 SVGRCSVPFG PPFQGMVDVS GTGTLSSQSYQ YEVCLTGGSG TNEFKFLKPI IPNFVAQGA 780  
 RVSEANPSFR KSFEFS

15 Seq ID NO: 285 DNA sequence  
 Nucleic Acid Accession #: NM\_001794.2  
 Coding sequence: 15..2765

20 1 11 21 31 41 51  
 CGCCGCGCGG GAAGATGACC GCGGCGCGCG CCGTGCTCCT TCTGTGCTC TCGCTCTCCG 60  
 GCGCGCTCCG GGCCTCAAT GAGGATCTTA CAACAGAGA GACCTGCAAG GCTGGGTCTT 120  
 CTGAAGATGA TTACACGGCA TTAATCTCCC AAAATATTCT AGAAGGGGAA AAGCTACTTC 180  
 25 AAGTCAAGTT CAGCAGCTGT GTGGGACCA AGGGGACACA ATATGAGACC AACAGCATGG 240  
 ACTTCAAGT TGGGGCAGAT GGGACAGTCT TCGCCACCCG GGAGCTGCAG GTCCTCTCCG 300  
 AGCAGTGGC GTTACAGGTG ACTGCATGGG ACAGCCAGAC AGCAGAGAAA TGGGACGCGG 360  
 TGGTGGGTT GCTGGTGGCC CAGACCTCGT CCCCGCACTC TGGACACAAG CCGCAGAAAG 420  
 GAAAGAAAGT CGTGGCTCTG GACCCCTCTC CGCCTCGAA GGACACCTGT CTGCGTGGC 480  
 30 CCCAGCACCA GAACGCCAAC GGGCTGAGG GGCACAAACG GGAGCTGGTC ATCCCGCCCA 540  
 TCAACGTGCC CGAGAAGTGG CGCGGGCCCT TCCCGCAGCA GCTCGTAGG ATCCGCTCCG 600  
 ACAAGAGCAA TGACATCCCC ATCCGGTACA GCATCACGGG AGTGGGGGCC GACCAGCCCC 660  
 CCAATGAGGT CTTCAGCAT GACTCCATGT CCGGCCGGAT GTACGTACA AGGCCCATGG 720  
 ACCGGAGGGA GCAGCTCTCT TACCACTCC GAGCCACGCG TGTGGACATG AATGGCAACA 780  
 35 AGGTGAGAAA CCCCATCGAC CTGTACATCT AGTCATCGA CATGAATGAC AACCGCCCTG 840  
 AGTTCATCAA CCAAGTCTAC AACGGCTCCG TGGACGAGGG CTCCAAGCCA GGCACCTACG 900  
 TGATGACCGT CACGGCCAAC GATGCTGAGC ACAGCACCCG GGCCCAACGG ATGGTGGGGT 960  
 ACCGGATCGT GACCCAGACC CCACAGAGCC CGTCCCAGAA TATGTTTACC ATCAACAGCG 1020  
 40 AGACTGGAGA TATGCTCACA GTGGCGGCTG GCCTGGACCG AGAGAAAGTT CAGCAGTACA 1080  
 CAGTCATCGT TCAGGCCACA GATATGGAAG GAAATCTCAA CTATGGCCTC TCAACACAG 1140  
 CCACAGCCAT CATCAGCGTG ACAGATGTGA ATGACAACCC GCCAGAATT ACOCGCCAGCA 1200  
 CGTTTGACGG GGAGGTCCCC GAAACCCGCG TGGAGACCGT GGTCCGAAAC CTCAGCGTGA 1260  
 TGGACCGAGA TCAGCCCCAC TCTCCAAACT GGAATGCGGT TTACCGCATC ATCAGTGGGG 1320  
 ATCCAGCGGA GCAGCTTCCG TCCCGCACAG ACCCGGTAAC CAACGAGGGC ATGGTCACCG 1380  
 45 TGGTGAAGGC AGTCGACTAC GAGCTCAACA GAGCTTTTCT GCTGACAGTG ATGGTGTCCA 1440  
 ACCAGGCGCC CCGTGGCCAGC GGAATCCAGA TGTCTTTCCA GTCCACGSCA GGGGTGACCA 1500  
 TCTCCATCAT GGACATCAAC GAGGCTCCCT ACTTCCCTC AAACACACAG CTGATCCGCC 1560  
 TGGAGGAGGG CGTCCCGCCC GGCACCGTGC TGACCAAGTT TTCACTGTG GACCTTGACC 1620  
 50 GGTTCATGTA CAGGCTGTG AGATACTCAA AGCTGTGAGA CCCAGCGAGC TGGCTGCACA 1680  
 TCAATGCCAC CAACGCCAGC ATCACCAGCG CGGCAGTGCT GGACCGTAG TCCCTCTACA 1740  
 CCAGAAACAA CGTCTACGAG GCCACCTTCC TGGCAGCTGA CAATGGGATA CCCCAGGCCA 1800  
 GCGGCACCGG GACCTCCAGC ATCTATCTCA TTGACATCAA CGACACGCC CCTGAGCTGC 1860  
 TGCCCAAGGA GCGCGAGATC TGGGAGAAGC CCAACCTGAA CGCCATCAAC ATCAGCGCGG 1920  
 CGAGCGCTGA CGTGGACCCC AACATCGGCC CCTACGTCTT CGAGCTGCCC TTTGTCCCGG 1980  
 55 CGCGCGTGGC GAAGAACTGG ACCATCACCC GCCTGAAAGG TGACTATGCC CAACTCAGCT 2040  
 TGGCATCCT GTACCTGGAG CCGCGGATGT ATGACGTCCC CATCATGTC ACAGACTCTG 2100  
 GAAACCTTCC CCGTGTCCAC AGTCCATCA TCAAGTCAA GGTGTGCCA TGTGATGACA 2160  
 ACGGGGAGCT CACCAACATT GCGCGAGTGG CAGCGGTGG TCTGGGACCC GGTGCCATCG 2220  
 TGGCATCTCT CATCTGCATC CTATCTCTGC TGACCATGGT CCGTGTGTT GTCATGTGGA 2280  
 60 TGAAGCGCG AGAGAAGGAG CGCCACAGA AGCAGCTGCT CATTGACCCC GAGGACGAGC 2340  
 TCCGCGACAA CATCTCAAG TATGACGAGG AAGCGGTGG CGAGGAGGAC CAGGACTACG 2400  
 ACCTCAGCCA GCTGCAGCAG CCGGAAGCCA TGGGGCACGT GCCAAGCAA GCCCTGGCG 2460  
 TCGCTCGCGT GGATGAGCGG CCGGTGGGCG CTGAGCCCCA GTACCGGATC AGGCCCATGG 2520  
 TGCGCACCCC AGGCACATC GGTGACTTCA TCAATGAGGG ACTCGCGCT GCTGACAAAG 2580  
 65 ACCCCACGCC ACCCCCTAT GACTCCCTGC TGGTCTTCCA CTACGAGGG AGCGGCTCCA 2640  
 CGCAGGCTC CGTCAGCTCC CTGAACATCAT CCACTTCGCG GGACCAAGAC TACGATTACC 2700  
 TCAACGACTG GGGGCCAGCA TTCAAGAAGC TGGCGGACAT GTATGGAGGT GGTGAAGAGG 2760  
 ATTGACTGAC CTGCTATCTT CGGACCGAAG TGAGAGCCGT GCTCGGAGCG CGGAGGAGCA 2820  
 GGACTGAGCA GAGGCGGCGG GTCTTCCCGA CTCCCTGCGG CTGTGCTCTT AGTGTGTTA 2880  
 70 GGAGGCCCCC CAATCCACAC GTTGAAGTGT CTAGCATGAG CACCCACCCC CACAGCGCCC 2940  
 TGCACCGCGC CGCTGCCAG CACCGCGCTG GCTGGCAGTG AAGGACAGCA AGAGGCACTC 3000  
 TGTCTTCACT TGAATTTCCT AGAACAGAAG CACTGTTTTT AAAAAAAAAA AAAAAAAG 3060  
 AAG

75 Seq ID NO: 286 Protein sequence  
 Protein Accession #: NP\_001785.2

80 1 11 21 31 41 51  
 MTAGAGVLLL LLSLSGALRA HNEDLTRET CKAGFSEDDY TALISQNI LEKLLQVKFS 60  
 SCVGTGKTGY ETNSMDFKVG ADGTVFATRE LQVPSEVAF TVTAWDSQTA EKWDVAVRLL 120  
 VAQTSSPHSG HKPQKGGKVV ALDPSPPPKD TLLPWPQHQN ANGLRRRKR D WVIPPINVPE 180  
 NSRGPPFQQL VRIRSDKND IPIRYSITGV GADQPPMEVF SIDSMGRMY VTRPMDREEH 240  
 ASYHLRAHAV DMNGKNVENP IDLYIYVIDM NDNRPFINQ VYNGSVDEGS KPGTYVMVT 300  
 ANDADDSTTA NGMVRYRIVT QTPQSPSQNM FTINSETGDI VTVAGLDRE KVQYTVIVQ 360

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60

```

ATDMEGNLNY GLSNTATAII TVTDVNDNPP EFTASTFAGE VPENRVETVV ANLTVMDRQQ 420
PHSPNWNNAVY RIISGDPSPGH FSVRTDPVTN EGMVTVVKAV DYELNRAFML TVMVSNAQPL 480
ASGIQMSFQS TAGVTISIMD INEAPYFPPN HKLIRLEEGV PPGTVLTTPS AVDPDRFMQQ 540
AVRYSKLSDP ASWLHINATN GQITTAVALD RESLYTKNNV YEATFLAADN GIPPASGTGT 600
LQIYLIDIND NAPELLPKEA QICEKPNLNA INITAADADV DPNIGPYVFE LPFVPAVRK 660
NWTITRLNGD YAQLSLRILY LEAGMYDVPI IVTDSGNPPI SNTSIIKVKV CPCDDNGDCT 720
TIGAVAAAGL GTGAIVAILI CILILLTMVL LPVMMMKRRE KERHTKQLLI DPEDDVDRDNI 780
LKYDEEGGGE EDQDYDLSQL QQPEAMGHVP SKAPGVRRVD ERPVGAEPQY PIRPMVPHPG 840
DIGDFINEGL RAADNDPTAP PYDSLLVPDY EGSGSTAGSV SSLNSSSSGD QDYDYLNDWG 900
PRFKKLADMY GGGGEED

```

Seq ID NO: 287 DNA sequence  
Nucleic Acid Accession #: AF152495.1  
Coding sequence: 1..2397

15  
20  
25  
30  
35  
40  
45  
50  
55  
60

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGGCCG GAGAGGGGAA GGAGCGCGTT CCGAAACAAA GGCAAGTCCT GATATCTTT 60
GTTTTGCTCG GCATAGCTCA GGCTAGTTGC CAGCCTAGGC ACTATTCAGT GGCCGAGGAA 120
ACGGAGAGTG GCTCCTTTGT GGCCAAATTG TTAAGAGACC TGGGGCTGGA GATAGGAGAA 180
CTTGCTGTGA GGGGGGCCAG GGTGCTTTCC AAAGSAAAAA AAATGCATTT GCAGTTCGAT 240
AGGCAGACCG GGGATTGTGT GTTAAATGAG AAATTGGACC GGGAGGAGCT GTGCGGCCCC 300
ACAGAGCCCT GTGTCCTACC TTCCAGGTG TTAGTAGAAA ATCCCTTGCA GTTTTTTCAG 360
GCGAGCTAC  GGATTAGGGA CGTAAATGAT CATTCCCCAG TTTCTCTAGA CAAAGAAATA 420
CTTTGAAAA  TTCCAGAAAG TATCACTCCT GGAACACTTT TCTTAATAGA ACGTGCCAG 480
GACTTGGATG TAGGAACCAA CAGTCTCCAA AATTACACAA TCAGTCCCAA TTTCACCTTT 540
CATCTTAATT TACAGACAG TCTCGATGGC ATAATATTAC CACAGCTGGT GCTGAACAGA 600
GCCCTGGATC GCGAGGAGCA GCGTGAGATC AGGTAAACCC TCACAGCGCT AGATGGCGGG 660
AGTCCACCCA GGTCCGCGAC GGCCTCGTA CCGATTGAAG TTGTGGACAT CAATGACAA 720
GTCCAGAGT  TTGCAAGCT GCTCTATGAG GTCCAGATCC CCGAGGACAG CCGCTTGA 780
TCCAGGTTG  CCACTGCTCT TGCCAGGGAT TTAGACATTG GAACTAATGG AGAAATATCT 840
TATGCATTTT CCAAGCATC TGAAGACATT CGCAAAACGT TTCGATTAG TGCAAAATCG 900
GGAGAAGTGC TTTTAAGACA GAACTGGAT TTGCAATCCA TCCAGACATA CACAGTAAAT 960
ATTGAGCGCA CAGATGTGTG GGCCTATCT GGAACCTGTG TGGTATTGT CCAAGTGATG 1020
GATTGGAATG ACAAATCTCC GGAACAACT ATGTCGACAC TTATCAATCA GATCCAGAA 1080
AACTTGCAGG ACACCTCAT TGCTGTATTC AGCGTTTCAG ATCCTGACTC CGGAGACAAC 1140
GGAAGGATGG TGTGCTCCAT CCAAGATGAT CTCTCTTTT TCTTGAACCC TTCTGTTGAG 1200
AACTTTTACA CTCTGGTGT AAGCACGGCC CTGGACCGGG AGACCGAGTC AGAATACAAC 1260
ATCACCATCA CCGTCACCGA CTTCGGGACA CCCAGGCTGA AAACCGAGCA CAACATAACC 1320
GTGCTGGTCT CCGAGCTCAA TGACAAACGCC CCCGCTTCA CCCAAACCTC CTACACCTG 1380
TTGCTCCGGG AGAACAACAG CCCCCTGCTG CACATCGGCA CGGTGAGCGC CACAGACAGA 1440
GACTCGGGCA CCAAGCGCCA GTTCACTTAC TCGCTGCTGC CGCCCCAGGA CCGGCACCTG 1500
CCCTCGCTCT CCTCTGCTC CATCAACGCG GACAAAGGCC ACCTGTTGCG TCTCCAGTGG 1560
CTGGAATACG AGCCCTGCA GCGTTCGAG TTCGCGTGG GCGCCGCGA CCGCGCTCC 1620
COGGCGTTGA GCAGCGAGGC GCTGGTGGCG GTGCTGTGTC TGGACGCCAA CGACAACCTG 1680
CCCTTCGTGC TGTACCCGCT GCAGAACGGC TCCGCGCCCT GCACCGAGCT GGTGCCCGG 1740
GCGGCGAGC CGGGCTACCT GGTGACCAAG GTGGTGGCGG TGGACGGCGA CTCGGGCGAG 1800
AAGCGCTGGC TGTGTGTACA GCTGCTCAAG GCCACGGAGC CCGGCTGTGT CCGGCTGTGG 1860
GCGCAATATG GCGAGGTGCG CACCGCCAGG CTGCTGAGG AGCGGAGCGC TGCCAAGCAG 1920
AGGCTGGTGG TGCTGTGCAA GGACAATGCG GAGCCTCCGC GCTCGGCCAC GSCCAACGCT 1980
CACGTGCTCC TGGTGGAGCG CTCTCCCGAG CCTACCTGCT TGCTCCCGGA GCGGCGACCG 2040
GCCAGGCCCC AGGCGGACTT GCTCACCGTC TACCTGTGTT TGGCGTTGCG CTCGGTGTCT 2100
TGCTCTCTCC TCTTCTCGGT GCTCCTGTTT GTGGCGGTGC GGCTGTGAG GAGGAGCAGG 2160
GCGGCTCTCG TGGGTGCTGT CTGCTGCCCC GAGGGCCCCC TTCCAGGGCA GATGGTGGAC 2220
GTGAGCGGCA CCGGACCCCT GTCCCAGAGC TACCAGTACG AGGTGTGTCT GACTGAGGCG 2280
TCCGGGACAA ATGAGTTCAA GTTCTGAAG CCAATTATCC CCAACTTCGT TGCTCAGGGT 2340
GCAGAGAGGG TTAGCGAGGC AAATCCCACT TTCAGGAAGA GCTTTGAATT CACTTAA

```

Seq ID NO: 288 Protein sequence  
Protein Accession #: AAD43756.1

65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
MEAGEGKERV PKQRQVLIFP VLLGLAQASC QPRHYSVAEE TESGSFVANL LKDLGLEIGE 60
LAVRGARVVS KGKIQHLQPD RQTGDLLENE KLDREELCGP TEPCLVPQV LLENPLQFFQ 120
AELRIRDVND HSPVFLDKEI LLKIPESITP GTTFLIERAQ DLDVGTNSIQ NYTISPNFHF 180
HLNLQDSLGG IILPQLVLNR ALDREEQPEI RLTLTALDGG SPFRSGTALV RIEVVINDIN 240
VPEFAKLLYE VQIPEDSPVG SQVAIVSARD LDIGTNGEIS YAFSQASEDI RKTFRLSAKS 300
GELLRLQKLD PESIQTYTVN IQATDGGGLS GTCVVFQVM DLNDNPPELT MSTLINQIPE 360
NLQDTLIAVP SVSDPDSGDN GRMVCISQDD LPFFLKPSVE NFYTLVISTA LDRETRSEYN 420
ITITVDFGT PRLKTEHNIT VLVSVDVNDNA PAFTQTSYTL FVRENNSPAL HIGSVSATDR 480
DSGTNAQVTV SLLPPQDPHL PLASLVSINA DNHLFALQS LDYEALQAFE FRVGAADRGS 540
PALSSEALVR VLVLDAANDS PFVLYPLQNG SAPCTELVPR AAEPGYLVTK VVAVDGDSGQ 600
NAWLSYQLLK ATEPGLFGVW AHNGEVRTAR LLRERDAAKQ RLVLVLDKNG EPPRSATATL 660
HVLVLVDGFSQ FYLLLPAPAP AQAQADLLTV YLVVALASVS SLFLPSVLLF VAVRLCRRSR 720
AASVGRCSVP EGPFPQGMVD VSGTGLSQS QYEVCLTGG SGTNEPKFLK PIIPNFVAQG 780
AERVSEANPS FRKSFET

```

Seq ID NO: 289 DNA sequence  
Nucleic Acid Accession #: NM\_018674.1  
Coding sequence: 390..2009

1 11 21 31 41 51  
| | | | | |

5	CGGAGCACAT	GCTGAGCGGA	GCGGCTGGGG	CTGGCGGGCG	TGGCGGAGCA	GCGCTCGCTC	60
	CCTCGCTCAC	TCGCTCGCTC	GCAGGGACAC	ACGCAGGGGC	TGACAGCTGT	GCTGGTGCTG	120
	ATAGAGGAAG	CCACAGGAG	ACGATCGAGG	AGAGAGACAA	GCGGCAGCAG	AGGCAGCAGC	180
	GGCAGAGGCA	GCACAGGGC	TGCGGAGCTG	CTGGGAGTGG	GAGTGACTCC	CCCACTCGG	240
	GCCCCAACC	TGTCCTGTG	CTCTTCCGCG	TGCGCTGAG	TTAGAAGAG	CAGCCGCTGC	300
	CACCACTGCC	ACTCGGGAGG	GCACCAGGGC	TGCTGGCTAG	GGAGGGACAG	GGCAGGGAGG	360
	CTCTGGCCAG	TCCGAGCAGC	CGGGGACAGA	TGCGGATCGA	GATTGTGTGC	AAAATCAAAT	420
	TTGCTGAGGA	GGATGCGAAA	CCCAAGGAGA	AGGAGGCAGG	GGATGAGCAG	AGCCTCCTCG	480
10	GGGCTGTGTC	CCCTGGAGCA	GCCCCCGAG	ACCTGGCCAC	CTTTGCCAGC	ACCAGCACC	540
	TGATGGTCTG	GGGCCGGGCC	TGTGGCCAG	GCCCCACGG	ACTGCGCAGA	ACCCTGTGGG	600
	CACCTGGCCCT	ACTCACCTCG	CTGGCTGCCT	TCTGTATCCA	GGCGGCTGSC	CTGGCCCGGG	660
	GCTACCTGAC	CCGCGCTCAC	CTGGTGGCAA	TGGACCCCGC	TGCCCCAGCC	CCAGTGGCGG	720
	GCCTCCCGGC	TGTCAACCTC	TGCAATATCA	ACCGCTTCGG	GCATTCCGCA	CTCAGCGATG	780
15	CCGACATCTT	CCACTGGGCC	AATCTGACAG	GGCTGCCGCC	CAAAGACCGG	GATGGGCACC	840
	GTGCGGCTGC	AGTCCGCTAC	CCAGAGCCTG	ACATGCTAGA	CATCCTCAAC	CGCACTGGCC	900
	ACCAGCTCGC	CGACATGCTT	AAGAGCTGCA	ACTTCAGTGG	GCATCACTGC	TCCGCCAGCA	960
	ACTTCTCTGT	GGTCTATACT	CGCTATGGGA	AGTGTATCAC	CTTCAACGCG	GACCCGCGGA	1020
	GCTCGCTGCC	CAGCCGGGCA	GGGGGCGATG	GCAGTGGCCT	GGAGATCATG	CTGACATCTC	1080
20	AGCAGAGGGA	GTACTCTGCC	ATCTGGAGGG	AGACAAATGA	GACGTCGTTT	GAGGCAGGTA	1140
	TTGCGGTGCA	GAGCCACAGC	CAGGAGGAGC	CGCCCTACAT	CCACCAGCTG	GGGTTGCGGG	1200
	TGTCCCGCAG	CTTCCAGACC	TTTGTGTCTT	GCCAGGAACA	GCGGCTGACC	TACCTGCCCC	1260
	AGCCCTGGGG	CAACTGCGCG	GCAGAGAGTG	AGCTCAGGGA	GCCTGAGCTT	CAGGGCTACT	1320
	CGGCCCTACAG	TGTGTCTGCG	TGCCGGCTGC	GCTGTGAAAA	GGAGGCCGTG	CTTCAGCGCT	1380
25	GCCACTGCCG	GATGGTGAC	ATGCCAGGCA	ATGAGACCAT	CTGCCCAACA	AATATCTACA	1440
	TCGAGTGTGC	AGTCCGCTAC	CTGACTCCG	TGGGTGGGGG	CCCTGAGGGC	CGGTGCTTCT	1500
	GCCCCAACC	CTGCAACCTG	ACACGCTATG	GGAAAGAGAT	CTCCATGGTC	AGGATCCCCA	1560
	ACAGGGGCTG	AGCCCGGTAC	CTGGGAGGGA	AGTACAACCG	CAACGAGACC	TACATACGGG	1620
	AGAACTTCTT	GCTCTAGATG	GTCTTCTTTG	AGGCCCTGAC	CTCTGAAGCC	ATGAGAGCAG	1680
30	GAGCAGGCTA	TGGCTGTGCA	CGCCCTGTGG	GAGACCTCGG	GGGACAGATG	GGCCTGTTC	1740
	TTGGGGCCAG	CATCTCAAG	TTGCTGGAGA	TCTCGACTA	CATCTATGAG	GTGTCTGGG	1800
	ATCGACTGAA	GCGGGTATGG	AGCGCTCCCA	AGACCCCTCT	GCGGACCTCC	ACTGGGGGCA	1860
	TCTCCACTTT	GGGGCTTCAG	GAGCTGAAGG	AACAGAGTCC	CTGCCGAGC	CTGGGCGGAG	1920
	CGGAGGGTGG	GGGGGTGAGC	AGTCTGCTCC	CCAATCACCA	CCACCCCCAC	GGTCCCCGAG	1980
35	GAGGTCTCTT	TGAAGATTTT	GCTTGTCTAG	ACGGTGTGCT	GACTGAAAGG	ACCCAGGAGT	2040
	CTGGGACCCG	TCTGGGATC	CCAGCACAT	TCTCTGTCTC	CTGGGAGAGG	CCGGGGGGCG	2100
	GTGCTCACTG	GGAGGGCCAG	GACTCAGTTC	CTGCTCTCAT	CCTCCCCCTG	CCTGATGTCA	2160
	GCTGCTTTGC	ACAAAGGTCC	TTCTTGTCCA	CACCCCTTAT	CCCCAGGCTG	GTGCCCCGGG	2220
40	AGGGCTGGAG	ACAGGGCCAT	GGGCCCTCAC	GGAGAGGAAG	GGAAAGGAAG	AGAGGGGAGG	2280
	GGAGGATAGA	GCCCATCCCA	GCCGGGGAGG	GGGAGCCCTC	TGTACATTTG	TAAATATTTA	2340
	GGGAAAGCCG	GGTGGGGGGA	GGGATACAG	ATGTAGAAGG	TGGGTAGGGC	TACAGGGGTG	2400
	GGTGATTAG	GGACAGCCAG	GGTCCAGCC	CCAATGTGAG	CAGGATAGGG	AGAGCCCCAG	2460
	GACTCAGGAG	TGCTGGGCTG	GTCTACTTTC	CTGCCCTCTC	CCAGGCCCCAG	CTCCCCCTTT	2520
45	GGCAGGGGGA	GGGATGTGCC	CAGCAGGCTC	GGCCAGCTC	CCAGTTCCCC	CTGACCCAGC	2580
	CCACCCCTTA	GAGTCCCTTC	TATAGGGAGG	GGCAGGAGA	CCTTCCAGAC	TTGGGCTGAG	2640
	CTTGAGGGT	GGGAAGGGAG	CCTTCTCAGT	CCTCTCTCCC	TCCAGTCTGA	TTTTATAAAG	2700
	TGCTGACGAG						

Seq ID NO: 290 Protein sequence  
Protein Accession #: NP\_061144.1

50	1	11	21	31	41	51	
	MPHIEIVCKIK	FAEEDAKPKE	KEAGDEQSLI	GAVAPGAAPR	DLATFASTST	LHGLGRACGP	60
	GPHGLRRLTLW	ALALTLTLAA	FLYQAAGLAR	GYLTRPHLVA	MDPAPAPVA	GFPVAVLNCNI	120
55	NFRFRHSALSD	ADIFHLANIT	GLPPKDRDGH	RAAGLRYPPE	DMVDILNRTG	HQLADMLKSC	180
	NFSGHHCASAS	NFSVVYTRYG	KCYTFNADPR	SSLPSPRAGGM	GSGLIMLMDI	QOEYLPINR	240
	ETNETSPFAG	IRVQIHSQEE	PPYIHLQGF	VSPGFQTFVS	QOEQLTYLPL	QPWGNCRAS	300
	ELREPLEPQCF	SAYSASACRL	RCEKEAVLQR	CHCRMVHMPG	NETICPPNIY	IECADHTLDS	360
60	LGGPEPGLQCF	CPTPQNLTRY	GKEISMVRIP	NRGSAARYLAR	KYNRNETYIR	ENPLVLVDFP	420
	EALTSEAMEQ	RAAYGLSALL	GDLGGMGLF	IGASILTLLE	ILDYIYEVSW	DRLKRVRWRP	480
	KTPLRTSTGG	ISTLGLQELK	EQSPCPSLGR	AEQGGVSSLL	PNHHHPGPP	GGLFEDFAC	

Seq ID NO: 291 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 62..895

65	1	11	21	31	41	51	
	CACCTGCTCTG	AGAATTGTG	AGCAGCCCTT	AACAGGCTGT	TACTTCACTA	CAACTGACGA	60
	TATGATCATC	TATATTTACT	TATTTCTCTT	GCTATGGGAA	GACACTCAAG	GATGGGGATT	120
70	CAAGGATGGA	ATTTTTTATA	ACTCCATATG	GCTTGAACGA	GCAGCCGGTG	TGTACACAG	180
	AGAAGCACGG	TCTGGCAAT	ACAAGCTCAC	CTACGCAGAA	GCTAAGCGCG	TGTGTGAATT	240
	TGAAGCGCGC	CATCTCGCAA	CTTACAAGCA	GCTAGAGGCA	GCCAGAAAAA	TTGGATTCTA	300
	TGTCTGTGCT	GCTGGATGGA	TGGCTAAGGG	CAGAGTTGGA	TACCCCATTC	TGAAGCCAGG	360
75	GCCCACTCTG	GGATTGTGAA	AACTGGCAT	TATTGATTAT	GGAATCCGTC	TCAATAGGAG	420
	TGAAGATGAG	GATGCCATTT	GCTACAACCC	ACACGCAAG	GAGTGTGGTG	GCGTCTTTAC	480
	AGATCCAAAG	CAATTTTTTA	AATCTCCAGG	CTTCCCAAT	GAGTACGAAG	ATAACCAAT	540
	CTGCTACTCG	CACATTAGAC	TCAAGTATGG	TCAGCGTATT	CACCTGAGTT	TTTTAGATTT	600
80	TGACCTTGAA	GATGACCCAG	GTGCTTGGC	TGATTATGTT	GAAATATATG	ACAGTTACGA	660
	TGATGTCAT	GGCTTTGTGG	GAAGATACTG	TGGAGATGAG	CTTCCAGATG	ACATCATCAG	720
	TACAGGAAAT	GTCATGACCT	TGAAGTTTCT	AAGTGATGCT	TCAGTGACAG	CTGGAGGTTT	780
	CCAAATCAAA	TATGTTGCAA	TGGATCTCTG	ATCCAAATCC	AGTCAAGGAA	AAAATACAG	840
	TACTACTTCT	ACTGGAATA	AAAACCTTTT	AGCTGGAAGA	TTTAGCCACT	TATAAAAAA	900
	AAAAAAGGA	TGATCAAAAC	ACACAGTGTT	TATGTTGGAA	TCTTTTGAA	CTCCTTTGAT	960

CTCACTGTGA TTATTACAT TTATTTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020  
TAGGAAAAAT TGGAAAAAT AGGAAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080  
ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTT TTCTTTCAGT CATTTTTCTA 1140  
TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTGTCAT TTGAAATTTT GGAATCCTGC 1200  
TCTATGTACA GTTTTGTATT ATACTTTTAA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260  
TCATTGATTA TTCTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320  
TGTTTATGTC ATTATTTAAG CCTGTCTCTA TTGTTGGAAT TTCAGTTCAT TTTCATAAAT 1380  
ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA

Seq ID NO: 292 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
| | | | |  
15 MIILYLFL LLWEDTQGWG KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEP 60  
EGGHLATYKQ LEARKIGIFH VCAAGWMAKG RVGYPIVKPG PNCQFGKTGI IDYGI RLNR 120  
ERWDAYCYNP HAKCEGCVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180  
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKLFL SDASVTAGGF 240  
QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSLH

Seq ID NO: 293 DNA sequence  
Nucleic Acid Accession #: NM\_007115.1  
Coding sequence: 69..902

25 1 11 21 31 41 51  
| | | | |  
GAATTCGCAC TGCTCTGAGA ATTGTGAGC AGCCCTTAAC AGGCTGTTAC TTCCTACAA 60  
CTGACGATAT GATCATCTTA ATTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120  
GGGGATTCAA GGATGGAATT TTTCACTAAT CCATATGGCT TGAACGAGCA GCCGGTGTGT 180  
30 ACCACAGAGA AGCAGGGTCT GGCAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT 240  
GTGAATTTGA AGCCGGCCAT CTCGCACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG 300  
GATTTCATGT CTGTCTGCTT GGTATGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360  
AGCCAGGCCC CAATCATGTA TTTGGA AAAA CTGGCATTAT TGATTATGGA ATCCGCTCTCA 420  
ATAGGAGTGA AAGATCGGAT GCCTATTGCT ACAACCCACA CGCAAGGAG TGTGGTGGCG 480  
35 TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540  
ACCAATCTCG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTAC CTGAGTTTIT 600  
TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660  
GTTACGATGA TGTCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720  
40 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780  
GAGGTTTCCA AATCAAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840  
ATACAAGTAC TACTTCTACT GGAATATAAA ACTTTTATAG TGGAGATTT AGCCACTTAT 900  
AAAAA AAAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAACTTT TGGAACTCCT 960  
TTGATCTCAC TGTATTATTT AACATTATTT TATTATTTT CTAAATGTGA AAGAAATACA 1020  
45 TAATTTAGGG AAAATGGGAA AATATAGGAA ACTTTAAACG AGAAATGAA ACCTCTCATA 1080  
ATCCCACTGC ATAGAAATAA CAAGCGTTAA CATTTCATA TTTTTCCTT TCAGTCATT 1140  
TTGTATTTGT GGTATGTGTA TATATGTACC TATATGTATT TGCATTGAA ATTTTGGAA 1200  
CCTGCTTAT GTACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260  
TGAATCAATT GATTATCTA CAAAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320  
50 ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTCAG GTCATTTTCA 1380  
TAAATATTGT TGAATAAAT ATCCTTGGGA ATTC

Seq ID NO: 294 Protein sequence  
Protein Accession #: NP\_009046.1

55 1 11 21 31 41 51  
| | | | |  
MIILYLFL LLWEDTQGWG KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEP 60  
EGGHLATYKQ LEARKIGIFH VCAAGWMAKG RVGYPIVKPG PNCQFGKTGI IDYGI RLNR 120  
60 ERWDAYCYNP HAKCEGCVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180  
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKLFL SDASVTAGGF 240  
QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSLH

Seq ID NO: 295 DNA sequence  
Nucleic Acid Accession #: NM\_001218.2  
Coding sequence: 116..1180

70 1 11 21 31 41 51  
| | | | |  
GTACTCGCCA CGGCACCCAG GCTGCGCGCA CGCGGTCCCG GTGTGCAGCT GGAGAGCGAG 60  
CGGCCACCGG GAGCCCCCGG CACAGCCCCG GCCCGCCCCG CAGGAGCCCG CGAAGATGCC 120  
CGGCGCAGC CTGACACCGG CGGCGGTGCT CCTGCTGGTG ATCTTAAAGG AACAGCCTTC 180  
CAGCCCGGCC CCAGTGAACG GTTCCAAGTG GACTTATTTT GGTCTTGATG GGGAGAAATG 240  
75 CTGTTCCAAAG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCCATAG ACCTGCACAG 300  
TGACATCCTC CAGTATGACG CCGACCTCAC GCCCTCTGAG TTCCAAGGCT ACAATCTGTC 360  
TGCCAAACAG CAGTTTCTCC TGACCAACAA TGGCCATTCA GTGAAGCTGA ACCTGCCCTC 420  
GGACATGCAC ATCCAGGGCC TCCAGTCTCG CTACAGTGCC ACGCAGCTGC ACCTGCACTG 480  
GGGGAACCG AATGACCCCG ACGGCTCTGA GCACACCGTC AGCGGACAGC ACTTCGCGC 540  
CGAGCTGCAC ATTGTCCATT ATAACCTAGA CCTTATCCT GACGCCAGCA CTGCCAGCAA 600  
80 CAGTCAGAA GGCCCTCGTG TCCTGGCTGT TCTCAITGAG ATGGGCTCCT TCAATCGTTC 660  
CTATGACAAG ATCTTCAGTC ACCTTCAACA TGTAAGGTAC AAAGGCCAGG AAGCATTCTG 720  
CCCGGATTTC AACATTGAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACCGCTACCG 780  
GGGTCCTGCT ACCACACCCC CTTCGAACCC CACTGTGCTC TGGACAGTTT TCCGAAACCC 840  
CGTGCAAAAT TCCACAGAGC AGCTGCTGCG TTTGGAGACA GCGCTGTACT GCACACACAT 900



5  
10  
15  
20  
25  
30

```

GGAGGACCCCT TCCCCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTCGATGA 960
GAGGCTGGTA TACACCTCCT TCTCCCAAGT GCAAGTCTGT ACTGCGGCAG GACTGAGTCT 1020
GGGCATCATC CTCTCACTGG CCTGGCTGG CATTCTTGGC ATCTGTATTG TGGTGGTGGT 1080
GTCCATTGG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA 1140
CAAGCCAGCC ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCCGGA GCTCCCGGCC 1200
ACATCCAGGA AGGACCTTGC TTTGGACCTT ACACACTTGG GCTCTCTGGA CACTTGCAC 1260
ACCTCAAGGT GTTCTCTGTA GCTCAATCTG CAAACATGCC AGGCCTCAGG GATCCTCTGC 1320
TGGGTGCTC CTTCGCTTGG GACCATGGCC ACCCCAGAGC CATCCGATCG ATGGATGGGA 1380
TGCACTCTCA GACCAAGCAG CAGGAATTCA AAGCTGCTTG CTGTAACGTG GTGAGATTGT 1440
GAAGTGTCT GAATTTCTGA ATCACAACCC AAGCCATGCT GGTGGGCCAT TAATGGTTGG 1500
AAAAACATTT CATCCGGGGC TTTGCCAGAG CGTGCTTTCA AGTGTCTTGG AAAGTCTGCT 1560
GCTTCTCCAA GCTTTCAGAC AAGAATGTGC ACTCTCTGCT TAGGTTTTCG TTGGGAAACT 1620
CAACTTCTTT CCTCTGGAGA CCGGCATCT CCCTCTGATT TCCTTCTGCT ATGACAAAAC 1680
CTTTAATCTG CACCTTACAA CTCGGGGACA AATGGGGACA GGAAGATCA AGTTGTAGAG 1740
AGAAAAAAGA AAACAAGAGA TATACATTGT GATATATTAG GGACACTTTC ACAGTCTCTG 1800
CCTCTGGATC CACAGACCTT CACAGACCTT AGGGAATGGC AGGTTCAAGT TCCACTTCTT 1860
GGTGGGGAG AGAAGGGAGA GAGAGCTAGA GGGACAAAGA GAATGAGAAG ACATGGATGA 1920
TCTGGGAGAG TCTCACTTTG GAATCAGAAT TGGAAATACA TTCTGTTTAT CAAGCCATAA 1980
TGTAAGGACA GAATAATACA ATATTAAGTC CAAATCCAAC CTCCTGTCTG TGGAGCAGTT 2040
ATGTTTTATA CTCTACAGAT TTTACAAATA ATGAGGCTGT TCCTTGAAAA TGTGTGTTG 2100
CTGTCTCTG GAGGAGACAT GAGTTCCGAG ATGACCCAAT CTGCCTTTGA ATCTGGAGGA 2160
AATAGGCAGA AACAAAATGA CTGTAGAACT TATCTCTGT AGGCCAAAT TCATTTCCAGC 2220
CACTTCTGCA GGATCCCTAC TGCCAACCTG GAATGGAGAC TTTTATCTAC TTCTCTCTCT 2280
CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTC AGCTATAAAA GCAGGAGGTT 2340
ATCTGTGAG GGGGCTGGCA TCATGTATT AGGGGCAAGT AATAATGGAA TGCTACTAAG 2400
ATACTCCATA TTCTTCCCCG AATCACACAG ACAGTTTCTG ACAGGCGCAA CTCCTCCATT 2460
TTCTTCCGCG AGGTGAGAAC CCTGTGGAGA TGAGTCAAGT CCATGACTGA GAAGGAACCG 2520
ACCCCTAGTT GAGAGCACTT TGCACTTCCC CGAGAACTTT CTGATTACCA GTCTCATTTT 2580
GACAGCATGA AATGTCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTTC TTCTACTCTT 2640
CCCTCTGACT CTAAAGATT TCTCTCTGG AATCGCTTGA ACCCAGGAGG CGCAGGTTGC 2700
AGTAAGCCAA GGTCAATGCCA CTGCACTCTA GCCTGGGTGA CAGAGCGAGA CTCATCTCA 2760
AAAAAATAAA AAAAA

```

Seq ID NO: 296 Protein sequence  
Protein Accession #: NP\_001209.1

40  
45

```

1 11 21 31 41 51
| | | | |
MPRRSLHAAA VLLLVILKEQ PSSPAPVNGS KWTYFGPDGE NSWKKYPSC GGLLQSPIDL 60
HSDILQYDAS LTPLEFQGYN LSANKQPLLT NNGHVSVKLN PSDMHIQGLQ SRYSATQLHL 120
HWGNPNDFHG SEHTVSGQHF AAEHLIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSFN 180
PSYDKIFSHL QHVYKQGEA FVPGFNIEEL LPRTAEYR YRGLSTTPPC NPTVLWTVFR 240
NPVQISQEL LALLETALYCT HMDPSPREM INNFRQVQKF DERLVYTSFS QVQVCTAAGL 300
SLGIILSLAL AGILGICIVV VVSIWLFRRK SIKKGDNGKV IYKPATKMET EARA

```

Seq ID NO: 297 DNA sequence  
Nucleic Acid Accession #: NM\_006632.1  
Coding sequence: 377..1582

50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ACGCGTCCGC CCAACGCTCC GCCACGCGGT CCGGTCCGGG CCAGAGCGCA GGTGTACCTG 60
GGCGCCGTGC TGGAGACCTT GACCGCCGAG ATCCTGGAGC TGGCTGGCAA CCGGCGCCGC 120
GACAAGAAGA CCGCATCAT CTGCGCCAC CTGTAGCTGG CCATTGCGAA CGGCGAGGAG 180
CTTAACAGAG TGCTGGGCGA AGTCACCATC GCGCAGGGCG GTGTCTGCCC CAACATTTCAG 240
GGCGTGCTTC TGCCCCAGAA GACCAAGAGC CACCACAAG CCAAGGGTGA AAACCATTC 300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCCACAG CAAGGGAGAG 360
CAAGAAGCCA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT 420
ATGTTCTGCT CGCTATGGAA TAGCCCTGCT CTTACATTTC TGCAATTTC CAACGATAGC 480
ACAAAATGTC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACAA GCCCTCAATC 540
CCAGCTCAAT GATTCTCTG AGGTGCTGCC TGTGACTCA TTTGGTGGCC TAAGTAAAGC 600
CCCAAGAGT CTTCTGCGAA AGTCCCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA 660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT 720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCAATTAGT GAAACCCCTG GGTGGCCCTT 780
TGTTCTCTAT ATCTTTGGAG GTGTTGGCTG TGTCTGCTGC CTTCTCTGGT TTGTTGTGAT 840
TTATGATGAC CCTTTTCTT ATCCATGGAT AAGCACCTCA GAAAAAGAA ACATCATATC 900
CTCCTTGAAA CAACAGGTCT GGTCTTCTAA GCAGCCTCTT CCAATCAAG CTATGCTCAG 960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC 1020
AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA 1080
TGGACTTCTA TCTGCCCTTC CTTTATTGT TGCCCTGGGT ATAGGCAAGG TGGGAGGCTA 1140
TCTGGCAGAT TTCTTCTTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTGCCAC 1200
AATTTTAGGA AGTCTCCCT CTTGAGCACT CATGTGTCT CTGCCTTACC TCAATTCCGG 1260
CTATATCACC CCAACTGCCT TGCTGACGCT CTCTTGCGGA TTAAGCACAT TGTGTCACTG 1320
AGGGATTAT ATCAATGTCT TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
ATCAAGAGGA TTTTCGAGCA TAGCACCTGT CATTGTACCC ACTGTACGG GATTTCCTT 1440
TAGTCAGGAC CCTGAGTTTG GGTGGAGGAA TGTCTTCTC TTGCTGTTG CCGTTAACCT 1500
GTGAGGACTA CTCTTCTACC TCATATTGG AGAAGCAGAT GTCCAAGAA GGGCTAAAGA 1560
GAGAAACTC ACTGTTTTAT GAAGTTATCC CACCTTGGAT GGAAAAGTCA TTAGGCACCG 1620
TATTGCATAA AATAGAAGGC TTCCTGTATG AATATACCAG TGAAAAGATT TTTTTCCT 1680
GTGGCTCTT TCAATTATGA GATCAGTTCA TTATTTTATT CAGACTTTT TTTGAGAGAA 1740
ATGTAAGATG AATAAAAATT CAAATAAAAT GATAACTAAG AAAAAATAAA AAAAA

```

Seq ID NO: 298 Protein sequence  
Protein Accession #: NP\_006623.1

```

1      11      21      31      41      51
|      |      |      |      |      |
5  MQVDETLIPR KGPSLCSARY GIALVLHFCN FTIAQNVIM NITMVAMVNS TSPQSQLNDS 60
SEVLVDSFSG GLSKAPKSLP AKSSILGGQF AIWEKWPPO ERSRLCSIAL SGMLLGCTA 120
ILIGGFISET LGWPFVFIYF GVGVCVCLL WFWVIYDDPF SYPWISTSEK EYIISSLKQQ 180
VGSSKQPLPI KAMLRSLPIW SICLCFSHQ WLVTMVVYI PTYISSVYVH NIRDNGLLSA 240
LPFIWVWIG MVGGYLADFL LTKKFLRLTV RKIATILGSL PSSALIVSLP YLNSGYITAT 300
ALLTLSCGLS TLQSGSIYIN VLDIAPRYSS FLMGASRGFS SIAPVIVPTV SGFLLSQDPE 360
10 FGWRNVFLL FAVNLLGLLF YLIFGEADVQ EWAKERKLTR L

```

Seq ID NO: 299 DNA sequence  
Nucleic Acid Accession #: NM\_003058.1  
Coding sequence: 145..1812

```

1      11      21      31      41      51
|      |      |      |      |      |
20  GGCCTGCCG TGAAGGCTGG TCACTTGCG AGGTAAACT CCTCTTTGA CTTCTGGCCA 60
GGGTTTGTG TGAGCTGGCT GCAGCCGCT TCAGCCCTGC TCGGGGCACG TCGGGCAGCC 120
TCGGGCCCTC CTGCCCTGCG GATCATGCC ACCACCGTGG ACGATGTCCT GGAGCATGGA 180
GGGGAGTTTC ACTTTTTCOA GAAGCAAATG TTTTCTCTCT TGGCTCTGCT CTCGGCTACC 240
TTGCGGCCCA TCIACGTGGG CATGCTCTTC CTGGGCTTCA CCCCTGACCA CGGCTGCGCG 300
AGCCCGGAG TGCCCGAGCT GAGTCTGCG TGCGGCTGGA GTCTGCGAGA GGAAGTGAAC 360
TACACGGTGC CGGCCCCAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420
GAGTGGAGCT GGAACCAAG CACCTTTGAC TCGTGGGACC CCTGGCCAG CCTGGACACC 480
AACAGGAGCC GCCTGCCACT GGGCCCTGCG CGGACCGGCT GGGGTACGA GACGCTGGC 540
TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAACT CCTGGATGTT GGACCTATTC 600
CAGTCATCAG TGAATGTAGG ATTCTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660
AGGTTTGGCC GTAAGCTCTG CCTCTAACT ACAGTCTCCA TAAATGCTGC AGCTGGAGTT 720
CTCATGCCCA TTTCCCAAC CTATACGTGG ATGTTAATTT TTCGCTTAAT CCAAGGACTG 780
GTCAGCAAAG CAGCTGGTGT AATAGGTAC ATCCTGATTA CAGAAATTGT TGGCGGAGA 840
TATCGGAGAA CAGTGGGGAT TTTTACCAA GTTGCCATA CAGTTGGGCT CTTGGTGCTA 900
GCTGGGTGG CTACGCACT TCCTCACTGG AGGTGGTGG AGTTACAGAT TGCTCTGCC 960
AACTTCTTCT TCTGCTCTA TTAAGTGGT ATACCTGAGT CTCCAGGTG GCTGATCTCC 1020
CAGAATAAGA ATGCTGAAG CATGAGAATC ATTAAGCACA TCGCAAAGAA AAATGGAAAA 1080
TCTCTACCCG CTCTCTTCA GCGCTGAGA CTTGAAGAGG AAAGTGGCAA GAAATTGAAC 1140
CCTTCATTTC TTGACTTGGT CAGAAGTCT CAGATAAGGA AACATACTAT GATATTGATG 1200
TACAACTGGT TCAGAGCTC TGTGCTCTAC CAGGGCTTCA TCATGCACAT GGGCCTTGCA 1260
GGTGACAATA TCACTCTGGA TTCTCTTAC TCTGCTCTGG TTGAATCCC AGCTGCTTTC 1320
ATGATCATCG ATGCTGAAG CCGCATCGGA CGCGTTTACC CTTGGGCTGC ATCAATATG 1380
GTTGCAGGGG CAGCTGTCT GGCCTCAGTT TTTATACCTG GTGATCTACA ATGGCTAAA 1440
ATTATTATCT CATGCTTGGG AAGAATGGG ATCACAATGG CCTATGAGAT AGTCTGCTG 1500
GTCAATGCTG AGCTGTACCC CACATTCTT AGGAATCTTG GCGTCCACAT CTGTCTCTCA 1560
ATGTGTGACA TTGGTGGCAT CATCACGCCA TTCCTGTCT ACCGCTCAC TAACATCTGG 1620
CTGAGCTTCC CGCTGATGGT TTTGGGGTA CTTGGCTTGG TTGCTGGAGG TCTGGTGTCT 1680
TTGCTTCCAG AAATCAAAGG GAAAGCTTGG CTTGAGACCA TCGAGGAAGC CGAAATATG 1740
CAAAGACCAA GAAAAATAA AGAAAAGATG ATTTACCTCC AAGTTCAGAA ACTAGACATT 1800
CCATTGAATC AAGAAGAGAG ACCGTTGCTG CTGTGATGAC CTAGCTTTGA TGGCAGCAG 1860
ACCAAAGATA GAAATCCCTG CACTCATCAC AAAGCCCAT AACTCAACC AAATTAACC 1920
CTGAGCCCTC TCAAGCTAGG TCTACAGCCA GTGGAGTCTA TTGTACACTG TGGAAAAATA 1980
CCCATGGGAC CAGATCTCTG CAAATCTTTC CAGCTCACTT TATTCTCAGC ATTCTTAGGA 2040
CATTTGACAT TGGTTTTCTG GAGGGTTTTT TTTCCGATCT TTGTATTTT TTAATTTGA 2100
TTCTTTTCTT TGTCAATGCTA GCAACAGAA TACATAGGGG AACTGTGGGC TAGGCAANA 2160
AAATAGAAAA AGTGTGAAAA ACAGTAAAGT TGGGAGAGGA GCATCTATT TCTTAAAGAA 2220
55 ATAAACACC NAAAAACAAA AAAAAAAA AAAAAA

```

Seq ID NO: 300 Protein sequence  
Protein Accession #: NP\_003049.1

```

60 1      11      21      31      41      51
|      |      |      |      |      |
MPTTVDDVLE HGGEFHFQK QMFLLALLS ATFAPYVGI VFLGFTPDHR CRSPGVAELS 60
LRGWSPAEE LNYTVPGPG AGEASPRQR RYVDWNQST FDCVDPLASL DTNRSLPLG 120
PCRDGWVYET PGSSIVTEFN LVCAANSWLD LQSSVNVGF FIGSMSIGYI ADRFGRKLCL 180
LTTVLNAAA GVLMAISPTY TWMLIFRLIQ GLVSKAGWLI GYILITEFVG RRYRRTVGIF 240
YQVATVGLL VLAGVAYALP HWRNLQFTVA LPNFFFLYY WCIPESPRWL ISQNKNAEAM 300
RIIKHAKQN GKSLPASLR LRLEESTGKX LNPSFLDLVR TPQIRKHTMI LMYNWFTSSV 360
LYQGLIMHG LAGDNIYLDY FYALVEFPA AFMIILTIDR IGRYPWAAS NMVAGAACLA 420
SVFIPGLQW LKIIISCLGR MGITMAYEV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480
70 TPFLVYRLTN INLEPLMVF GVLGLVAGGL VLLLPETKPK ALPETIEEA NMQRPRNKKE 540
RMIYLVQVQL DIPLN

```

Seq ID NO: 301 DNA sequence  
Nucleic Acid Accession #: NM\_012206.1  
Coding sequence: 52..1131

```

75 1      11      21      31      41      51
|      |      |      |      |      |
GTTACCCAGC ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT 60
CAAGTGGTCA TCTTAAGCCT CATCCTACAT CTGGCAGATT CTGATGCTG TCTGTAAAG 120
GTTGGTGGAG AGGCAGGTCC ATCTGTCACT CTACCCCTGC ACTACAGTGG AGCTGTCACT 180
TCAATGTGCT GGAATAGAGG CTCATGTTCT CTATTCACAT GCCAAATGG CATGTCTGG 240
ACCAATGGAA CCCACGTGAC CTATCGGAAG GACACAGGCT ATAAGCTATT GGGGACCTT 300
TCAAGAAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACG TGGCTATAT 360
80

```

5 TGTGTCCGTTG TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCATTGGAG 420  
 ATTGTGCCAC CCAAGGTCCAC GACTACTCCA ATTGTACAA CTGTTCCAAC CGTCACGACT 480  
 GTTCGAAAGA GCACCACTGT TCCAAAGACA ACGACTGTTC CAACGACAAC TGTTCACAA 540  
 ACAATGAGCA TTCCAACGAC AAGACTGTT CCGACGACAA TGAATGTTTC AACGACAAAG 600  
 AGCGTTCCAA CGACAACGAG CATTCCAACA ACAACAAGTG TTCCAGTGAC AACAAACGGTC 660  
 TCTACCTTTG TTCTCTCAAT GCCTTTGCCG AGGCAGAAC ATGAACAGT AGCCACTTCA 720  
 CCAATCTTAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGAGAG AATAAGGAGA 780  
 GAACCCACCA GCTCACCATT GTACTCTTAC ACACACAGAT GGAATGACAC CGTGACAGAG 840  
 TCTTCAGATG GCCTTTGGAA TAACAATCAA ACTCAACTGT TCCTAGAACA TAGTCTACTG 900  
 10 ACGGCCAATA CCACTAAAGG AATCTATGCT GGAGTCTGTA TTTCTGTCTT GGTGCTTCTT 960  
 GCTCTTTTGG GTGTCTCAT TGCCAAAAGG TATTTCTTCA AAAAGGAGGT TCAACAACCTA 1020  
 AGTGTTCAT TTAGCAGCCT TCAAATTAAA GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080  
 CAAGCAGAAG ACAATATCTA CATTGAGAAT AGTCTTTATG CCACGGACTA AGACCCAGTG 1140  
 GTGCTCTTTG AGAGTTTACG CCCATGACTG CAGAAGACTG AACAGGTATC AGCAGATCAG 1200  
 15 ATGTCTTTTA GACTCCAAGA CAATTTTCTT GTTTCAGTTT CATCTGGCAT TCCAACATGT 1260  
 CAGTGATACT GGGTAGAGTA ACTCTCCAC TCCAACTGT GTATAGTCAA CCTCATCATT 1320  
 AATGTAGTCC TAATTTGTTT TGCTAAACT GCCTCAATCC TTCTGATCAT TGCAGAGTTT 1380  
 TCTCTCAAC ATGAACACT TAGAATTGTA TGTCTCTT AGACCCCAT AATCTGTAT

20 Seq ID NO: 302 Protein sequence  
 Protein Accession #: NP\_036338.1

25 1 11 21 31 41 51  
 MHPQVILSL ILHLADSVAG SVKVGSEAGP SVTLPCHYSG AVTSMCWNRG SCSLFTCQNG 60  
 IVWTNGTHVT YRKDTRYKLL GDLSRRDVS LTIENAVSDS GVIYCCRVHR GWFNDMKITV 120  
 SLEIVPFPVT TPIVTVTPVT VTTVTRSTTV PTTTTPVTIT VPTTMSIPTT TTVPTTMTVS 180  
 TTTSTVPTTS IPTTSTVPVT TTVSTFVPPM PLPRQNHPEV ATSPSSPQPA ETHPTTLQGA 240  
 30 IRREPTSSPL YSYITDNDT VTESSDGLWN NNQTLFLEH SLLTANTTKG IYAGVCISVL 300  
 VLLALLGVII AKKYFFKKEV QQLSVSFSSL QIKALQNAVE KEVQEDNIY IENSLYATD

35 Seq ID NO: 303 DNA sequence  
 Nucleic Acid Accession #: NM\_001044.1  
 Coding sequence: 129..1991

40 1 11 21 31 41 51  
 ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGCGTGC 60  
 AAAGCCACAG CCCGGGCGGC CAGACCAAGA GGAAGAAGC ACAGAATTCC TCAACTCCCA 120  
 GTGTGCCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCGGTG GTGGCCCGGG 180  
 CTAAGGAGCC CAATGCCGTG GGGCCGAAGG AGGTGGAGCT CATCTTGTGC AAGGAGCAGA 240  
 ACGAGTGCA GCTCACCAGC TCCACCTCCA CCAACCCGCG CGAGAGCCCC GTGGAGGCCG 300  
 AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTCTCTCT GTCCGTCATT GGCCTTGTCTG 360  
 TGGACCTGGC CAACTCTGCG CGGTCCCCCT ACCTGTGCTA CAAAATGGT GGGGTGCGCT 420  
 45 TCCTGGTCCC CTACCTGCTC TTCATGCTCA TTGCTGGGAT GCCACTTTTC TACATGGAGC 480  
 TGGCCCTCGG CCAGTTCAAC AGGGAAGGGG CCGCTGGTGT CTGGAAGATC TGCCCCATAC 540  
 TGAAAGGTGT GGGCTTACAG GTCATCTCTA TCTCACTGTA TGTGGCTTC TTCTACAACG 600  
 TCATCATGCG GTGGGCGCTG CACTATCTCT TCTCTCTCT CACCAAGGAG CTCCCTGGA 660  
 TCCACTGCAA CAACTCTGCG AACAGCCCCA ACTGCTCGGA TGCCCATCTT GGTGACTCCA 720  
 50 GTGAGACAG CTGCGGCCCT AACGACACTT TTGGGACCA ACCTGCTGCC GAGTACTTTG 780  
 AACGTGGCGT GTGCACTCTC CACGAGAGCC ATGGCATOGA CGACCTGGGG CCTCGCGGCT 840  
 GGCAGCTCAC AGCCTCCCTG GTGCTGGTCA TGTGCTGCT CTACTTCAGC CTCTGGAAGG 900  
 GCGTGAAGAG CTTGCGGGAAG GTGGTATGGA TCACAGCCAC CATGCCATAC GTGTCTCTCA 960  
 55 CTGCCCTGCT CTTGCGTGGG GTCACTCTCC CTGGAGCCAT AGACGCGATC AGAGCATACC 1020  
 TGAGCGTTGA CTTCTACCGG CTCTGCGAGG CGTCTGTTTG GATTGACGGG GCCACCCAGG 1080  
 TGTGCTTCTC CTTGGGCGTG GGGTTCGGGG TGTCTGATCG CTTCTCCAGC TACAACAAGT 1140  
 TCACCAACAA CTGCTACAGG GACGCGATTG TCACCACTTC CATCACTCC CTGACGAGCT 1200  
 TCTCTCCGGG CTTCTGCTGC TTCTCTCTCC TGGGGTACAT GGCACAGAAG CACAGTGTGC 1260  
 60 CCACTCGGGA CGTGGCCAA GACGGGCCAG GGCTGATCTT CATCATCTAC CCGGAAGCCA 1320  
 TCGCCACGCT CCTCTGTCTC TCAGCCTGGG CGGTGGTCTT CTTCATCATG CTGCTCACCC 1380  
 TGGGTATCGA CAGCGCCATG GGTGGTATGG AGTCAGTGAT CACCGGGCTC ATCGATGAGT 1440  
 TCCAGCTGCT GCACAGACAC CGTGAGCTCT TCACGCTCTT CATGCTCCTG GCGACCTTCC 1500  
 TCCGTGCCCT GTTCTGCGTC ACCAACGGTG GCATCTACGT CTTCAOGCTC CTGACCCATT 1560  
 65 TTGCAGCCGG CAGTCCATCT CTCTTTGGAG TGCTCATCGA AGCCATCGGA GTGGCCTGGT 1620  
 TCTATGGTGT TGGGCAAGTT AGCGACGACA TCCAGCAGAT GACCGGGCAG GGGCCAGCC 1680  
 TGTACTGGCG GCTGTGCTCG AAGCTGGTCA GCCCTGCTT TCTCTGTTTC GTGGTCTGTG 1740  
 TCAGCATGTT GACCTTCAGA CCCCCCACT ACGGAGCCTA CATCTTCCCC GACTGGGCCA 1800  
 ACGCGCTGGG CTGGGTGATC GCCACATCCT CCATGGCCAT GGTGCCCATC TATGGGCGCT 1860  
 70 ACAAGTCTGT CAGCTGCCT GGGTCTTTTC GAGAGAACT GGCTACGCC ATTGCACCCG 1920  
 AGAAGGACCG TGAGCTGGTG GACAGAGGG AGGTGCGCCA GTTCAOGCTC GGCACAGG 1980  
 TCAAGGTGTA GAGGAGCAG AGACGAAGC CCCAGGAAGT CATCTGCAA TGGGAGAGAC 2040  
 ACGAACAAAC CAAGGAATC TAAGTTTGA GAGAAAGGAG GGCACCTTCT ACTCTTCAAC 2100  
 CTCTACTGAA AACACAAACA ACAGAGCAGA AGACTCTCTT CTTCTGACTG TTTACACCTT 2160  
 TCGTGCCGGG GAGGACACT CGCGGTGCTT TGTGTGCTG TAATAACGAC GTAGATCTGT 2220  
 75 GCAGCGAGGT CCACCCCGTT GTTGTCTCTG CAGGGCAGAA AAAGCTTAA CTTCTGCTG 2280  
 TCTGTGTGAG GCTCCCTCCC TCCCTGCTCC CTGCTCCCGG CTCTGAGGCT GCGCCAGGGG 2340  
 CACTGTGTTT TCAGGCGGGG ATCAGATGCC TTGTAGAAGC ACCTGCTGAG AATCCCGGTG 2400  
 CTCACAGTAG CTTCCTAGAC CATTTACTTT GCCCATATTA AAAAGCCAAG TGTCTGTCTT 2460  
 80 GGTTTAGCTG TGCAGAAGGT GAAATGGAGG AAACCAACAA TTCATGCAA GTCCCTTCCC 2520  
 GATGCGTGCC TCCAGCAGA GGCCTGAAAT TGAGGTTTCA GTTGACAT TGCACACACA 2580  
 GTCTGTTCAG AGGCATTGGA GGATGGGGGT CTTGGTATGT CTCACAGGA AATTCTGTTT 2640  
 ATGTCTTTCG AGCAGAGAGA AATAAACTC CTGAAACCA GCTCAGGCTA CTGCCACTCA 2700  
 GGCAGCTAGT GGTGCTTGTG GGTGAGGGA ACGGCTGAG AGGAGCGGTG CCTATCCCG 2760  
 GACGATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCG GACGATGCA GGGCCCCCAC 2820

5  
10  
15  
20

```

AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAG AGGAGCGTGT ACTACCCCAG 2880
AACGCATGCA GGGCCCCCAG AGGAGCGTGT ACTACCCCAG GACGCATGCA GGGCCCCCAG 2940
TGGAGCGTGT ACTACCCCAG GACGCATGCA GGGCCCCCAG AGGAGCGTGT CCTATCCCTG 3000
GACCGGACGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC CCCAGGACGC ATGCAGGGCC 3060
CCCACAGGAG CGTGTACTAC CCCAGGATGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC 3120
CCCAGGACGC ATGCAGGGCC CCCATGCAGG CAGCCTGCAG ACCAACACTC TGCCTGGCCT 3180
TGAGCGGTGA CCTCCAGGAA GGGACCCCAG TGGAAATTTA TTTCTCTCAG GTGCGTGCCA 3240
CATCAATAAC AACAGTTTTT ATGTTTGCGA ATGGCTTTT AAAATCATAT TTACCTGTGA 3300
ATCAAAACAA ATTCAAGAAAT GCAGTATCCG CGAGCCTGCT TGCTGATATT GCAGTTTTTG 3360
TTTACAAGAA TAAATTAGCAA TACTGAGTGA AGGATGTTGG CCAAAGCTG CTTTCCATGG 3420
CACACTGCCC TCTGCCACTG ACAGGAAAGT GGATGCCATA GTTTGAATTC ATGCTTCAAG 3480
TGGTGGGGCC TGCTTACGTG CTGCCCAGAG GCAGGGGGCC TGCAGGGCCA GTCATGGCTG 3540
TCCCCTGCAA GTGGACGTGG GCTCCAGGGA CTGGAGTGTG ATGCTCGGTG GGAGCCGTCA 3600
GCCTGTGAAC TGCCAGGACG CTGCAGTTAG CACAGAGGAT GGCTTCCCA TTGCTTCTG 3660
GGGAGGGACA CAGAGGACGG CTTCCCATC GCCTTCTGGC CGCTGCAGTC AGCACAGAGA 3720
GCGGCTTCCC CATTGCCTTC TGGGGAGGGA CACAGAGGAC AGTTTCCCA TCGCTTCTG 3780
GTTGTTGAAG ACAGCAGAGA GAGCGGCTTC CCCATCGCCT TCTGGGGAGG GGCTCCGTGT 3840
AGCAACCCAG GTGTTGTCCG TGTCTGTTGA CCAATCTCTA TTCAGCATCG TGTGGGTCCC 3900
TAAGCACAAT AAAAGACATC CACAATGGAA AAAAAAAG GAATTC

```

Seq ID NO: 304 Protein sequence  
Protein Accession #: NP\_001035.1

25  
30  
35

```

1 11 21 31 41 51
| | | | |
MSKSKCSVGL MSSVVAPAKE PNAVGPKEVE LILVKEQNGV QLTSSLTINP RQSPVEAQDR 60
ETWKKIDIFL LSVIGFAVDL ANVWRFPYLC YKNGGGAFIV PYLLFMVIAG MPLPYMELAL 120
GQFNREGAAG VKIKCPILKG VGFTVILISL YVGFFYNVII AWALHYLFSS FTTELPHIHC 180
NNSMNSPNCB DAHPGDSGSD SGLNDTFTGT TPAEYFERG VLHLHQSHGI DDLPGRWQL 240
TACLVLVIVL LYFSLWKGVK TSGKVVWITA TMPYVVLTL LRGVTLPGA IDGIRAYLSV 300
DFYRLCEASV WIDAATQVCF SLGVGFGVLI AFSSYNKFTN NCYRDAIVTT SINSLSFSS 360
GFVVFSLFGY MAQKHSVPIG DVAKDGPGLI FIITYEAIAT LPLSSAWAVV PFIMLLTLGI 420
DSAMGGMESV ITGLIDEFQL LHRHRELFLL FIVLATFLLS LFCVTNGGIY VFTLLDHFAA 480
GTSILEFVLI EAIGVAFWYF VQGFSDDIQO MTGQRPSLYW RLCWKLVSPP FLFFVVVSI 540
VTFRPHYGA YIFPDWALAL GWVIATSSMA MVPIYAAKPF CSLPGSFREK LAYAIAPKED 600
RELVDGRGEVR QFTLRHLKLV

```

Seq ID NO: 305 DNA sequence  
Nucleic Acid Accession #: NM\_001216.1  
Coding sequence: 43..1422

45  
50  
55  
60  
65  
70

```

1 11 21 31 41 51
| | | | |
GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 60
AGCCCTCGGC TCCTCTGTGT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCACAGAGT TGGCCCGGAT GCAGGAGGAT 180
TCCCTCTGGG GAGGAGGCTC TTCTGGGAA GATGACCCAC TGGGCGAGGA GSATCTGCCC 240
AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAAGCCAG 420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
CGCCCTTGCC CCGGGGTGTC CCCAGCCTGC GCGGGCGCT TCCAGTCCCC GGTGGATATC 540
CGCCCTGAGC GAGGCGCTTC CTGCCCAGGC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG 600
CTCCCGCCGC TCCAGAACT CGCCTCGGCC AACATGGGCC ACAGTGTGCA ACTGACCCCTG 660
CCTCTGGGCG TAGAGATGGG TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGAGCACA CTGTGGAAGG CCACCGTTTC 780
CCTGCGGAGA TCCAGCTGGT TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCGCTG 840
GGGCGCCCGG GAGGCGCTGC CGTGTGGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
AGTGCCATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
CAGTCTCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC 1080
CAGACAGTGA TGCTGAGTGC TAAAGCAGTC CACACCTCT CTGACACCTT GTGGGGACCT 1140
GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGAGCGAGC CTTTGAATGG GCGAGTGATT 1200
GAGGCTCTCT TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCTCCT TTTTGTCTGC 1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGSTA ACTGTCCTGT CCGTCTCATT 1500
ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT

```

Seq ID NO: 306 Protein sequence  
Protein Accession #: NP\_001207.1

75  
80

```

1 11 21 31 41 51
| | | | |
MAPLCPSFWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPIG GSSSGEDDPL 60
GEEDLPSEED SPREDPPGE EDLPGBEDLP GEEDLPEVKP KSEEGSLKL EDLPTVEAPG 120
DPQEPQNNAR RDKEGDQSH WRYGGDPPWP RVSPACAGRP QSPVDIRPQL AAFCPALRPL 180
ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGRFY RALQLHLHWG AAGRPGESEH 240
VEGHRFPAPL FVVHLSTAFR RVDEALGRPG GLAVLAFLF EGPEENSAYE QLLSRLEBIA 300
EEGSETQVPG LDISALLPSD PSRYPYEGGS LITPPCAQGV IWTVFNQTMV LSAKQLHTLS 360
DTLWGPDSR LQINFRATQP LNRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
GLLFAVTSVA FLVQMRRQHR RGTGKGVSYR PAEVAETGA

```

Seq ID NO: 307 DNA sequence  
Nucleic Acid Accession #: NM\_003039.1  
Coding sequence: 76..1581

```

5      1      11      21      31      41      51
|      |      |      |      |      |
CCTCTCTCTC CATTAGTGC ACACGCTTACT TTGGCTAAAA GGAGGTGAGC GGCACCTCTGC 60
CCTTCCAGAG CAAGCATGGA GCAACAGGAT CAGAGCATGA AGGAAGGGAG GCTGACGCTT 120
GTGCTTGCCC TGGCAACCTT GATAGCTGCC TTTGGGTCAT CCTTCCAGTA TGGGTACAAC 180
10     GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAA TTTACAATGA GACTTACTAT 240
GGTAGGACCG GTGAATTAT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAAACGTG 300
TCCATGTTTC CATTTGGAGG GTTTATCGGA TCCCTCCTGG TCGGCCCTTT GGTGAATAAA 360
TTTGGCAGAA AAGGGGCTT GCTGTTCAAC AACATATTTT CTATCGTGCC TGCATCTTA 420
ATGGGATGCA GCAGAGTCGC CACATCATTT GAGCTTATCA TTATTCCAG ACTTTTGGTG 480
15     GGAATATGTG CAGGTGTATC TTCCAACGTG GTCCCCATGT ACTTAGGGGA GCTGGCCCCCT 540
AAAAACGCTG CGGGGGCTCT CGGGGTGGTG CCCAGCTCT TCATCACTGT TGGCATCCTT 600
GTGGCCAGTA TCTTTGGTCT TCGGAATCTC CTGCAAAACG TAGATGGCTG GCGCATCCTG 660
CTGGGCTGTA CCGGGGTCCC CGGGGGCTG CAGCTCCTTC TGCTGCCCTT CTTCCCGGAG 720
AGCCCCAGGT ACCTGCTGAT TCAGAAGAAA GACGAAGCGG CCGCCAGAA AGCCCTACAG 780
20     ACCTGTCGGG GCTGGGACTC TGTGGACAGG GAGGTGGCGG AGATCCGGCA GGAGGATGAG 840
GCAGAGAAGG CCGCGGGCTT CATCTCGTGT CTGAAGCTGT TCCGGATGCG CTCGCTGCGC 900
TGGCAGCTGC TGTCCATCAT CGTCTCATG GCGGCCAGC AGCTGTGCGG CGTCAACGCT 960
ATCTACTACT ACGGGGACCA GATCTACCTG AGCGCGGGG TGCGGAGGA GCACGTGCAG 1020
TAAGTGACGG CCGGCACCGG GCGCGTGAAC GTGGTCAATG CCTTCTGGC CGTGTTCGTG 1080
25     GTGGAGCTCC TGGGTGGGAG GCTGCTGCTG CTGCTGGGCT TCTCCATCTG CCTCATAGCC 1140
TGCTGGCTGC TCACTGCAGC TCTGGCACTG CAGGACACAG TGTCTGGAT GCCATACATC 1200
AGCATGCTCT GTGTCTCTC CTACGTCTCA GGCATGCCC TCGGGCCAGG TCCCATACCC 1260
CGCTGCTGTA CCGGAGTCTT CTCTCTGAGT TCCTCTCGGC CATCTGCTCT CATGGTGGGG 1320
GGCAGTGTGC ACTGGCTCTC CACTTCCACC GTGGGCTTGA TCTTCCCGTT CATCCAGGAG 1380
30     GGCTCGGGCC GTTACAGCTT CATTTGCTTC GCGGTGATCT GCCTCTCTAC CACCATCTAC 1440
ATCTTCTTGA TTGTCCCGGA GACCAAGGCC AAGACGTTC TAGAGATCAA CCAGATTTTC 1500
ACCAAGATGA ATAAGTGTG TGAAGTGTAC CCGGAAAAGG AGGAAGTCAA AGAGCTTCCA 1560
CCTGTCACTT CGGAACAGT ACTCTGGAGA GGAAGCCAGT GGAGCTGGTC TGCCAGGGGC 1620
TTCCCACTTT GCCTTATTTT TCTGACTTCT AGCTGTCTGT GAATATCCAG AAATAAAACA 1680
35     ACTCTGATGT GGAATGCAGT CCTCATCTCC AGCCTCCCCA CCCCAGTGGG AACTGTGCAA 1740
AGGGCTGGCT TGCTGTCTT GTCTCTCTC CATGTTGGCC CATGTTGGCC TGTCACCAGA 1800
CCCGAGTCAA TTAACAGCTT GGTCTCTCC TTTGCTGGTT CAGCCTTCGT GTGGCTCTCT 1860
GTAACGTGGC TCCACCTTGA TGGGTCAACC TTTGTGTGGC TCTGTGTAAC ATAACAACAA 1920
40     CAGTTACTAT AGTGTGAGA TGAAGGAAT CAAATTTTGC CAGAGAACT AACTCGTGG 1980
CCCCAACAGG TCTTCCGGGG CCATGGGCAT TTGTTTAGAG CCAATTCAT CCTCTTACCA 2040
GATCCTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAAT GACATCCAGA 2100
AAGCTGAGGA ACAGGTTCTT GTGGAGACAC TGAGTCAGAA TTCTTATCC AAATTAATTT 2160
GTTAGTGGA AATGGAATTG CTTCTGTGTA GTCAATAAAA TGAACCTGAT CACTTTTC

```

45 Seq ID NO: 308 Protein sequence  
Protein Accession #: NP\_003030.1

```

50     1      11      21      31      41      51
|      |      |      |      |      |
MEQQDQSMKE GRLTLVLALA TLIAAFSSSP QYGVNVAVN SPALLMQQFY NETYYYRTGE 60
FMEDPPLTLI WSVTVSMPPF GGFISGLLVG PLVNFGRKRG ALLFNNIFSI VPAILMGCSR 120
VATSFELIII SRLVLGICAG VSSNVVPMYL GELAPKLNLRG ALGVVPLQFI TVGILVAQIF 180
GLRNLILANVD GPILLGLTG VPAALQLLL PFPSPRYL LIQKDEAA KKAQLTLRGW 240
55     DSVDRVABEI RQEDAEKAA GFISVLKLER MSLRWQLLS IIVLMGGQQL SGVNAIYYA 300
DQIYLSAGVP EEHVQYVYTAG TGAVNVMVF CAVFVVELLC RRLILLIGFS ICLIACCVLT 360
AALALQDTHS WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFMVGGSVHW 420
LSNFTVGLIF PPIQEGGLPY SFIVFAVICL LTTIYIFLIV PETKAKTPIE INQIPTKMK 480
VSEVYPEKEE LKLEPPVTSE Q

```

60 Seq ID NO: 309 DNA sequence  
Nucleic Acid Accession #: NM\_001252.1  
Coding sequence: 138..719

```

65     1      11      21      31      41      51
|      |      |      |      |      |
GGCTGGTCCC CTGACAGGTT GAAGCAAGTA GACGCCAGG AGCCCCGGA GGGGGCTGCA 60
GTTTCTCTCC TTCTTCTCG GCAGCGCTCC GCGCCCCAT CGCCCCCTCT GCGCTAGCGG 120
AGGTGATGCG CGCGGCGATG CCGGAGGAGG GTTCGGGCTG CTGCGTGCGG CGCAGGCCCT 180
70     ATGGGTGCGT CTTGCGGGCT GCTTTGGTCC CATTTGGTGC GGGCTTGGTG ATCTGCTCG 240
TGGTGTGATC CAGCGCTTC GCACAGGCTC AGCAGCAGCT GCGCTGCGAG TCACTTGGGT 300
GGGACGTAGC TGAGCTGCAG CTGAATCACA CAGGACCTCA GCAGGACCCC AGGCTATACT 360
GGCAGGGGGG CCGCAGCTG GCGCGCTCT TCCTGCTATG ACCAGAGCTG GACAAGGGGC 420
AGCTAGCTAT CATTGTGAT GGCATCTACA TGGTACACAT CCAGGTGAGC CTGGCCATCT 480
75     GCTCCTCCAC GAGCGCTCC AGGCACCACC CCACCACCT GGCCTGGGA ATCTGCTCTC 540
CCGCTTCCCG TAGCATCAGC CTGCTGGTGC TCAGCTTCCA CCAAGTTGT ACCATTGCTT 600
CCGAGCGCTT GAGCGCCCTG GCGCGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC 660
TTTTGCTTTC CCGAAACACT GATGAGACCT TCTTTGGAGT GCAGTGGGTG CGCCCTGAC 720
CACTGCTGCT GATTAGGTTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAAA 780
80     AGTGTACACA CAGGGGCCAC CCGGGTGTGG GGTGGGAGTG TGGTGGGGGG TAGTGGTGGC 840
AGGACAAGAG AAGGCATTGA GCTTTTCTT TCATTTTCTT ATTAATAA

```

Seq ID NO: 310 Protein sequence  
Protein Accession #: NP\_001243.1

1 11 21 31 41 51  
 MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCQR FAQAQQQLPL ESLGWDVAEL 60  
 5 QLNHTGPQD PRLYWQGGPA LGRSFLHGPE LDKGQLRIHR DGIYMVHIQV TLAICSSTTA 120  
 SRHHPTTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLPSRN 180  
 TDETFFGVQW VRP

Seq ID NO: 311 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..3978

1 11 21 31 41 51  
 15 ATGGTGGGTG AAGGACCCTA CCTTATCTCA GATCTGGACC AGGAGGCGCG GCGGAGATCC 60  
 TTTGCAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGGGACC CTGTGCAAGG 120  
 TTAGCACCCA ACCCGGTGGA TGATGCCGGG CTACTCTCCT TCGCCACATT TTCCTGGCTC 180  
 AGCCCGGTGA TGGTGAAAGG CTACCGGCAA AGGCTGACCG TAGACACCCCT GCCCCCATTTG 240  
 TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCTTTTG GGTATGAAGAG 300  
 20 GTAGCAAGGG TGGTCTCTGA GAAGGCCTCT CTGAGCCACG TGGTGTGGAA ATTCCAGAGG 360  
 ACACGGGTGT TCATGGACAT CGTGGCCAAC ATCTGTGCA TCATCATGGC AGCCATAGGG 420  
 COGACAGTTC TCATTACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG 480  
 GTTGGCATTG GACTGTGAT AGCCCTTTT GCCACCGAGT TTACCAAGT CTCTTTTGG 540  
 GCGCTTGCTT GGGCCATCAA CTACCGCAG GCCATCCGCT TGAAGGTGGC GCTCTCCACC 600  
 25 TTGGTTTTTG AAAACCTAGT GTCCTTCAAG ACATTGACCC ACATCTCTGT TGGGAGGTTG 660  
 CTCATATATC TGTCAAGTGA TAGCTATTCT TTGTTTGAAG CTGCTTGTGT TTGCTCTTTG 720  
 CCAGCCACCA TCCCGATCCT AATGGTCTTT TGTGGGGCGT ACGCCCTTTT CATTCTGGGG 780  
 CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCCGTCCA GATGTTTATG 840  
 GCCAAGCTG ACTCAGCTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTTCA 900  
 30 ACAATGAATG AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCCTG GGAGAAATCT 960  
 TTTACCAACA CTATCCAAGC TATAAGAAGG AGGGAAGAA AATTACTGGA AAAAGCTGGA 1020  
 TTTGTCCAAA GTGGAAGTCT TGCCTGTGCC CCCATCGTGT CCACCATAGC CATCGTGTG 1080  
 ACATTATCCT GCCACATCCT CCTGAGACGC AAATCACCAG CACCCGTGGC ATTTAGTGTG 1140  
 ATTGCCATGT TTAATGTAAT GAAGTTTTC ATTGCAATCT TGCCCTTCTC CATCAAGCA 1200  
 35 TTGGCTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAGCCCTC 1260  
 CATCTTACA TCACCAACCC AGAAGACCCA GATAGTGTCT TGCTTTTAGC AAATGCCACC 1320  
 TTGACATGGG AGCATGAAGC CAGCAGGAAA AGTACCCCAA AGAATTGCA GAACAGAAA 1380  
 AGGCATTTAT GCAAGAAACA GAGGTGAGAG GCATACAGTG AGAGGAGTCC ACCAGCCAG 1440  
 GGAGCCATG GCGCTGACGA GCRAAGTGAC AGCCTCAAAT CGGTTCTGCA CAGCATAAGC 1500  
 40 TTTGGGTGAG GAAAGTTATG TCGTTATCCC GAAGCCACAG TCCTGGCTTG GAGGTGGCCA 1560  
 GCAGTGTGTG TTGGGAGAA CATCAGAGGA TACAGGCCTC ATGGATTTTC TGCTAAAGAC 1620  
 AAGGATGAAT CTAGAAGGCT TCTTACTTGG CCCCAAGAAG TGGATAGGAC TCAAGGGCA 1680  
 GCCAATATACC TGGGGAGAT CTGTTGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC 1740  
 GCTCTTGACG CTCTCTTAGG ACAGATGCAG CTGCAGAAAG GGGTGGTGGG AGTCAATGGA 1800  
 45 ACTTTGGCCT ACCTTTTACA GCAGGCATGG ATCTTTTATG GAAATGTGAG AGAAAACATA 1860  
 CTCTTTGAGG AAAAGTATGA TCACCAAAGG TATCAGCACA CAGTCCGCT CTGTGGCCTC 1920  
 CAGAAGGACC TGAGCAACCT CCCCTATGGA GACCTGACTG AGATTGGGGA GCGGGGCTC 1980  
 AACCTCTCTG GGGGGCAGAG GCAGAGGATT AGCCTGGCCC GCGCTGTCTA CTCGACCGT 2040  
 CAGCTCTACC TGCTGTGACGA CCCCTGTCTG GCGCTGGAGC CCCACGTGGG GAAGCAGCTC 2100  
 50 TTTGAGGAGT GCATTAAAGA GAOGCTCAGG GGAAAGACAG TCGTCTGTGT GACCCACAG 2160  
 CTACAGTCTT TACAGTCTTG TGATGAAGTT ATTTATTAG AAGATGGAGA GATTGTGAA 2220  
 AAGGGAACCC ACAAGGAGTT AATGAGGAG AGAGGGGCGT ATGCAAACT GATTCAAC 2280  
 CTGCGAGGAT TGCAAGTTCAA GGATCCTGAA CACCTTTACA ATGCAGCAAT GGTGGAAGCC 2340  
 TTCAAGGAGA GCGCTGCTGA GAGAGAGGAA GATGCTGGA TAATCGGGA CCTCCTTTCT 2400  
 55 CTCTTCACTG TGTTCCTCTT CCTCTGATG ATTGGCAGCG CTGCTTCTAG CAAGTGGTGG 2460  
 CTGGGTCTCT GGTGTGACAA GGGCTCACGG ATGACCTGTG GCGCCACAGG CAACAGGACC 2520  
 ATGTGTGAGG TCGGCGCGGT GCTGGCAGAC ATCGGTGAGC ATGTGTACCA GTGGGTGTAC 2580  
 ACTGCAAGCA TGGTGTTCAT GCTGGTGTGT GCGGTACCA AAGGCTTCGT CTCACCAAG 2640  
 ACCACACTGA TGGATCCTCT CTCTCTGCT GACACGCTGT TTGATAAGAT CTTAAAGAGC 2700  
 60 CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACCGTTT TTCCAAGGAT 2760  
 ATGACGAGC TGGATGTGAG GCTGCCGTTT CACGACAGGA ACTTTCTGCA GCAGTTTTTT 2820  
 ATGGTGGTGT TTAATCTCGT GATCTTGGCT GCTGTGTTTC CTGCTGTCTT TTTAGTCTG 2880  
 GCCAGCCTTG CTGTAGGCTT CTTTATTCTG TTACGATTT TCCACAGAGG AGTCCAGGAG 2940  
 CTCAGAAGG TGGAGAATGT CAGCCGCTCA CCCTGGTTCA CCCACATCAC CTCTCCATG 3000  
 65 CAGGCGCTGG GCATCATTTA CGCCTATGGC AAGAAGGAGA GCTGCATCAC CTATACTTCA 3060  
 TCCAAAGGCC TGTCAATGTC ATACATCATC CAGCTGAGCG GACTGCTCCA AGTGTGTGTG 3120  
 CGAACGGGAA CAGAGACGCA AGCCAAATTC ACCTCGGTGG AGCTGCTCAG GGAATACATT 3180  
 TCGACCTGTG TTCCTGAATG CACTCATCCC CTCAAAGTGG GGACCTGTCC CAAGGACTGG 3240  
 CCCAGCTGTG GGGAGATCAC CTTGAGAGAC TATCAGATGA GATACAGAGA CAACACCCCC 3300  
 70 CTGTCTCTG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTGGA 3360  
 AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTCGTCTGTG GGAGCCAGCC 3420  
 AGTGGCACA TCTTTATTGA TGAGGTGGAT ATCTGCATTC TCAGCTTGA AGACCTCAGA 3480  
 ACCAAGCTGA CTGTGATCCC ACAGATCCT GTCCGTGTTG TAGGTACAGT AAGGTACAAC 3540  
 TTGATCCCT TTGAGAGTCA CACCGATGAG ATGCTCTGGC AGGTTCTGGA GAGAATTC 3600  
 75 ATGAGAGACA CAATAATGAA ACTCCAGAA AAATTACAGG CAGAAGTCAC AGAAAATGGA 3660  
 GAAAATCTCT CAGTAGGGGA AOGTCAGCTG CTTTGTGTGG CCGGAGCTCT TCTCCGTAAT 3720  
 TCAAGATCA TTCTCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGC TGACACCCCTG 3780  
 GTTCAGAAC CAATCAAGA TGCCCTCAAG GGCTGCACTG TGCTGACCAT CGCCACCCG 3840  
 CTCACACAG TTCTCAACTG CGATCAGTCT CTGGTTATGG AAAATGGGAA GGTGATTGAG 3900  
 80 TTTGACAGC CTGAAGTCCT TGCAGAGAAG CCAGATTCTG CATTGCGAT GTTACTAGCA 3960  
 GCAGAAGTCA GATTGTAG

Seq ID NO: 312 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MVGEGPYLIS DLDQGRRRS FAERYDPSLK TMIFVRPCAR LAPNPVDDAG LLSFATFSML 60  
 5 TPVMVGYRQ RLTVDTLPPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVMKFQR 120  
 TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEFTKVFVW 180  
 ALAWAINYRT AIRLKVALLST LVFENLVSPK TLTHISVGEV LNILSSDSYS LFEAALFCPL 240  
 PATIPILMVF CAAYAFPIIG PTALIGISVY VIFIPVQMFM AKLNSAFRRS AILVTDKRVQ 300  
 TMNEFLTICR LIKMYAWEKS FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360  
 10 TLSCHILLRR KLTAFVAFSV IAFNVVMKFS IAILPFSIKA MAEANVLRR MKKILIDKSP 420  
 PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNK RHLCKQKQSE AYSERSPPAK 480  
 GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSAKD 540  
 KDESRLRLTW PQEVDRTORA AKYLKILGI CGNVGSGKSS LLAALLGQMQ LQKGVVAVNG 600  
 TLAYVQQAW IFHGNVRENI LFGEKYDHQR YQHTVRVQGL QKDLNLFPYG DLTEIGERGL 660  
 15 NLSGGQRQRI SLARAVYSR QLYLDDPLS AVDAHVGKHF FECEIKTLR GKTVVVLVTHQ 720  
 LQFLESCDEV ILLEDGEICE KGTHKELMEE RGRYAKLIHN LRGLQFKDPE HLYNAAMVEA 780  
 FKESPAEREE DAGIIGYLLS LFTVFLFLM IGSAAFSNWW LGLWLDKGRS MTCGPQGNRT 840  
 MCEVGAFLAD IGQHVYQWVY TASMVFMVLF GVTGKGFVFTK TTLMASSSLH DTVFDKILKS 900  
 PMEFFDTTPT GLHNRFSKD MDELDRVLPF HAENFLQOFF MVVFLVILA AVFPAVLV 960  
 20 ASLAVGFIL LRIFHRGVE LKVENVSRS PWFTHITSSM QGLGIHAYG KKECITYTS 1020  
 SKGLSLSYII QLSGLLQVCV RTGTETQAKP TSVELLREYI STCVPECTHP LKVGTCPKDW 1080  
 PSCGEITFRD QMRVYRDNTP LVLDLNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140  
 SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTVRYN LDFFESHTDE MLWQVLERTP 1200  
 MRDTIMKLPE KLQAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMSDKTDL 1260  
 25 VQNTIKDAFK GCTVLTIAHR LMTVLNCDHV LVMENGVIE FDKPEVLAEK PDSAFAMLLA 1320  
 AEVRL

Seq ID NO: 313 DNA sequence  
 Nucleic Acid Accession #: Z31560  
 Coding sequence: 1-966

1 11 21 31 41 51  
 CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCGCGG CCGCAGCAA 60  
 35 ACTTCGGGGG GCGGCGGCGG CAACTCCACC GCGGCGGCGG CCGGCGGCAA CCAGAAAAAC 120  
 AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CCGCAGCGG 180  
 CGCAAGATGG CCCAGGAGAA CCCAAGATG CACAACCTCG AGATCAGCAA GCGCCTGGGC 240  
 GCGGAGTGGG AACTTTTGTG GGAGACGGAG AAGCGGCGGT TCATCGACGA GGCTAAGCGG 300  
 CTGCGAGCGC TGCACATGAA GGAGCACCCG GATTATAAAT ACCGGCCCCG GCGGAAAACC 360  
 40 AAGAGCTCTA TGAAGAAGGA TAAGTACACG CTGCGCGCGG GGCTGTGGC CCGCGGCGGC 420  
 AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCGGCGCTGG GCGGCGCGGT GAACAGGCG 480  
 ATGGACAGTT ACGCGCACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC 540  
 CAGCTGGGCT ACCCGCAGCA CCGGGGCTCT AATGCGCAGC GCGCAGCGCA GATGCAGCCC 600  
 ATGCACCGCT ACGACGTGAG CGCCCTGCAG TACAACCTCA TGACAGCTC GCAGACCTAC 660  
 45 ATGAACGCGT CGCCACCTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT 720  
 CTGGGTCCA TGGGTTCGGT GGTCAAGTCC GAGGCGAGCT CCAGCCCCC TGTGGTTACC 780  
 TCTTCTCTCC ACTCCAGGCG GCGCTGCCAG GCGGCGGACC TCGGGGACAT GATCAGCATG 840  
 TATCTCCCCG GCGCGGAGGT GCGGGAACCC GCGGCCCCCA GCAGACTTCA CATGTCCAG 900  
 CACTACCAAG GCGGCGCGGT GCGGCGCAGC GCCATTAAAG GCACACTGCC CCTCTCAC 960  
 50 ATGTAGGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAGAAAAA ACGAGGGAAA 1020  
 TGGGAGGGGT GCAAAGAGG AGAGTAAGAA ACAGCATGGA GAAACCCCG TACGCTCAA 1080  
 AAAAA

Seq ID NO: 314 Protein sequence  
 Protein Accession #: CAA83435

1 11 21 31 41 51  
 HSARMYNMME TELKPPGPQQ TSGGGGNST AAAAGGNQKN SPDRVKRPMN AFMVNSRQR 60  
 60 RQMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKHP DYKVRPRKT 120  
 KTLMKDKYT LPPGILLAPG NSMASGVGVG AGLGAGVNR MDSYAHMNGW SNGSYMMQD 180  
 QLGYPPHPL NAHGAQMOP MHRVDVSALQ YNSMTSSQTY MNGSPYMS YSQQTPGMA 240  
 LSGMSVVK SSSSPFPVT SSSHSRAPC AGDLRDMISM YLPGAEPPEP AAPSRHMSQ 300  
 HYQSGVPVGT AINGTLPLSH M

Seq ID NO: 315 DNA sequence  
 Nucleic Acid Accession #: U91618  
 Coding sequence: 29..541

1 11 21 31 41 51  
 CGGACTTGGC TTGTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAATCC AGCTTGTATG 60  
 70 CATGCTACTC CTGGCTTTCA GCTCTCGGAG TCTGTGCTCA GATTGAGAAG AGGAAATGAA 120  
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180  
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGAGTCTT GTAAATAATT TGAACAGCCC 240  
 75 AGCTGAGGAA ACAGAGAGA TTTATGAAGA GGAGCTTGT GCAAGAAGGA AACTTCTAC 300  
 TGCTTAGAT GGTCTTAGCT TGAAGCAAT GTTGACATA TACCAGCTCC ACAAAATCTG 360  
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420  
 TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACGGCA 480  
 80 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540  
 AGAGAATAAA TCATTTATTT ACATGTGATT GTGATTATC ATCCCTTAT TAAATATCAA 600  
 ATTATATTG TGTGAAAAAT TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTT 660  
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA 720  
 TCTTCAAAAA AAAAAAATAA AATGGGGGCC GCAATT

Seq ID NO: 316 Protein sequence  
Protein Accession #: AAB50564

5 1 11 21 31 41 51  
MMAGMKIQLV CMLLLAPSSW SLCSDESEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60  
VCSLVNNLNS PAETGEVHE EELVARRKLP TALDGFSLA MLTIYQLHKI CHSRAFQHWE 120  
LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY

10 Seq ID NO: 317 DNA sequence  
Nucleic Acid Accession #: NM\_006536.2  
Coding sequence: 109..2940

15 1 11 21 31 41 51  
ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60  
ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120  
AGCATTCGAG GTCCCTATTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180  
20 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240  
ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAACAT TAAGGAAATG 300  
ATAACTGAAG CTTCAATTTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAAGAAAT 360  
ATAAAGATT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420  
TCATATGAAA AGGCAAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480  
TACACCTTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAAT ACATTTCATT CACACCTAAT 540  
25 TTCTACTGTA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCGGAGT GTTTGTCCAT 600  
GAATGGGCC ACCTCGTTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTTCTAC 660  
ATAAATGGGC AAAATCAAT TAAAGTGACA AGGTGTTTCT CTGACATCAC AGGCATTTT 720  
GTGTGTGAAA AAGGTCCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780  
GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840  
30 AGTTTATCTT CTGTGGTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900  
CTACAGAAC AGATGTGCAG CCTCAGAAAT GCATGGGATG TAATCACAGA CTCTGCTGAC 960  
TTTCACCACA GCTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCCCAAC ATTCTCGCTT 1020  
GTACAGGCTG GTGACAAAGT GGTCTGTGTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080  
GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTGTAA 1140  
35 ATTCATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAGG GAGAGATCAG AGCCACAGTA 1200  
CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCATCTGA 1260  
TCAGCTAAAA CAGACATCAG CATTTGTTC GGGCTTAAGA AAGGATTGGA GGTGGTTGAA 1320  
AAACTGAATG GAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAAGCG AGATGATAAG 1380  
40 CTTCTTGGCA ATGTCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440  
CTGGGTTTCT CTGACGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500  
TTCTTTGTTC CAGATATATC AAACCTCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560  
TCTGGAAGCT GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAGATGTC 1620  
AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680  
45 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTAT TATCTCTGAT 1740  
GGACGAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTGGGAC AGCTAGTCTT 1800  
TGGATTCCAG GAATGAGTAA CCGTGGGCAC TGGACTTACA CCGTGAACAA TACCCATCAT 1860  
TCTCTGCAAG CCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA 1920  
GCCACTGTGG AAGCCTTTGT GGAAGAGAGC AGCCTCCATT TTCCTCATCC TGTGATGATT 1980  
50 TATGCCAATG TGAACAGGG ATTTTATCCC ATTCCTAATG CCACTGTCAC TGCCACAGTT 2040  
GAGCCAGAGA CTGGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100  
GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTCTCT CCITTGCTGC AAATGGTAGA 2160  
TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCAGC CCACTCTATT 2220  
CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280  
55 GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGCTT TAGCCGAGTC 2340  
AGCTCAGGAG GCTCCTTTTC AGTGTGGGA GTTCCAGCTG GCCCCACCC TGAATGTGTT 2400  
CCACCATGCA AATATTATGA CCTGGAAGCT GTAAAGTAG AAGAGGAATT GACCCTATCT 2460  
TGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520  
AGTAAAGTTC TACAGATAT CCAAGATGAC TTTAACAATG CTAATTTAGT AAATACATCA 2580  
60 AAGCGAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTCTCACC CCAATTTCC 2640  
ACGAATGGAC CTGACATCA GCCAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700  
GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAATAT TGCCAGGCG 2760  
CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820  
GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTGCTC TTATTATAGT TGTGACACAT 2880  
65 CATACITTA GCAGGAAAAA GAGAGCAGAC AAGAAGAGA ATGGAACAAA ATTATTATAA 2940  
ATAAATATCC AAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000  
CATACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTACA 3060  
ATACAGATAA GATTTTACA TGGTAGATCA ACAATTCTTT TTGGGGGTAG ATTAGAAAAA 3120  
CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAGTAAT GTCTTTAAAG 3180  
70 GCAAGGGGAA GGTAAAGTC GGACCAAGT CAAGGAAAGT TTGTTTATT GAGGTGGAAA 3240  
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA 3300  
TCATTTAGTT ACTTTGATTA ATTTTCTTT TCTCTTATC TGTGCACTAG AGGTGCTTG 3360  
TTTACATGAA GATCATGCTA TATTTATAT ATGTAGCCCC TAATGCAAG CTCTTACCT 3420  
CTTGCTATTT TGTATATAT ATTTAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480  
75 TTTCACTGTA AGAGGTAAAC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540  
TTTATGACAA AGGTCTATTG AATTTATTG TNGTAAGTT TCTACTCCCA TCAAAGCAGC 3600  
TTTCTAAGTT TATGCTCTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660  
TACCTAGGAA A

80 Seq ID NO: 318 Protein sequence  
Protein Accession #: NP\_006527.1

1 11 21 31 41 51  
MTQRSIAGPI CNLKFVTLIV ALSSELPLFG AGVQLQDNQY NGLLIAINPO VPENQNLSN 60



	IKEMITEASF	YLFNATKRRV	FFRNIKILIP	ATWKANNNSK	IKQESYEKAN	VIVTDWYGAH	120
	GDDPYTLQYR	GCGKEGKYIH	FTPNFLNDN	LTAGYGSRRG	VVFVHEWAHLR	WGVFDEYNND	180
	KPFYINGQNK	IKVTRCSSDI	TGIFVCEKGP	CPQENCIIISK	LFKEGCTFIY	NSTQNATASI	240
5	MFMSQLSSVV	EFCNASTHNQ	EAPNLQNMCM	SLRSAMDVIT	DSADFHSFSP	MNGTELPPPP	300
	TFSLVQAGDK	VVCLVLDVSS	KMAEADRLQ	LQQAEEFYLM	QIVEIHTFVG	IASFDSKGEI	360
	RAQLHQINSN	DDRKLVLVSYL	PTTVSAKTDI	SICSGLKKGK	EVVEKLNGKA	YGSVMILVTS	420
	GDDKLGNLCL	PTVLSSGSTI	HSIALGSSAA	PNLEELSLRT	GGLKFPVPDI	SNSNSMIDAF	480
	SRISSTGDI	FQHQIQLEST	GENVKPHQL	KNTVTVDNTV	GNDTMFLVTW	QASGPPEIIL	540
10	FDPDGRKYIT	NNFITNLTPR	TASLWIPSTA	KPGHWITLNL	NTHHSLOALK	VTVTSRASNS	600
	AVPPATVEAF	VERDSLHFPH	PVMIIANVKQ	GFYPILNATV	TATVEPETGD	PVTLRLDDG	660
	AGADVINKDG	IYSRYPFSFA	ANGRYSLKVH	VNHSPSISTP	AHSIPGSHAM	YVPGYTANGN	720
	IQMNAPRKSV	GRNEEERKMG	FSRVSSGGSF	SVLGVPAPGH	PDVFPCKII	DLEAVKVEEE	780
15	LTLSTWAPGE	DFDQGGATSY	EIRMSKSLQN	IQDDFNNAIL	VNTSKRNPQQ	AGIREIPTFS	840
	PQISTNGPEH	QPNGETHESH	RIYVAIRAMD	RNSLQSAVSN	IAQAPLPIPP	NSDPVPARDY	900
	LILKGVLTAM	GLIGITCLII	VVTHHTLSRK	KRADKKENGT	KLL		
	Seq ID NO: 319 DNA sequence						
	Nucleic Acid Accession #: NM_000228.1						
	Coding sequence: 82..3600						
20	1	11	21	31	41	51	
	GCTTTCAGGC	GATCTGGAGA	AAGAACGGCA	GAACACACAG	CAAGGAAAGG	TCCTTCTCGG	60
25	GGATCACCCC	ATTGGCTGAA	GATGAGACCA	TTCTTCCTCT	TGTGTTTTCG	CCTGCTCGGC	120
	CTCTCGCATG	CCCAACAAGC	CTGCTCCCGT	GGGGCCTGCT	ATCCACCTGT	TGGGGACCTG	180
	CTTGTGGGA	GGACCCCGGT	TCTCOGAGCT	TCATCTACCT	GTGACTGAC	CAAGCCTGAG	240
	ACCTACTGCA	CCAGTAGTGG	CGAGTGGCAG	ATGAAATGCT	GCAAGTGTGA	CTCCAGGCAG	300
	CCTCACAACT	ACTACAGTCA	CCGAGTAGAG	AATGTGGCTT	CATCCTCGCG	CCCCATGCGC	360
30	TGGTGGCAGT	CCCAGAATGA	TGTGAACCTT	GTCTCTCTGC	AGCTGGACCT	GGACAGGAGA	420
	TTTCAGCTTC	AAGAAGTCAT	GATGGAGTTC	CAGGGGCCCA	TGCCCCCGCG	CATGCTGATT	480
	GAGCGCTCCT	CAGACTTCGG	TAAGACCTGG	CGAGTGTACC	AGTACTCTGC	TGCCGACTGC	540
	ACCTCCACTT	TCCCTCGGGT	CGCCGAGGGT	CGGCCCTCAG	GCTGGCAGGA	TGTTCTGGTC	600
	CAGTCCCTGC	CTCAGAGGCC	TAATGCACGC	CTAAATGGGG	GGAAGGTCCA	ACTTAACCTT	660
35	ATGGATTAG	TGTCTGGGAT	TCCAGCAACT	CAAAGTCAAA	AAATTCAAGA	GSTGGGGGAG	720
	ATCACAAACT	TGAGAGTCAA	TTTCAACAGG	CTGGCCCTCT	TGCCCCAAAG	GGGCTACCCAC	780
	CCTCCCAAGC	CGACTATGCG	TGTGTCCAG	CTCCGTCTGC	AGGGGAGCTG	CTTCTGTAC	840
	GGCCATGCTG	ATGCGTGC	ACCCAGCCT	GGGGCCTCTG	CAGGCCCTTC	CACCGCTGTG	900
	CAGGTCCACG	ATGCTGTGTG	CTGCCAGCAC	AACACTGCCG	GCCCAAAATG	TGAGCGCTGT	960
40	GCACCTTCT	ACAACAACCG	GCCTTGAGAG	CCGGCCGAGG	GCCAGGACGC	CCATGAATGC	1020
	CAAAGGTGGC	ACTGCAATGG	GCACTCAGAG	ACATGTCACT	TTGACCCCGC	TGTGTTTGCC	1080
	GCAGCCAGG	GGGCATATGG	AGGTGTGTGT	GACAATTGCC	GGGACACAC	CGAAGGCAAG	1140
	AACTGTGAGC	GGTGTGAGCT	GCACTATTTC	CGGAACCGGC	CGCCGGGAGC	TTCCATTTCAG	1200
	GAGACCTGCG	TCTCCTGCGA	GTGTGATCCG	GATGGGGCAG	TGCCAGGGGC	TCCCTGTGAC	1260
45	CCAGTGACCG	GGCAGTGTGT	GTGCAAGGAG	CATGTGCAGG	GAGAGGCGCT	TGACCTATGC	1320
	AAGCCGGGCT	TCAGTGGACT	CACCTACGCC	AACCCGAGG	GCTGCCACCG	CTGTGACTGC	1380
	AACATCTCGG	GGTCCCGGAG	GGACATGCCG	TGTGACGAGG	AGAGTGGCGC	CTGCCTTTGT	1440
	CTGCCCAAGC	TGTGGGTGCC	CAAAATGTAC	CAGTGTGCTC	CCTACCACTG	GAAGCTGGCC	1500
	AGTGCCACG	GCTGTGAAC	GTGTGCTGCG	GACCCGCACA	ACTCCCTCA	GCCCAAGTGC	1560
50	CAACCACTTC	ACAGGGCAGT	GCCTGTGCGG	GAAGGCTTTG	GTGGCCTGAT	GTGCAGCGCT	1620
	GCAGCCATTC	GCCAGTGTCC	AGACCGGACC	TATGGAGAGC	TGGCCACAGG	ATGCCGAGCC	1680
	TGTGACTTGC	ATTTCGGGGG	AACAGAGGGC	CCGGGCTGCG	ACAAGGCATC	AGGCCTGTGC	1740
	CTCTGCCGCC	CTGGCTTGAC	CGGGCCCCGC	TGTGACCACT	GCCAGCGAGG	CTACTGCAAT	1800
	CGCTACCGCG	TGTGCGTGGC	CTGCCACCTT	TGCTTCAGAG	CCTATGATGC	GGACCTCCGG	1860
55	GAGCAGGCCC	TGCGCTTTGG	TAGACTCCGC	AATGCCACCG	CCAGCCTGTG	GTGAGGCGCT	1920
	GGGCTGGAGG	ACCGTGGGCT	GGCTCCCGG	ATCCTAGATG	CAAAGAGTAA	GATTGAGCAG	1980
	ATCCAGCTCG	TTCTCAGCAG	CCCGCAGTGC	ACAGAGCAGG	AGGTGGCTCA	GSTGGCCAGT	2040
	GCCATCCTCT	CCCTCAGGGG	AACTCTCCAG	GGCCTGCAGC	TGGATCTGCC	CCTGGAGGAG	2100
	GAGAGCTGTG	CCCTCCGAGT	AGACCTGGAG	AGTCTTGACA	GAAGCTTCAA	TGCTCTCCTT	2160
60	ACTATGTATC	AGAGGAAGAG	GGAGCAGTTT	GAATAAATAA	GCAGTGTCTA	TCCTTCAGGA	2220
	GCCTTCCGGA	TGCTGAGCAC	AGCCTACGAG	CAGTCAGCCC	AGGCTGCTCA	GCAGGTCTCC	2280
	GACAGCTCGC	GCCTTTTGA	CCAGCTCAGG	GACAGCCGGA	GAGAGGCAGA	GAGGCTGGTG	2340
	CGCAGGCGCG	GAGGAGGAGG	AGGCACCGGC	AGCCCCAAGC	TTGTGGCCCT	GAGGCTGGAG	2400
	ATGTCTTCGT	TGCTTGACCT	GACACCCACC	TTCAACAAGC	TCTGTGGCAA	CTCCAGGCAG	2460
65	ATGGCTTGCA	CCCCAATATC	ATGCCCTGGT	GAGCTATGTC	CCCAAGACAA	TGGCAGAGCC	2520
	TGTGGCTCCC	GCTGACGGGG	TGTCTTCCC	AGGCGCGGTG	GGGCTTCTT	GATGGCGGGG	2580
	CAGGTGGCTG	AGCAGCTGCG	GGGCTTCAAT	GCCCAGCTCC	AGCGGACCAG	GCAGATGATT	2640
	AGGGCAGCCG	AGGAATCTGC	CTCACAGATT	CAATCCAGTG	CCCAGCGCTT	GGAGACCCAG	2700
70	GTGAGCGCCA	GCCGCTCCCA	GATGGAGGAA	GATGTGAGAC	GCACACGGCT	CCTAATCCAG	2760
	CAGGTCCGGG	ACTTCCCTAAC	AGACCCCGAC	ACTGATGCAG	CCAATATCCA	GGAGGTGAGC	2820
	GAGGCGGTGC	TGGCCCTGTG	GCTGCCACCA	GACTCAGCTA	CTGTTCTGCA	GAAGATGAAT	2880
	GAGATCCAGG	CCATTGACAG	CAGGCTCCCC	AACGTGGAGT	TGTTGCTGTC	CCAGACCAAG	2940
	CAGGACATTG	CGCGTGGCGG	CCGGTTGCAG	GCTGAGGCTG	AGGAAGCCAG	GAGCCGAGCC	3000
	CATGCACTGG	AGGGCCAGGT	GGAAGATGTG	GTTGGGAACC	TGCGGCAGGG	GACAGTGGCA	3060
75	CTGCAGGAAG	CTCAGGACAC	CATGCAAGGC	ACCAGCGGCT	CCCTTCGGCT	TATCCAGGAC	3120
	AGGGTGTGCT	AGGTTTCAGCA	GGTACTGCGG	CCAGCAGAAA	AGCTGGTGAC	AAGCATGACC	3180
	AAGCAGCTGG	GTGACTTCTG	GACACGGATG	GAGGAGCTCC	GCCACCAAGC	CCGGCAGCAG	3240
	GGGCGAGAGG	CAGTCCAGGC	CCAGCAGCTT	GCGGAAGGTG	CCAGCGAGCA	GGCATTGAGT	3300
80	GCCCAAGAGG	GATTTGAGAG	AATAAAACAA	AAGTATGCTG	AGTTGAAGGA	CCGGTTGGGT	3360
	CAGAGTTCCA	TGCTGGGTGA	GCAGGCTGCC	CGGATCCAGA	GTGTGAAGAC	AGAGGCGAGG	3420
	GAGCTGTTTG	GGGAGACCAT	GGAGATGATG	GACAGGATGA	AAGACATGGA	GTTGGAGCTG	3480
	CTGCGGGGCA	GCCAGGCCAT	CATGCTGCGC	TGCGCGGACC	TGACAGGACT	GGAGAAGCGT	3540
	GTGGAGCAGA	TCGGTGAACA	CATCAATGGG	CGCGTGTCTT	ACTATGCCAC	CTGCAAGTGA	3600
	TGCTACAGT	TCCAGCCCGT	TGCCCACTCT	ATCTGCGGCC	TTTGCTTTTG	GTTGGGGGCA	3660
	GATTGGGTTG	GAATGCTTTC	CATCTCCAGG	AGACTTTCAT	GCAGCTTAAA	GTACAGCCTG	3720

5 GACCACCCCT GGTGTGTAGC TAGTAAGATT ACCCTGAGCT GCAGCTGAGC CTGAGCCAAT 3780  
 GGGACAGTTA CACTTGACAG ACAGAGATGG TGGAGATTGG CATGCCATTG AACTAAGAG 3840  
 CTCTCAAGTC AAGGAAGCTG GGCTGGGCAG TATCCCCGC CTTTAGTTCT CCACTGGGGA 3900  
 GGAATCTCG ACCAAGCACA AAAACTTAAC AAAAGTGATG TAAAAATGAA AAGCCAAATA 3960  
 AAAATCTTG G

Seq ID NO: 320 Protein sequence  
 Protein Accession #: NP\_000219.1

10 1 11 21 31 41 51  
 MRPFLLCFA LPGLLHAQQA CSRGACYPPV GDLLVGRTRF LRASSTCGLT KPETYCTQYG 60  
 EQQMKCKCD SRQPHNYSH RVENVASSG PMRWWSQND VNPVSLQLDL DRRFQLQEVN 120  
 15 MEFGQPMFAG MLIERSSDFG KTRVYQYLA ADCTSTFPRV RQGRPSQSWD VRCQSLPQRP 180  
 NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240  
 VSQRLRQSGC FCHGHADCA PKPGASAGPS TAVQVHDCV CQHNTAGPNC ERCAFPYNNR 300  
 PWRPAEGQDA HECQCDNCG HSETCHFDPA VFAASQAYG GVCNDCRDHT EGNKNCERQCL 360  
 HYFRNRFPQA SIQETCISCE CDFDGAFFGA FCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420  
 20 TYANPQGGHR CDCNLSRRR DMPDEESGR CLCLPNVVGK KCDQCAPYHW KLASGGQCEP 480  
 CACDPHNSPQ FTVQPVHRAV PCREGEFGLM CSAAAIRQCP DRTYGDVATG CRACDCDFRG 540  
 TEGPGCDKAS GRCLCRPGLT GPRCDQCRG YCNRPVPCVA CHPCFQTYDA DLREQALRFG 600  
 RLNRNATSLW SGPGLDRGL ASRILDAKSK IEQIRAVLSS PAVTEQEVQA VASAILSLRR 660  
 TLQGLQLDLP LEEETLSLPR DLESILDRSFN GLLTMYQKRK EQFEKISSAD PSGAFRMLST 720  
 25 AYEQSAQAQ QVSDSSRLD QLRDSRREAE RLVRQAGGGG GTGSPKLVAL RLEMSLPLD 780  
 TPTFNKLCGN SRQMACTPIS CPGLCPQDN GTACGSRCRG VLRAGGAFV MAGQVAEQLR 840  
 GFMAQLQRT RQIRAAEESA SIQSSAQRL ETQVSASRSQ MEEDVRRTRL LIQVQVDFLT 900  
 DPDTAAATIQ EVSEAVLAW LPTDSATVQ KMNEIQIAA RLPNVDLVLS QTKQDIARAR 960  
 RLQAEAEAR SRAHAEVGGQ EDVVGRLRQ TVALQEAQDT MQGTSRLRL IQDRVAEVQO 1020  
 30 VLRPAEKLV SMTKQIGDFW TRMEELRHOA RQQAEGAVQA QQLAEGASEQ ALSAQEGFER 1080  
 IKQKYAELKD RLQSSMLGE QGARIQSVKT EABELFGETM EMDRMKDMB LELLRGSQAI 1140  
 MLRSADLTGL EKRVEQIRDH INGRVLYYAT CK

Seq ID NO: 321 DNA sequence  
 Nucleic Acid Accession #: NM\_001944.1  
 Coding sequence: 84..3083

35 1 11 21 31 41 51  
 40 TTTCTTAGA CATTAACTGC AGACGGCTGG CAGGATAGAA GCAGCGGCTC ACTTGGACTT 60  
 TTTCCACAGG GAAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG 120  
 CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAATTGCG AATAGAGACT AAAGGTCAAT 180  
 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAGAAGAG GCAAAAACGT GAATGGGTGA 240  
 AATTTCCTCA ACCCTGCAGA GAAGGAGAAG ATAACCTCAA AAGAAACCCA ATTGCCAAGA 300  
 45 TTACTCTAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360  
 ATCAGCCGCC TTTTGGAAATC TTTGTGTGTG ACAAAAACAC TGGAGATATT AACATAACAG 420  
 CTATAGTCGA CGGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTCGGGCT CTAATGCCCC 480  
 AAGGACTAGA TGTAGAGAAA CCACCTATAC TAACGGTTAA AATTTTGGAT ATTAATGATA 540  
 ATCTCTCAGT ATTTTACAAA CAAATTTTCA TGGGTGAAAT TGAAGAAAAT AGTGCCCTCA 600  
 50 ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACCCAC TTGAATTCTA 660  
 AAATTGCGTT CAAATTTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCCTAAGCA 720  
 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTCTCTTGA CCGAGAGCAA GCTAGCAGCT 780  
 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT 840  
 GTAATATTAA AGTGAAGAGT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900  
 55 CAGCACTGAT TGAAGAAAAT ATTTTAAGTT CTGAATTACT TCGATTTCAA GTAACAGATT 960  
 TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGGAAATGAAG 1020  
 GAAATTGGTT TGAATACAA ACTGATCCTA GAACATAATG AGGCATCCTG AAAGTGGTGA 1080  
 AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAACCTTAG TATTGCTGTC AAAAACAAG 1140  
 CTGAATTTC AACTTCAGTT ATCTCTCGAT ACGAGTTCA GTCAACCCCA GTCAACATTC 1200  
 60 AGGTAATAAA TGTAGAGAA GGAATTGCAT TCGTCTCTG TTCCAAGACA TTTACTGTGC 1260  
 AAAAAAGCAT AAGTAGCAAA AAATTGGTGG ATTATATCCT GGGAAACATAT CAAGCCATCG 1320  
 ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAAAATATG CATGGGACGT AACGATGGTG 1380  
 GATACCTAAT GATTGATTCA AAAACTGCTG AAATCAAAAT TGTCAAAAT ATGAACCGAG 1440  
 ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500  
 65 CGGTAATAAC TTCTACAGGC ACGGTATATG TTAGAGTACC CGATTTCAT GACAATTGTC 1560  
 CAACAGCTGT CCTCGAAAAA GATGAGTTT GCAGTTCTTC ACCTTCCGTG GTTGTCTCCG 1620  
 CTAGAACACT GAATAATAGA TACACTGSCC CCTATACATT TGCACTGGAA GATCAACCTG 1680  
 TAAAGTTGCC TGCCGTATGG AGTATCACAA CCCTCAATGC TACCTCGGCC CTCCTCAGAG 1740  
 70 CCCAGGAACA GATACCTCTC GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA 1800  
 ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT CTGTGAGTGT GACAACAGGG 1860  
 GCATCTGTGG AACTCTCTAC CCAACCAAA GGCCTGGGAC CAGTATGGC AGGCCGCACT 1920  
 CAGGAGGCT GGGGCTGCCC GCCATGCGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT 1980  
 TGGCCCCCTT TCTGCTGTTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040  
 75 TGGTCTTTAT CCACTTCTCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100  
 GAGCCCATCC TGAGACAAG GAAATCACAA ATATTGTGT GCTCTCTGTA ACAGCCAATG 2160  
 GAGCCGATTT CATGGAAGT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCG 2220  
 TGGAGGACAC TTCAGGAATG GAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 2280  
 GTGCTGACAG CTTTGCAACA GGGCAGGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340  
 80 CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAACCAT GAGAACAAGG CATTCCACTG 2400  
 GAGGAACCAA TAAGACTACG GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT 2460  
 TTTCTCAGAA AGCTTTGACC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520  
 TGTGATCTTA TGATAATGAA GGCGCAGATG CCACTGCTTC TCCTGTGGGC TCGTGGGTT 2580  
 GTTGCAATTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640  
 TTAATAAATG TGCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAAAGG GTTCAGCCAC 2700  
 CCTCTAAGA CAGCGTTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA 2760

5  
10  
CAGGATTGTG TAAGTGCCAG ACTTTGTGAG GAAGTCAAGG AGCTTCTGCT TTGTCCGCCT 2820  
CTGGGTCTGT CCAGCCAGCT GTTTCATCC CTGACCCTCT GCAGCATGCT AACTATTAG 2880  
TAACGGAGAC TTACTCGGT TCTGGTTCCC TCGTGCAACC TTCCACTGCA GGCTTTGATC 2940  
CACTTCTCAC ACAAATGTG ATAGTGACAG AAAGGTGAT CTGTCCATT TCCAGTGTT 3000  
CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAG 3060  
ATCCTTGCTC CCGTCTAATA TGACCAGAAAT GAGCTGGAAT ACCACACTGA CCAAATCTGG 3120  
ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATAATT 3180  
TGCCACTTAT TAGCTTCTCT CATAAACTGA TCACGATTAT AAATTAATG TTTGGGTTC 3240  
TACCCCAAAA GCAATATGTT GTCATCTCTA ATTCTCAAGT ACTATTCAA TTTAGTATA 3300  
TCTTAAAGTT TTCAAAACC CTAATATCAT ATTCCG

Seq ID NO: 322 Protein sequence  
Protein Accession #: NP\_001935.1

15  
20  
25  
30  
35  
MMGLPFRITG ALAIFVWVIL VHGLRIETK GQYDEEEMTN QQAKRRQKRE WVKFAKPCRE 60  
GEDNSKRNPFI AKITSDYQAT QKITRISGV GIDQPPFGIF VVDKNTGDIN ITAIVDREET 120  
PSFLITCRAL NAQGLDVEKP LILTVKILDI NDNPPVPFSQQ IFMGEIEENS ASNSLVMILN 180  
ATDADEPNHL NSKIAFKIVS QEPAGTFMFL LSRNTGEVRT LTNSLDREQA SSYRLVVSQA 240  
DKDGBGLSTQ CECNIVKIDV NDNFPMFRDS QYSARIEENI LSSELLRFQV TDLDEEYTDN 300  
WLAVYEFTSG NEGNWFEIQT DPRTNESILK VVKALDYEQL QSVKLSIAVK NKAEPHQSVI 360  
SRYRVQSTPV TIQVINVRER IAFRPASKTF TVQKGISSKK LVDYILGTQY AIDEDTNKAA 420  
SNVKYVMGRN DGGYLMIDSK TAEIKFVKNM NRDSTFIVNK TITAEVLAI D EYTGKTSTGT 480  
VYVRVPDFND NCPTAVLEKD AVCSSSPSVV VSARTLNNRY TGPYTFALD QPVKLPAVWS 540  
ITTLNATSLA LRAQEGIPPG VYHISLVLT D SQNRCMPR SLTLEVQCQD NRGICGTSYP 600  
TTSFGTRYGR PHSGRLGPA IGLLLGLLLL LLLAPLLELT CDCGAGSTGG VTGGFIPVPD 660  
GSEGTIHQNG IEGAHPEDE ITNVCVPPVT ANGADFMESSE EVCNTYARG TAVEGTSQME 720  
MTTKLGAATE SGGAGFATG TVSGAASGFG AATGVGICSS GQSGTMRTRH STGGINKDYA 780  
DGAISMFLND SYFSQKAFAC AEEDDGGQAN DCLLIYDNAG ADATGSPVGS VGCCSFIADD 840  
LDDSFLLDSLQ PKFKKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPLEV QQTGFVKCQT 900  
LSGSQASAL SASGSVQPAV SIPDPLQHG N YLVTETYSAS GSLVQPSTAG FDLPLTQNYI 960  
VTERVICPIS SVPGNLAGPT QLRGSHMLC TEDPCSRLI

35  
Seq ID NO: 323 DNA sequence  
Nucleic Acid Accession #: XM\_058069.2  
Coding sequence: 1..1413

40  
45  
50  
55  
60  
65  
ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCTGAAC 60  
AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATT 120  
TATGCGCTTG AGATAAACAA ACTTCCAGTG ACAAATGA ATATAGTGG AAACCTAATG 180  
AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTAGCCGG GCACTGGAC 240  
ACATCTACCC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCCGATGT CCATCATTT 300  
AGGGAATGCG CAGSGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360  
TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAGC TTTCCAAGTA 420  
TGGAGTAATG TTACCCCTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTG 480  
GTGGTTTGTG CCGGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540  
CTAGCCCATG CTTTTGGACC TGGATCTGGC ATTTGGAGGGG ATGCACATT CCATGAGGAC 600  
GAATTCCTGA CATACATTG AGGAGGCACA AACTTGTTC TCACTGCTGT TCACGAGAT 660  
GGCCATTCTT TAGGTCTTGG CCATCTAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC 720  
AAATATGTTG ACATCAACAC ATTTCGCTC TCTGCTGATG ACATACGTGG CATTCACTCC 780  
CTGTATGGAG ACCCAAAGA GAACCAACGC TTGCCAAATC CTGACATTC AGAACAGCT 840  
CTCTGTGACC CCAATTGAG TTTTGTGCT GTCACTACCG TGGGAATTA GATCTTTTTC 900  
TTCAAGACA GOTTCTCTG GCTGAAGGT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960  
ATTTCTTCTT TATGGCCAAC CTTCGCCATC GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020  
AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080  
GAGCCAAAT ATCCCAAGAG CATACATTCT TTTGGTTTTC CTAACCTTGT GAAAAAATT 1140  
GATGCAGCTG TTTTAAACC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACAGTAT 1200  
TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCTGGTT ATCCCAACT GATTACCAAG 1260  
AATCTCAAG GAATCGGGCC TAAATTTGAT GCAGTCTTCT ACTCTAAAA CAAATCTAC 1320  
TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAAAG TATCACCAAA 1380  
ACACTGAAAA GCAATAGCTG GTTTGGTTGT TGA

Seq ID NO: 324 Protein sequence  
Protein Accession #: P39900

70  
75  
80  
MKFLILLILQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60  
KEKIQEMQHF LGLKVTQQLD TSTLEMMHAP RGVDPDVHFP REMPGGPVWR KHYITYRINN 120  
YTPDMNREOV DYAIRKAFQV WSNVTPKFS KINTGMADIL VVFARGAGD FHAFDGKGGI 180  
LAHAFPGPGSG IGDHAHDED EFWTHSGGT NLFLTAVHEI GHSGLGHSS DPKAVMPTY 240  
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300  
FKDRFPWLK SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360  
EFNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420  
NFQGIQPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC

Seq ID NO: 325 DNA sequence  
Nucleic Acid Accession #: NM\_024423.1  
Coding sequence: 64..2590

1 11 21 31 41 51

	GGCAGGTCTC	GCTCTCGGCA	CCCTCCCGGC	GCCCAGCTTC	TCCTGGCCCT	GCCCCGATC	60
	CCGATGGCCG	CCGCTGGGCC	CCGGCGCTCC	GTGCGGGAG	CCGCTGCCT	GCATCTGCTG	120
5	CTGACCCCTG	TGATCTTCAG	TCGTGATGGT	GAACCTGCA	AAAAGGTGAT	ACTTAATGTA	180
	CCTTCTAAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTTGGAAGA	GTGCTTCAGG	240
	TCTGCAGACC	TCATCCGGTC	AAGTGATCCT	GATTTTCAGAG	TTCTAAATGA	TGGGTTCAGT	300
	TACACAGCCA	GGGCTGTGTC	GCTGCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
	GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
10	TCGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
	ATTCTTGTCT	CTATGCAAGA	GAATTCCTTG	GGCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
	GAATCTGATG	CAGCAGAGAA	CTATCTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
	AAAGAACCTT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GAATCTATT	TTGCACTCGG	660
	CCTGTGATC	GTGAAGAATA	TGATGTTTT	GATTGATTG	CTTATGCTC	AACTGCAGAT	720
15	GGATATTTCAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAAC	780
	CACCTGTTT	TGCAGAAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAGTAG	TAGACCTGGT	840
	ACTACAGTGG	GGGTGGTTTG	TGCCACAGAC	AGAGATGAAC	CGGACACAAT	GCATACGGCG	900
	CTGAATACAG	GCATTTTGCA	CGAGACACCA	AGGTCACTG	GGCTCTTTTC	TGTGCATCCC	960
	AGCACAGGCG	TAATCACCAC	AGTCTCTCAT	TATTTGGACA	GAGAGGTTGT	AGACAAGTAG	1020
20	TCATTGATAA	TGAAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
	ACTTGTATCA	TAAACAGTAA	AGATTCAAAT	GATAATGCAC	CCACTTTTCAG	ACAAAATGCT	1140
	TATGAAGCAT	TTGTAGAGGA	AAATGCATT	AATGTGGAAA	TCCTACGAAT	ACCTATAGAA	1200
	GATAAGGATT	TAAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCAATTT	AAAGGGAAAT	1260
	GAATAATGGAC	ATTTCAAAT	CAGCACAGAC	AAAGAACTA	ATGAAGGTGT	TCTTTCTGTT	1320
25	GTAAAGCCAC	TGAATTTATGA	AGAAAACCGT	CAAGTGAACC	TGGAATTTGG	AGTAAACAAT	1380
	GAAGCGCCAT	TTGCTAGAGA	TATTTCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGGTTACA	1440
	GTTCAATGTA	GGGATCTGGA	TGAGGGGCTT	GAATGCACCT	CTGAGGCCCA	ATATGTGCGG	1500
	ATTAAGAAAT	ACTTAGCAGT	GGGGTCAAA	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	1560
	AATAGAACTG	GCATTTGTTT	AAGGTACAAA	AAATTGCATG	ATCTTAAAGG	TTGGATCACC	1620
30	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
	CCCAAAAATG	AGTTGTATAT	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
	ACTGGAACAT	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAAGTTTC	CCAATACCTC	TCCAGAAATC	1920
35	AGTAGACGTG	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCGCTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGATA	TACCATTCTT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
	GCACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACTTGGG	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTCG	TCCTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
40	GGGAAACGTT	TTCTGAAGA	TTTAGCACAG	CAAACTTAA	TTATATCAA	CACAGAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTTATGA	CCCAACTAC	CAACAACCTC	2340
	AGCCAGGTTT	TTTGTGTGAC	TATGGGATCA	GGAATGAATA	ATGGAGGGCA	GGAAACCAAT	2400
	GAATATGATG	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGGATG	CCTGCAAGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACITACTCG	2520
45	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGAAGAT	CCATTAGAGG	ACACACTGGT	2580
	TAAATAATTA	ACATAAAGAA	AATTCATCG	ATGTAATCAG	AATGAAGACC	GCATGCCATC	2640
	CCAGGATTAT	GTCTCTCACT	ATCACTATGA	GGGAAGAGGA	TCTCCAGCTG	GTCTGTGGG	2700
	CTGCTGAGT	GAAGAAGCAG	AAGAAGATGG	CCTTGACTTT	TTAAATAAAT	TGGAACCCAA	2760
	ATTATTATCA	TTAGCAGAGG	CATGCACAAA	GAGATAATGT	CACAGTGCTA	CAATTAGGTC	2820
50	TTTGTGAGAC	ATTCTGGAGG	TTTCAAAAA	TAATATTGTA	AAGTTCAATT	TCAACATGTA	2880
	TGTATATGAT	GATTTTTCCT	TCAATTTTGA	ATTATGCTAC	TCACCAATTT	ATATTTTAA	2940
	AGCCAGTTGT	TGCTTATCTT	TTCCAAAAG	TGAAAATGT	TAAACAGAG	AACTGGTAAA	3000
	TCTCAAACTC	CAGCAGTGGA	ATTAAGGCTC	CTAAGCATC	TGCTCTTTT	TTTTTTTACG	3060
	GATATTTTAG	TAAATAAAT	GCTGGATAAA	TATTAGTCCA	ACAATAGCTA	AGTTATGCTA	3120
55	ATATCACATT	ATTATGTATT	CACITTAAGT	GATAGTTTAA	AAAATAAACA	AGAAATATTG	3180
	AGTATCACTA	TGTGAAGAAA	GTTTTGGAAG	AGAAACCAAT	AAGACTGAAT	TAAATTAATA	3240
	ATGTTGCAGC	TCATAAAGAA	TTGGGACTCA	CCCTTACTGC	ACTACCAAT	TCATTTGACT	3300
	TTGGAGGCAA	AATGTGTGTA	AGTGCCCTAT	GAAGTAGCAA	TTTTCTATAG	GAATATAGTT	3360
	GGAAATAAAT	GTGTGTGTGT	ATATTATTAT	TAATCAATGC	AATATTAAAA	ATGAATAGAG	3420
60	AACAAAGAGG	AAATGTGTAA	AACTTGAAG	TGAGGCTGGG	GTATAGTTTG	TCCTACAATA	3480
	GAAAAAGAG	AGAGCTTCTT	AGGCTGCGC	TCTTAAATGC	TGCATTATAA	CTGAGTCTAT	3540
	GAGGAATAG	TTCTGTGCTA	ATTGTGTAA	TTTGTTTAAA	ATTGTAATA	AATTAACCTT	3600
	TTCTGGTTTC	TGTGGGAAGG	AAATAGGGAA	TCCAATGGAA	CAGTAGCTTT	GCTTTGCACT	3660
	CTGTTTCAAG	ATTTCTGCTG	CCACAAGTTA	GTAGCAAACT	GGGGAATACT	CGCTGCAGCT	3720
65	GGGGTTCCTT	GCTTTTGTGT	AGCAAGGGTC	CAGAGATGAG	GTGTTTTTTT	CGGGGAGCTA	3780
	ATAACAAAA	CATTTTAAAA	CTTACCTTTA	CTGAAGTTAA	ATCTCTATT	GCTGTTTCTA	3840
	TTCTCTCTTA	TAGTGACCAA	CATCTTTTAA	ATTAGATGCC	AAATAACCAT	GTCTCTCTAG	3900
	AGTTTAGAGG	CTAGAGGGAG	CTGAGGGGAG	GATCTTACTG	AAAGCACCTT	GGGGAGATTG	3960
	ATTGTCTCTA	AACCTAAGCC	CCACAACTT	GACACCTGAT	CAGGTCTGGG	AGCTACAAAA	4020
70	TTTCATTTTT	CTCTCTACTG	CCCTCTCTCT	GAGTGGCATT	GGCCTGAATC	AAGGAAAGCC	4080
	AGGCCCTGTG	GGCCCCCTTC	TTTGGGCTTT	CTGCTAAAGC	AACACCTCCA	GCAGAGATTG	4140
	CCTTAAGTGA	CTCCAGGTTT	TCCACCATCC	TTGAGGTTGA	ATTAATTTTT	AATCAGTTTG	4200
	CTTTCTCCAG	AGAAATTTTA	AAATAATAGA	AGAAATAGAA	ATTTTGAATG	TATAAAGAA	4260
	AAAGATCAAG	TGTGCTATT	AGAACAGAGG	GAACCTTGGG	AGAAAGCAGC	CCAAGTAGGT	4320
75	TATTTGTACA	GTGAGAGGGC	AACAGGAAGA	TGCAGGCTTT	CAAGGGCAAG	GAGAGGCCAC	4380
	AAGGAATATG	GGTGGGAGTA	AAAGCAACAT	CGTCTGCTTC	ATACCTTTTC	CTAGGCTTGG	4440
	CACCTGCTTT	TCCTTTCTCA	GGCCAAATGG	AACCTGCCAT	TGAGTCCGGT	GAGGGATCAG	4500
	CCAACCTCTT	CTCTATGCTC	CACCTTATT	GGAGTGAGAA	ATCAAGGAGA	CAGAGCTGAC	4560
	TGCTAGTGA	GCTCTGAAGC	ATTGTCAGGA	TGAGCCTGAA	CTGGTTGTGC	AGAACAAACA	4620
80	AGGCATTTCAT	GGGAATTTGT	GTATTCCTTC	TGCAGCCCTC	CTTCTGGGCA	CTAAGAGGTT	4680
	CTATGAATTA	AATGCCCTAT	TAAATTTCTG	ATTTATTCCT	ACATTTTCTG	TTTTCTAATT	4740
	TGACCTTAAA	ATCTATGTGT	TTTAGACTTA	GACTTTTTAT	TGCCCCCCCT	CCCTTTTTTT	4800
	TTGAGACCGA	GTCTGCTCTC	GAGCAGCAGG	CTGGAGTGCA	GTGGCTCCGA	TCTCTGCTCA	4860
	CTGAAGCTC	CGGCTCCGGG	GTTCTATGCA	TTCTCTGCTC	TCAGCCTCTC	GAGTAGCTGG	4920
	GACTACAGGC	CCCCACCACC	ACGCCCGGCT	AATTTTTTGT	ATTTTAAATA	GAGACGGGGT	4980

Seq ID NO: 326 Protein sequence  
Protein Accession #: NP\_077741.1

Seq ID NO: 327 DNA sequence  
Nucleic Acid Accession #: NM\_001941.2  
Coding sequence: 64..2754

1079

	GTAAAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATTGG AGTAAACAAT	1380
	GAAGGCGCAT TTGCTAGAGA TATTCGCCAG GTGACAGCCT TGAACAGAGC CTGGTTTACA	1440
	GTTCATGTGA GGGATCTGGA TGAGGGGCGT GAATGCACTC CTGCAGCCCA ATATGTGCGG	1500
5	ATTAAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA	1560
	AATGAGAAATG GCAATGGTTT AAGGTACAAA AAATTGCATG ATCCTAAAGG TTGGATCACC	1620
	ATTGATGAAA TTTCAGGGTC AATCATAACT TCCAAAATCC TGGATAGGGA GGTGAAACT	1680
	CCCAAAATG AGTTGTATAA TATTACAGTC CTGGCAATAG ACAAGATGA TAGATCATGT	1740
	ACTGGAACAC TTGCTGTGAA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA	1800
10	GAATATGTAG TCATTGCAA ACCAAAATG GGGTATACCG ACATTTTAGC TGTTGATCCT	1860
	GATGAACCTG TCCATGGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC	1920
	AGTAGACTGT GGAGCTCAC CAAAGTTAAT GATACAGCTG CCCGCTTTTC ATATCAGAAA	1980
	AATGCTGGAT TTCAAGAATA TACCATTCTT ATTACTGTAA AAGACAGGGC CGGCCAAGCT	2040
	GCAACAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTCGTGCG	2100
15	ACTTCAAGGA GTACAGGAGT AATACTTGA AAATGGGCAA TCCTTGCAAT ATTACTGGGT	2160
	ATAGCACTGC TCTTTCTGT ATTGCTAAT TTAGTATGTG GAGTTTITGG TGCAACTAAA	2220
	GGGAAACGTT TTCTGAAGA TTTAGCACAG CAAAACCTAA TTATATCAAA CACAGAAGCA	2280
	CCTGGAGACG ATAGAGTTGT CTCTGCCAAT GGATTATGA CCCAACTAC CAACAACTCT	2340
	AGCCAAGGTT TTGTGGTATC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAACCAATT	2400
20	GAATGATGA AAGGAGGAAA CCAGACCTTG GAATCCTGCC GGGGGGCTGG GCATCATCAT	2460
	ACCCCTGGACT CCTGCAGGGG AGGACACAG GAGGTGGACA ACTGCAGATA CACTTACTCG	2520
	GAGTGGACA GTTTTACTCA ACCCGTCTC GGTGAAAAAT TGCATCGATG TAATCAGAAT	2580
	GAAGACCGCA TGCCATCCCA AGATTATGTC CTCACITATA ACTATGAGGG AAGAGGATCT	2640
	CCAGCTGGTT CTGTGGGCTG CTGCAGTGAA AAGCAGGAAG AAGATGGCCT TGACTTTTAA	2700
25	AATAATTTGG AACCACAAAT TATTACATTA GCAGAAGCAT GCACAAAGAG ATAATGTCAC	2760
	AGTGCTACAA TTAGGCTCTT GTCAGACATT CTGGAGGTTT CCAAAAATAA TATTGTAAAG	2820
	TTCAATTTC AATGTATGT ATATGATGAT TTTTCTTCTA ATTTTGAATT ATGCTACTCA	2880
	CCAATTATA TTTTAAAGC CAGTTGTGTC TTATCTTTTC CAAAAGTGA AAAATGTTAA	2940
	AACAGACAAC TGGTAAATCT CAAACTCCAG CACTGGAATT AAGGTCTCTA AAGCATCTGC	3000
30	TCITTTTTTT TTTTACGGAT ATTTTAGTAA TAAATATGCT GGATAAATAT TAGTCCAACA	3060
	ATAGCTAAGT TATGCTAATA TCACATTATT ATGTATTAC TTTAAGTAT AGTTTAAAAA	3120
	ATAAACAGA AATATTGAGT ATCACTATGT GAAGAAAGTT TTGGAAGA AACAATGAAG	3180
	ACTGAATTAA ATTAATAATG TTGCAGCTCA TAAAGAAATG GGACTCACCC CTACTGCACT	3240
	ACCAAAATCA TTGACTTTTG GAGGCAAAAT GTGTTGAAGT GCCCTATGAA GTAGCAATTT	3300
35	TCTATAGGAA TATAGTTGGA AATAAATGTG TGTGTGTATA TTATTATTA TCAATGCAAT	3360
	ATTTAAATG AAATGAGAAC AAAGAGGAAA ATGGTAAAAA CTGAAATGA GGCTGGGGTA	3420
	TAGTTTGTCC TACAATAGAA AAAAGAGAGA GCTTCTTAGG CCTGGGCTCT TAAATGCTGC	3480
	ATTATAACTG AGTCTATGAG GAAATAGTTC CTGTCCAATT TGTGTAATTT GTTTAAATTT	3540
	GTAAATAAT TAACTTTTTC TGGTTTCTGT GGGAAAGGAAA TAGGGGAATCC AATGGAAACG	3600
40	TAGCTTTGCT TTGCAGTCTG TTTCAAGATT TCTGCATCCA CAAGTTAGTA GCAAACTGGG	3660
	GAATACTGCG TGCAGCTGGG GTTCCCTGCT TTTTGTAGC AAGGGTCCAG AGATGAGGTG	3720
	TTTTTTTCGG GGAGCTAATA ACAAAACAT TTTAAAACTT ACCTTTACTG AAGTTAAATC	3780
	CTCTATTGCT GTTCTATTTC TCTCTATAG TGACCAACAT CTTTTTAATT TAGATCCAAA	3840
	TAAACATGTC TCTCTAGAGT TTAGAGGCTA GAGGGAGCTG AGGGGAGGAT CTTACTGAAA	3900
45	GCACCCCTGG GAGATTGATT GTCCCTTAAAC CTAAGCCCCA CAAACTTGAC ACCTGATCAG	3960
	GTCTGGGAGC TACAAAATTT CATTTTCTC CTCAGTCCCC TTCTTCTGAG TGGCATTGGC	4020
	CTGAATCAAG GAAAGCCAGG CCTGTGGGCG CCCCTTCTTT CGGCTTCTG CTAAGCAAC	4080
	ACCTCCAGCA GAGATTCCCT TAAGTGACTC CAGGTTTTCC ACCATCCTTC AGCGTGAATT	4140
	AATTTTTAAT CAGTTTGTCT TCTCCAGAGA AATTTTAAAA TAATAGAAGA AATAGAAATT	4200
50	TTGAATGTAT AAAAGAAAAA GATCAAGTTG TCAATTTAGA ACAGAGGGA CTTTGGGAGA	4260
	AAGCAGCCCA AGTAGGTTAT TTGTACATC AGAGGGCAAC AGGAAGATGC AGGCCTTCAA	4320
	GGGCAAGGAG AGGCCACAAG GAATATGGGT GGGAGTAAAA GCAACATCGT CTGCTTCATA	4380
	CTTTTTCTTA GGCTTGGCAC TGCCTTTTCC TTTCTCAGGC CAATGGCAAC TGCCATTGTA	4440
	GTCCGGTAGG GGATCAGCCA ACCTCTTCTC TATGGCTCAC CTTAATTGGA GTGAGAAATC	4500
55	AAGGAGACAG AGCTGACTGC ATGATGAGTC TGAAGGCATT TGCAGGATGA GCCTGAACTG	4560
	GTGTGTCAGA ACAAACAAGG CATTCTAGG AATTGTTGTA TTCTTCTGCG AGCCCTCCTT	4620
	CTGGGCCTTA AGAAGGTCTA TGAATTAAAT GCCTATCTAA AATTCTGATT TATTCTTACA	4680
	TTTTCTGTTT TCTAATTTGA CCTTAAATC TATGTGTTTT AGACTTAGAG TTTTATTGCT	4740
	CCCCCCCCCT TTTTTTTTTG AGACGGAGTC TCGCTCTGAC GCACAGGCTG GAGTGCAGTG	4800
60	GCTCCGATCT CTGCTCACTG AAAGCTCCGC CTCCCGGTT CATGCCATT TCCTGCCTCA	4860
	GCCTCCTGAG TAGCTGGGAC TACAGGCGCC CACCACCAG CCGGCTAAT TTTTGTATT	4920
	TTTAATAGAG ACGGGGTTTC ACTGTGTTAG CCAGGATGGT CTGCATCTCC TGACCTCGTG	4980
	ATCCGCTGCG CTGCGCTCC CAAAGTGCTG GGATTACAGG CATGACCCAC CGCTCCCGGC	5040
	CTGTPTTCC GTTTAAAGTC GTCTTCTTT AATGTAATCA TTTTGAACAT GTGTGAAAGT	5100
65	TGATCATACG AATTGGATCA ATCTGAAAT ACTCAACCA AAGACAGTCG AGAAGCCAGG	5160
	GGGAGAAAGA ACTCAGGGCA CAAAATATTG GTCTGAGAAAT GGAATTTCTT GTAAGCCTAG	5220
	TTGCTGAAAT TTCTGCTGT AACCAGAAGC CAGTTTTATC TAAAGGCTAC TGAACACCCC	5280
	ACTGTGTTTT GCTCACTCCC TCACTCACCG ATCAAAACCT GCTACCTCCC CAAGACTTTA	5340
	CTAGTCCGCA TAAACTTTCT CAAAGAGCAA CCAGTATCAC TTCCCTGTTT ATAAACCTC	5400
70	TAACCATCTC TTTGTTCTTT GAACATGCTG AAAACCACTT GGTCTGATG TATGCCCGAA	5460
	TTTGTAAATC TTTTCTCTCA AATGAAAATT TAATTTTAGG GATTCAITTC TATATTTTCA	5520
	CATATGTAGT ATTATTATT CTTATATGT GTAAGGTGAA ATTTATGGTA TTTGAGTGTG	5580
	CAAGAAAAATA TATTTTAAA GCTTTCAATT TTCCCCAGT GAATGATTGA GAAATTTTAA	5640
	TGTAATAATA CAGAATGTTT TTTCTTACTT TTATAAGGAA GCAGCTGTCT AAAATGCAGT	5700
75	GGGGTTTGT TTGCAATGTT TTAACACAG TTTTAGTATT GCTATTAAAA GAAGTTACTT	5760
	TGCTTTTAAA GAAACTTGGC TGCTTAAAT AAGCAAAAAT TGGATGCATA AAGTAATATT	5820
	TACAGATGTG GGGAGATGTA ATAAACAAT ATTAACCTGG TTTCTGTGTT TTGCTGTATT	5880
	TAGAGATTAA ATAACTTCAA GATGATCACT TTGCAAAATT ATGCTTATGG CTGGCATGGA	5940
80	AATAGAAATA CTCATTTAG TCTTTGTGT ATTAATGGGG AATATTTTGG ACAAATGTTT	6000
	ATTATCAAT TGTGCACATC ATTAATATAT ATTGTAATGT TGGGAAGAGA TCACTATTTT	6060
	GAAGCACAGC TTTACAGATG AGTATCTATG ATACATATGT ATAATAAATT TTGATCGGGT	6120
	ATTAAAGTA TTAGAAGGTG GTTATAATTG CAGAGTATTC CATGAATAGT ACACGTACAC	6180
	AGGGGTTTTA CTTTGAGGAG CAGTGTATGC AAGGGAAAC ATGAGTTAAA AAGAAAGCA	6240
	GGCAATTATG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATCCCTGA ACTTTAATGA	6300
	CAAGATGATC CAACATAAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG	6360

5  
10  
AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420  
AGCCTTACAT TTAAATATAG GTTGAACCAA AATTTCAAIT CCAGTAACIT CTATTGTAAC 6480  
CATTATTTIT GTGTATGTCT TCAAGAATGT TCATTGGATT TTGTTTGTGA ATAGTAAAT 6540  
ACCGATACA TTTCAGTGT CCTCAGTAT TGATTGGIT GAATATTGGG TCATAATGGT 6600  
TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660  
TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAATCAAT 6720  
GAACATGCC AGCCTCATGG GGTGTGTGAA TGATTAATAT AGTTAATATA CCTAAAGTAC 6780  
ATAGAACT CCCTGCACAT AGTAAAGAA TTATAAGTGT GAGGTAGTTG GTAAATATAT 6840  
GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTT AGGGAAATAA AGTTTGTGCA 6900  
TATATATAAT CCGGAACAT G

Seq ID NO: 328 Protein sequence  
Protein Accession #: NP\_001932.1

15  
20  
25  
30  
1  
11 21 31 41 51  
MAAAGPRRSV RGAVCLHLLT TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60  
ADLIRSSDPD PRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS 120  
KTRHRTETVL RRAKRWAPI PCSMQENSLG PFPLFLQOVE SDAQNYTVF YSISGRGVDK 180  
EPLNLFYIER DTGNLFCTRP VDREYDVDFD LIAYASTADG YSADLPPLP IRVEDENDNH 240  
PVFTEIYNF EVLESSRPGT TVGVVCATDR DEPDTHMTRL KYSILQOTPR SPGLFSVHPS 300  
TGVITTVSHY LDREVDVKYS LIMKVQMDG OFFGLIGTST CIITVDSND NAPTFRQNAV 360  
EAFVEENAFN VEILRTPIED KDLINTANWR VNFTILKNE NGHPKISTDK ETNEGVLVSV 420  
KPLNVEENRQ VNLEIGVNE APPARDIPRV TALNRALVTV HVRDLDEGPE CTAAQYVRI 480  
KENLAVGSKI NGYKAYDPEN RENGRLRYKK LHPDKGWTI DEISGSIITS KILDREVETP 540  
KNELYMITVL AIDKDDRSCT GTLAVNIEDV NDNPPFELQE YVVICPKMG YTDILAVDPD 600  
EPVHGAPFFX SLNPTSPEIS RLWSLTKVND TAARLSYQKN AGFQETIPI TVKDRAGQAA 660  
TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATGK 720  
KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTNNSS QGFCGTMSGG MKNGGQETIE 780  
MMKGNQTLB SCRAGHHHT LDSCRGGHTE VDNCRYTYSE WHSFTQPRLG EKLHRCNQNE 840  
DRMPSQYVL TYNVEGRGSP AGSVGCCSEK QEEDGLDFIN NLEPKFITLA EACTKR

35  
Seq ID NO: 329 DNA sequence  
Nucleic Acid Accession #: NM\_016583.2  
Coding sequence: 72..842

40  
45  
50  
55  
60  
1  
11 21 31 41 51  
GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60  
TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGCTCT CTACGGGCTG TTAGCCCCAGA 120  
CCATGGCCCA GTTGGAGGCG CTGCCCGTGC CCTCGGACCA GACCCTGCC TTGAATGTGA 180  
ATCCAGCCCT GCCCTTGAAT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240  
ATGGCCTGCT GTCTGGGGCG CTGTTGGGCA TTCTGGAAA CTTCCGCTC CTGGACATCC 300  
TGAAGCCTGG AGGAGGTACT TCTGGTGCC TCCTTGGGGG ACTGCTTGA AAGTGACGT 360  
CAGTGATTC TGGCTGAAC AACATCATG ACATAAAGT CACTGACCC CAGCTGCTGG 420  
AACTTGGCTC TGTGAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480  
TAAAGTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540  
TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGTGCC 600  
TTGTGACTG CACCATTCC CCTGGAAGCC TGCAAATTC TCTGCTTGA GCACTTGGCC 660  
CCTCCCATC TCAAGTCTT CTGGACAGCC TCACAGGAT CTTGAATAA GTCCCTGCCTG 720  
AGTTGGTCA GGGCAACGTG TGCCCTCTGG TCAATGAGT TCTCAGAGC TTGGACATCA 780  
CCTGTGTGA TGAATGTGT AACATGCTGA TCCACGACT ACAGTTGTG ATCAAGTCT 840  
AAGCCTTCCA GGAAGGGGCT GGCTCTGCT GAGCTGCTC CCACTGTCTA CAGATGGCTG 900  
GCCCATGTG TGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCTT 960  
TCCACACAGG CGTGTGTAA ATCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTG 1020  
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA

60  
Seq ID NO: 330 Protein sequence  
Protein Accession #: NP\_057667.1

65  
70  
1  
11 21 31 41 51  
MFQGTGLIVF YGLLAQTMAG PGLFVPLDQ TLPLVNPAL PLSPTGLAGS LINALSNGLL 60  
SGGLLILEN LPLLDILKPG GGTSGGLISG LLGKVTSVIP GLNNIIDIKV TDPOLLELGL 120  
VQSPDGHRLY VTIPLGIKLQ VNTPLVGASL LRLAVKLDIT ABILAVRDKQ ERIHLVLGDC 180  
THSPGLQIS LLDGLGLPLI QGLLDSLTI LNKVLPVLQ GAVCPVNEV LRGLDITLVH 240  
DIVNMLHGL QFVIK

75  
Seq ID NO: 331 DNA sequence  
Nucleic Acid Accession #: NM\_004363.1  
Coding sequence: 115..2223

80  
1  
11 21 31 41 51  
CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60  
TCCTGGAAT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120  
TCTCCCTCGG CCCCTCCCA CAGATGGTGC ATCCCTGGC AGAGGCTCCT GCTCAGAGCC 180  
TCATTCTAA CCTTCTGGAA CCCGCCACC ACTGCCAAGC TCACTATTGA ATCCAGCCG 240  
TTCAATGTG CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACAATCTGCC CCAGCATCTT 300  
TTTGCTACA GCTGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAT TATAGGATAT 360  
GTAATAGGAA CTCACAGAG TACCCAGGG CCGCATACA GTGGTCAGA GATAATATAC 420  
CCCAATGCAT CCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCTA 480

CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540  
 GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600  
 GTGGCCTTCA CCGTGAACCT TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660  
 CAGAGCCTCC CGGTGAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720  
 5 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAATGTG AAACCCAGAA CCCAGTGAGT 780  
 GCCAGGGCGA GTGATTGAGT CATCTGAAAT GTCTCTATG GCCCGGATGC CCCCAACCATT 840  
 TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAAACTGTA ACCTCTCCGT CCACGCAGCC 900  
 TCTAACCCAC CTGCACAGTA CTCTGGTITT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960  
 10 GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020  
 AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080  
 CCCAAACCCCT TCATCACCAG CAACAACCTCC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140  
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200  
 CTCCCGGTCA GTCCAGGCT GCAGCTGTCC AATGACAACA GGACCCCTAC TCTACTCAGT 1260  
 15 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAAT AAGTGTGTAG 1320  
 CACAGCGACC CAGTCATCCT GAATGTCTTC TATGGCCCG AGACCCCCAC CATTTCCCCC 1380  
 TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CTGCCCATGC AGGCTCTAAC 1440  
 CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACTCC AGCAACACAC ACAAGAGCTC 1500  
 TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560  
 20 GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCCAAG 1620  
 CCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680  
 TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740  
 GTCAGTCCCA GGTCTGAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTGACA 1800  
 AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860  
 25 GACCCAGTCA CCTGTGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920  
 TCGTCTTACC TTTCCGGAGC GAACCTCAAC CTCCTCTGCC ACTCGGCCTC TAAACCATCC 1980  
 CCGCAGTATT CTTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040  
 GCCAAATACA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTTGGCTACT 2100  
 GGCCGCAATA ATTCTCATGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT 2160  
 30 CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220  
 TAGCAGCCCT GGTGTAGTGT CTTCATTTC GGAAGACTGA CAGTTGTTT GCTTCTCTCT 2280  
 TAAAGCATTT GCAACAGCTA CAGCTAAAAA TGTCTCTTT ACCAAGGATA TTTACAGAAA 2340  
 AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAACCCCA TCTCTACTAA 2400  
 AAATACAAA ATGAGCTGGG CTTGGTGGCG CGCACCTGTA GTCCAGTTA CTCGGGAGGC 2460  
 35 TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520  
 ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAGAC 2580  
 TCTGACCTGT ACTCTGAAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640  
 AACTTTAATG AACTAATCGA CAGCTTCATG AAATGTCCA CCAAGATCAA GCAGAGAAAA 2700  
 TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTIA AATGCTCTGT 2760  
 40 TTCCAGATT TCAGAAACT TTTTCTTT TAAGCTATCC ACTCTACAG CAATTGTATA 2820  
 AAATATACTT TGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGTGCTCTCC 2880  
 AGACTTGGGA AACTATTAT GAATATTAT ATGTATGGT AATATAGTTA TTGCACAAGT 2940  
 TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 332 Protein sequence  
 Protein Accession #: NP\_004354.1

1 11 21 31 41 51  
 MESPSAPPFR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVENLPQ 60  
 50 HLFQYSWYKG ERVDGNRQII GYVIGTQAT PGPAYSGREI IYPNASLLIQ NIIONDTGEY 120  
 TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPEVDK DAVAFTCEPE TQDATYLVWV 180  
 NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGPDAP 240  
 TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGTFQS TQELFIPNIT VNNSSGYTCQ 300  
 55 AHNSTGLNLR TTVTTITYYA EPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLVWVNN 360  
 QSLFVSPRLQ LSNDRNLTLL LSVTRNDVGP YEOGIQNELS VDHSOPVILN VLYGPDPTI 420  
 SPSYTYRPG VNLNLSCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480  
 NSAGHSRTT VKTITVSSEL PKPSSISNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540  
 LPVSPRLQLS NGNRLTLFEN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600  
 60 PDSSYLSGAN LNLNLSCHASN PSPQYSWRIN GIPQHTQVL FIAKITFNNN GTYACFVSNL 660  
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGA LI

Seq ID NO: 333 DNA sequence  
 Nucleic Acid Accession #: NM\_006952.1  
 Coding sequence: 11..793

1 11 21 31 41 51  
 AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTGTC TTCCAGGGCC TGCTGATTTT 60  
 70 TGAAATGTG ATTATTGGIT GTTGGGCGAT TGCCCTGACT GCGGAGTGCA TCTTCTTGT 120  
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180  
 GGCTGCGCTGG ATCGGCATAT TTGTGGGCGT CTGCTCTTTC TGCTGTCTG TTCTAGGCAT 240  
 TGTAGGCATC ATGAAGTCCA CGAGGAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT 300  
 75 AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360  
 ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGGCC CTCCAAACAA 420  
 TGATGACCAG TGGAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480  
 CAATTGCTGT GCGGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTCCGGAC 540  
 TGAGAAATAAT GATGCTGACT ATCCCTGGCC TGTCAATGC TGTGTTATGA ACAATCTTAA 600  
 80 AGAACCTCTC AACCTGGAGG CTGTGAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660  
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTGG CTGCTTGGG 720  
 ATTTGCCATT CTCTGCTGGA CTTTGTGGGT TCTCTGGGT ACCATGTCTT ACTGGAGCAG 780  
 AATTGAATAT TAAGAA

Seq ID NO: 334 Protein sequence  
 Protein Accession #: NP\_008883.1



1 11 21 31 41 51  
 5 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60  
 IGIFVIGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TORDEFTENL 120  
 FLKQMLERYQ NNSPPNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180  
 DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVANWGFPAI 240  
 LCWTFWVLLG TMFYWSRIEY

10 Seq ID NO: 335 DNA sequence  
 Nucleic Acid Accession #: NM\_002638.1  
 Coding sequence: 120..473

15 1 11 21 31 41 51  
 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CGGCCCTGGA GCCAGGCCAA 60  
 GCTGGAGTCG ATAAAGATTG GTATGGCCCT AGCTCTTAGC CAAACACCTT CCTGACACCA 120  
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTCTCTCAT CGCTGGGACG CTGGTTCTAG 180  
 AGGCAGCTGT CACGGAGATT CCTGTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240  
 20 TCAATGGACA AGATCCGCTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300  
 CGCAAGAGCC AGTCAAGGT CCAAGCTTCC CAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360  
 TCCGGTGGCG CATGTTGAAT CCCCTAACC GCTGCTGAA AGATACTGAC TGCCCAAGAA 420  
 TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480  
 25 CGGTCTTTCG TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCATCTGGT CCTAAGTCCC 540  
 TGCTGCCCTT CCCCTTCCA CACTGTCCAT TCTTCTCTCC ATTACAGATG CCCACGGCTG 600  
 GAGCTGCCTC TCTCATCCAC TTTCACATAA A

30 Seq ID NO: 336 Protein sequence  
 Protein Accession #: NP\_002629.1

35 1 11 21 31 41 51  
 MRASSFLIVV VFLLIAGTLVL EAAVTGVVPVK GQDITVKGRVP FNGQDPVKQ VSVKQGDVKV 60  
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDITDCPG IKKCEGSGS MACFVFPQ

40 Seq ID NO: 337 DNA sequence  
 Nucleic Acid Accession #: NM\_001793.2  
 Coding sequence: 71..2560

40 1 11 21 31 41 51  
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGGCCGTGCG GGCAGCTGCT TCACCCCTCT 60  
 CTCTGCAGCC ATGGGGCTCC CTCTGGGACC TCTCGCGTCT CTCTCTCTTC TCCAGGTTTG 120  
 45 CTGGCTGCAG TGCCCGGCGT CCGAGCCGTG CCGGGCGGTC TTGAGGGAGG CTGAAGTGAC 180  
 CTGGAGGGCG GGAGGGCGCG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240  
 CTGCCCTGGG CAGAGGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300  
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360  
 ATCCAAAGCT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420  
 TGAATAATGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480  
 50 AGACACCAAG ATTTTCTACA GCATCAGGGG CGCGGGGCA GACAGCCCCC CTGAGGGTGT 540  
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600  
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGTGCTCT CAGTGGAGGA 660  
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAAATGAC CACAAGCCCA AGTTTACCCA 720  
 55 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTTCTG TGATGCAGGT 780  
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTGG CTTACTCCAT 840  
 CCATAGCCAA GAACCAAGG ACCCACAGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900  
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960  
 CATCCAGGCG ACAGACATGG ATGGGGACGG CTCACCAACC ACGGCAGTGG CAGTAGTGGA 1020  
 60 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTGAACCCC CAGAAGTACG AGGCCCATGT 1080  
 GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140  
 CAACCTACCA GGTGGCGGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATT 1200  
 TACCATCACC ACCCACCTGT AGAGCAACCA GGGCATCTCT ACAACCGAGA AGGTTTGGGA 1260  
 TTTTGAGGCG AAAAACCAGC ACACCTGTGA CGTTGAAAGT ACCAACGAGG CCCCCTTTGT 1320  
 65 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGTCCAC GTGGAGGATG TGAATGAGGC 1380  
 ACCTGTGTTT GTCCCACTCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440  
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAGGAG AATCAAAGA TCAGCTACCG 1500  
 CATCTGAGA GACCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560  
 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTGTGAGG AACAACTCT ATGAAGTCAT 1620  
 70 GGTCTTGGCC ATGGCAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680  
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC GTTCAGATCA CCATCTGCAA 1740  
 CCAAGCCCT GTGGCCAGG TGCTGAACAT CAGGACAAG GACCTGTCTC CCCACACCTC 1800  
 CCCTTTCAG GCCCAAGCTA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860  
 GGAAGGTGAC ACAGTGGTCT GTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920  
 75 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980  
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAGGGAG GTTTCATCT 2040  
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGCTGC TTTTGTGTT 2100  
 GAGAAAGAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGGTGACAA 2160  
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCAACCA 2220  
 80 GCTCCACCGA GGTCTGAGG CAGGCGCGGA GGTGGTCTC CGCAATGACG TGGCAACCAAC 2280  
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAA CAGATGAAA TCGCAACTT 2340  
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACA GCCCCGCCCT ACACACCTC 2400  
 CTGTGGTGTG GACTATGAGG GCAGCGGCTC CGAGCGCGCG TCCCTGAGCT CCCTCACCTC 2460  
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGGCTTCAA 2520  
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTGCC TGCAGGGCTG 2580

5  
10  
GGGACCAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640  
GACTTCGGAG CTGTGCAGGA AGTGCCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700  
ACGTTAGAGT GGTGCTTCCT TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760  
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCTCAG AGGCCAAGTT TCCAGAGGCC 2820  
TCTTACCTGC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCTGCT GTGACTGACC 2880  
TACAGTGGAC TTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940  
TTTTTTTAA GCTATCTCA AAACGTTAGA GAAAGTTCTT CAAAGTGCA GCCCAGAGCT 3000  
GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTCCAGAC CCAATGCCT CCCATTGCGA 3060  
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGCCC CCTATTTTT TATTTTCCCT 3120  
GTTCGTTGC TATAGATGAA GGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180  
TAAAGAAACT TTTCACAGAA AAAAA

Seq ID NO: 338 Protein sequence  
Protein Accession #: NP\_001784.2

15  
20  
25  
30  
1 11 21 31 41 51  
MGLPRGPAS LLLLQVCWLQ CAASEPCRAV PREAEVTLEA GGAEQEPGQA LGKVPMGCPG 60  
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDV VAPISVPENG 120  
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGNLLN KPLDREEIAK 180  
YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
DEDDAIYTN GVVAYSIHSQ EPKDPHLMF TIHRSTGTIS VISSGLDREK VPEYTLTIOA 300  
TDMGDGSGST TAVAVVEILD ANDNAPMFDQ QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360  
AWRATYLLMG GDDGDHFTIT THPESNQIIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480  
DPAGWLANDP DSGQVTAVCT LDREDBQFVR NNIYEVMLA MDNGSPPTTG TGTLLLLTLD 540  
VNDHGFVPEP RQITICNQSP VRQVLNITDK DLSPTSPFF AQLTDDSDIY WTAEVNEEGD 600  
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDQ HGHVETCPGP WKGGFILFVL 660  
GAVLALLFL LVLALLVRKK RKIKEPLLLP EDDTRDNVVF YGEEGGGEED QDYDITQLHR 720  
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 339 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..672

35  
40  
45  
50  
1 11 21 31 41 51  
ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GGCGCGGCC CCGGGGCGGG 60  
CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGGCG GGAGGCTGCG AAGGTTCCAG 120  
AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180  
CTGCTGCGCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240  
GCGAGACAAC GAGATCCAGA GGACTCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300  
TGTATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATGG 360  
ACAGAGCCAT ACTCGGTAT AGCGGCCGTG AAAATATTT CACGTTTTT CATGGTTGCG 420  
AAGCAGTGCT CGGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480  
CTCTGGAAG AGCCCATGCC CTCTTTTAC CTCAAGTGT GTAAAATTG CTACTGCAAT 540  
TTAGAGGGGC CACCTACAA CTCATCAGT TTCAAAGAA ATGCTGGGAG CATGGGTGAG 600  
AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATGCG AGCGCGCCTC 660  
AGCTGTCTT GA

Seq ID NO: 340 Protein sequence  
Protein Accession #: Eos sequence

55  
60  
1 11 21 31 41 51  
MRLLRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRFFQ KGGEGAPRAD PPWAPLGTM 60  
LLALLLVVL PRVWTDANLT ARQDPEDSQ RTDEGDNVW CHVCEENTF EQCNPRCKW 120  
TEPYCVIAAV KIFPRPFMVA KQCSAGCAAM ERPKPEEKRF LLEPMPPFY LKCKKIRYCN 180  
LEGPPINSSV FREYAGSMGE SCGGLWLAIL LLLASIAAGL SLS

Seq ID NO: 341 DNA sequence  
Nucleic Acid Accession #: XM\_035292.2  
Coding sequence: 53..1576

65  
70  
75  
80  
1 11 21 31 41 51  
GCTCGCTGGG CCGCGGCTCC CGGCTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60  
TGCGGGCCCG AAGCGGCGCG GCTAGCGGC GCGGCGGCGG GAGGAGAAGG AAGAGGCGCG 120  
GGAGAAGATG CTGGCGCCCA AGAGCGCGGA CGGCTCGGCG CCGGAGGCG AGGGCGAGGG 180  
CGTGACCTCT CAGCGGAACA TCAGCTGCTT CAACGGGCTG GCCATCATCG TGGGGACCAT 240  
TATCGGCTCG GGCATCTTCT TGAAGCCAC GGGCGTCTC AAGGAGGCG GCTCGCGGG 300  
GCTGGGCGCT GTGGTGTGGG CCGGCTGCGG GGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360  
CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420  
CTACGGCTCG CTGCGCGCCT TCTCTAAGCT CTGGATCGAG CTGCTCATCA TCGGCGCTTC 480  
ATCGCAGTAC ATCGTGGGCC TGGTCTTCGC CACCTACCTG CTCAGCGCG TCTTCCCCAC 540  
CTGCGCGGTG CCGGAGGAGG CAGCCAGCT CCGGCGCTGC CTCTGGTGTG TGCTGCTCAC 600  
GGCGGTGAAC TGTCTACAGG TGAAGGCCCG CACCGGGTGC CAGGATGCTT TTGCGCGCG 660  
CAAGCTCTCT GCCCTGGGCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720  
TGTGTCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGATG TGGGGACCAT 780  
TGTGCTGGA TTATACAGCG GCCTCTTTCG CTATGGAGGA TGAATTAAT TGAATTTCTG 840  
CAGAGAGGAA ATGATCAACG CCTACAGAAA CCGCGCCCTG GCCATCATCA TCTCCCTGCC 900  
CATCGTGAGC CTGGTGTAGG TGCTGACCAA CCTGGCCTAC TTCACCAACC TGTCACCGA 960  
GCAGATGCTG TCGTCCGAGG CCGTGGCGGT GCACTTGGG AACTATCACC TGGGCGTCAT 1020

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```
GTCTGGATC ATCCCCGCT TCGTGGGCT GTCTGCTTC GGCTCCGTC ATGGGTCCCT 1080
GTTACATCC TCCAGGCTCT TCTTCGTGG GTCCCGGAA GCCACCTGC CTCCATCCT 1140
CTCCATGAT CACCAACAG TCCTCACCC CGTGCCGTC CTCGTGTCA CGTGTGTGAT 1200
GACGCTGCT TACGCTTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TCGTGGGCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTAGC CGGCCATCA AGGTGAACCT GGCCCTGCT GTGTCTTCA TCCTGGCCTG 1380
CCTCTTCTG ATCGCCGCT CTCTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCA 1440
CATCATCTC AGCGGCTGC CGTCTACTT CTTCGGGTC TGGTGGAAA ACAAGCCAA 1500
GTGGCTCCTC CAGGCATCT TCTCCAGAC CGTCTGTGT CAGAAGCTCA TGCAGGTG 1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC
```

Seq ID NO: 342 Protein sequence

Protein Accession #: XP\_035292.2

1 11 21 31 41 51  
MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60  
GTIIGSGIFV TPTGVLEKAG SPGLALVWMA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120  
LEVYGSLEPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLV 180  
LITAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240  
GNIVLALYSY LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300  
STEQMLSSEA VAVDFGNYHL GVMSNIIIPV VGLSCFGSVN GSLFTSSRLF FVSGREGHLP 360  
SILSMIHPLQ LTFVPSLVPT CVMTLLYAFS KDIFSVINFF SPFNWLCVAL AITGMINLRH 420  
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECCI GFTIILSGLP VYFFGVWWRN 480  
KPKWLLQGIF STTVLCQKLM QVVPQET

Seq ID NO: 343 DNA sequence

Nucleic Acid Accession #: NM\_005268.1

Coding sequence: 168..989

1 11 21 31 41 51  
TAAAAAGCAA AAGAATTGCG GGCCGCGTCG ACACGGGCTT CCCGAAAAC CTTCCTCCGCT 60  
TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCTCTATTGC CGGCTGCTGG GAGCCAGGAG 120  
AGCCCTGAGG AGTATGTCAC CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180  
TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240  
TGCTCTGGT CTTCATCTTC GCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300  
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCGTCT 360  
TTGATGAGTT CTTCCTCTGT TCCCATGTGC GCCTCTGGGC CTGTCAGCTT ATCTCTGTGA 420  
CATGCCCTCG ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480  
ACCGAGAAGC CCATGGGAGG AACAGTGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540  
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT 600  
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAGTGGCC 660  
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCTATCT CAAGCCCTCA GAGAAGAACA 720  
TTTTTACCTT CTTCATGTGT GCCACAGCTG CCATCTGCAT CTGCTCAAC CTCTGGAGC 780  
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840  
TGTGACACGT TCATCACCCT CACGGTACCA CTTCTTCTG CAAACAAGAC GACCTCTTTT 900  
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCCGCCCT 960  
GAGACCATGT GAAGAAACCC ATCTTGTGAG GGGCTGCGCT GACTGGTCTG GCAGGTTGGG 1020  
CCTGGATGGT AGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080  
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCTAGTCC 1140  
TCAACTCCAG CCACCTGCC CAGCTCGAG GCACCTGGCC AGTTCCCTCT CTGCTCTGCA 1200  
GCTCGGTTTC CTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC

Seq ID NO: 344 Protein sequence

Protein Accession #: NP\_005259.1

1 11 21 31 41 51  
MNWSIFEGLL SGVNYSTAF GRIWLSLVFI FRVLVYLVA ERVWSDDHKD FDCNTRQPGC 60  
SNVCFDEFPF VSHVRLNALQ LILVTCPSLL VVMHAYREV QEKHREAHG ENSGRLYLNP 120  
GKRGGLWWT YVCSLVFKAS VDIAPLYVPH SFYPKYILPP VVKCHADPCP NIVDCPISKP 180  
SEKNIFTLFM VATAAICILL NLVELIYLV KRCHECLAAR KQAMCTGHH PHGTTSSCRQ 240  
DILLSGDLIF LGSDSHPLLL PDRPRDHVK TIL

Seq ID NO: 345 DNA sequence

Nucleic Acid Accession #: NM\_002391.1

Coding sequence: 26..457

1 11 21 31 41 51  
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACTCTCTC 60  
CGCCCTGCTG GCGCTCACTT CCGCGSTGCG CAAAAGAAA GATAAGGTGA AGAAGGGCGG 120  
CCCGGGGAGC GAGTGGCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180  
CGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCCAAGCC CAGCGCATCC GGTGAGGGT 240  
GCCCTGCAAC TGAAGAAGG AGTTTGAGC GACTGCAAG TACAAGTTT AGAACTGGGG 300  
TGCGTGTGAT GGGGGCAGC GCACCAAGT CCGCCAAGC ACCCTGAAGA AGGCGCGCTA 360  
CAATGCTCAG TGCAGGAGA CCATCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420  
AAAGGCCAAA GCCAAGAAAG GGAAGGAAA GGAAGTACG CCAAGCTGG ATGCCAAGGA 480  
GCCCTGGTGT TCACATGGG CTTGGCCAG CCCTCTCTCT CCCAGGCCG AGATGTGAAC 540  
CACCAGTGCC TTCTGTCTG TGTGTAGCT TAATCAATCA TGCCCTGCTT TGTCTCTCTC 600  
ACTCCCAAGC CCCACCCCTA AGTGCCCAA GTGGGAGGG ACAAGGGATT CTGGGAAGCT 660  
TGAGCTCCAG CCAAGCAAT GTGAGTCCA GAGCCGCTT TTGTCTCTCC CCACAAATTC 720  
ATTACTAAGA AACACATCAA ATAACTGAC TTTTCCCCC CAATAAAGC TCTCTTTTT 780

TAATAT

Seq ID NO: 346 Protein sequence  
Protein Accession #: NP\_002382.1

1 11 21 31 41 51  
MQHRGFLLLT LLALLALTSV VAKKKDKVKK GPGSECAEW AWGPTPSSK DGVGFREGT 60  
CGAQTQRIIC RVPCNWKKEF GADCKYKPEW WGACDGGTGT KVRQGLTKKA RYNAQCQETI 120  
RVTKPCTPKT KAKAKAKGK GKD

Seq ID NO: 347 DNA sequence  
Nucleic Acid Accession #: NM\_006783.1  
Coding sequence: 1..786

1 11 21 31 41 51  
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTACT CACCAGCATC 60  
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120  
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTGCTCTGCA ACACACTGCA ACCGGGATGC 180  
AAAAATGTGT GCTATGACCA CTTTTCCCG GTGTCCACA TCCGGCTGTG GGCCTCCAG 240  
CTGATCTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCTTA CTACAGGCAC 300  
GAAACCACTC GCAAGTTTCA GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360  
ATTAAAAAGC ACAAGTTTCG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420  
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480  
TACCACCTGC CTGCGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCTT TGTGACTGC 540  
TTTATTTCTA GGCCACACGA GAAGACCGTG TTTACCATTT TTATGATTTT TGCCTCTGTG 600  
ATTTGCATGC TGCTTAACTG GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTATGG 660  
AGATCAAGA GAGCAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720  
CAGATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780  
AGCTAA

Seq ID NO: 348 Protein sequence  
Protein Accession #: NP\_006774.1

1 11 21 31 41 51  
MDWGLRFTI GGVNKHSTSI GKVVITVIFI FRVMILVVA QEVWGDEQED FVCNTLQPGC 60  
KNVCYDHPFH VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKPRRGE KENDFKDIED 120  
IKKHVRIEG SLWYTTSSSI FFRIFEEAEP MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180  
FISRPTKTV FTIFMISASV ICMILNVAE CYLLKVCFR RSKRAQTQKN HPNHALKESK 240  
QNEANLISD SGQNAITGFP S

Seq ID NO: 349 DNA sequence  
Nucleic Acid Accession #: NM\_002571.1  
Coding sequence: 99..587

1 11 21 31 41 51  
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCCTCTGC 60  
TCACCCCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120  
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180  
ACATCTCCCT CTGCGCAGA CTGAAGGCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240  
CCACCCCGGA GGACAACTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTGT 300  
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360  
TGGCGAAGCA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCTGTTT CTCTGCCTAC 420  
AGGACACCC CACCCCATC CAGAGCATGA TGTGCCAGTA CTGGCCAGA GTCTGTGTGT 480  
AGGACGATGA GATCATGCAG GGATTCTCA GGGCTTTCAG GCCCTGCCCC AGGCACCTAT 540  
GGTACTTGCT GGACTTAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCT 600  
CCAGGAAGAC CAGACTCCCA CCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCC 660  
TTTCAAAGAA TAAACACAGC TCAGAAGACG ATGACGTGTT CATCTGTGTC GCCATCCCC 720  
TCTGTCTGCA CACTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780  
GCAGAGGTTA TTAATAAACC CTGGAGCAT G

Seq ID NO: 350 Protein sequence  
Protein Accession #: NP\_002562.1

1 11 21 31 41 51  
MDIPQTKQDL ELPLKAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR 60  
WENNSCVEKK VLGEKGTGNPK KFKINYTVAN EATLLDITDY NFLPLCLQDT TPIQSMHCQ 120  
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLRQMEEPK RF

Seq ID NO: 351 DNA sequence  
Nucleic Acid Accession #: NM\_006500.1  
Coding sequence: 27..1967

1 11 21 31 41 51  
ACTTGGCTCT GCGCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60  
TGGCGCGCTG CTGCTGCTGT CCTCGCGTGG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120  
CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180  
AGTCCCAAG CAACCTCAGC CATGTGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240  
TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGAGTAC GAGCAGCGGC 300

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55

TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC 360  
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGGC 420  
TCTACAAAGC TCCGAGGAGG CCAACATACC AGGTCAACCC CTTGGGCATC CTTGTGAACA 480  
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCAAG 540  
TCATCTGGTA CAAGAAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCACT 600  
CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660  
TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAATACCCGG CTGCCAGTGT 720  
GGAACCATAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG 780  
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840  
GTTTGCTGTA TGGCAACCTT CCACCACTCT TCAGCATCAG CAAGCAGAAC CCCAGACCA 900  
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CCTGCCCGGA 960  
AGGAACACAG TGGGCGCTAT GAATGTCAAG CCTGGAACCT GGACACCATG ATATCGCTGC 1020  
TGAGTGAACC ACAGGAACCTA CTGGTGAACCT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080  
CCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140  
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAAGT GCTGGAAGG GGGCCTGTGC 1200  
TTCAGTTGCA GGTGTTGAA CGGGAGGCAG GAGGCGGCTA TCGCTGCGTG CGCTCTGTGC 1260  
CCAGCATACC CGGCCTGAAC CGCACACAGC TGGTCAAGCT GGCCATTTTT GGGCCCCCTT 1320  
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAGAGAAA TATGGTGTG AATCTGTCTT 1380  
GTGAAGCGTC AGGGCACCCC CGGCCACCA TCTCTGGAA CGTCAACGGC ACGGCAAGTG 1440  
AACAGACCA AGATCCACAG CGAGTCTCTG GCACCTGAA TGTCTCTGTG ACCCCGAGGC 1500  
TGTGAGGACA AGTGTGTGAA TGCACGGCCT CCAACGACCT GGGCAAAAAC ACCAGCATCC 1560  
TCTTCTGGA GCTGGTCAAT TTAACCAACC TCACACAGA CTCCACACA ACCACTGGCC 1620  
TCAGCACTTC CACTGCCAGT CCTCATACCA GAGCCAACAG CACTCCACA GAGAGAAAGC 1680  
TGCCGGAGCC GGAGAGCCGG GGCCTGGTCA TCGTGGCTGT GATTGTGTGC ATCTCTGTCT 1740  
TGGCGGTGCT GGGCGCTGTC CTCTATTTC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC 1800  
GCTCAGGACA TTAGGACCTG AGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG 1860  
TTAAGTCAGA TAAGCTCCCA GAAGAGATGG GCCTCTCTGA GGGCAGCAGC GGTGACAGA 1920  
GGGCTCCGGG AGACCAGGGA GAGAAATACA TCGATCTGAG GCATTAGCCC GGAATCACTT 1980  
CAGCTCCCTT CCTGCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG 2040  
CCTCCAAAGG GACTAGAGAG AAGCCTCTCT CTCCCTCAC CTGCACACCC CCTTTCAGAG 2100  
GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA 2160  
GTCCACCACC ATCTCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCAGTCTCT 2220  
CCGAGCGGGT AGGAGAGTTT CTTCGAGAAC GTGTTTTTTC TTTACACACA TTATGGCTGT 2280  
AAATACCTGG CTCTGCGCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCTGCC 2340  
CAAAGGCTGG CTTCACCAT CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC 2400  
GCCTGCTCAT GTTGAAGTGC CTGTTTACA CCGCTCCGG AGAGCACCCC AGCGGCATCC 2460  
AGAAGCAGCT GCAGTGTGTC TGCCACCACC CTCTGCTCG CCTCTTCAA GTCTCTGTG 2520  
ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCTAT CCTTAAAGA TACGTGCGG 2580  
GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGGGGCGGA 2640  
TCACAAAGTC AGGACAGAGC CATCTGGCT AACACGCTGA AACCTGTCT CTACTAAAA 2700  
TACAAAAAAA AATTGACTAG GCGTAGTGGT TGGCACTAT AGTCCAGCT ACTCGGAAGG 2760  
CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC 2820  
CACTGCATCT CAGCCTGGGC AACACAGCGA GACTCGCTCT CGAGGAAAAA AAAAGAAAA 2880  
ACGCGTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTGGAG TTCAGGTGAA TTAGCCTCAA 2940  
TCCCGGTGTT CACTGCTCC CATAGCCCTC TTGATGGATC ACGTAAACT GAAAGGCAGC 3000  
GGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAGC TATGGTTATA 3060  
TTAGCACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAAGG CCCAAATGAG 3120  
AGAATGGTAT TTAGGGATGG AAAACGGGGC CTGGCTAGAG CTTGGGTGT GTGTGTCTGT 3180  
CTGTGTGAT GCATACATAT GTGTGATAT ATGGTTTTGT CAGGTGTGTA AATTGCAAAA 3240  
TTGTTCTCTT TATATATGTA TGTATATATA TATATGAAA TATATATATA TATGAAAAA 3300  
AAAGCTTAAT TGTCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACACAGG 3360  
AACCTGGGGG CCTGTGAAAC TACAACCAA AGGCACCAA AACGTTTCC AGTTGGCAGC 3420  
AGAGATCAGG GGTATCTCT GCTTCTGAGC AATGGCTCA AGCTCTACCA GAGCAGACAG 3480  
CTACCTACT TTTAGCAGC AAAAGCTCCC GTATGACGCA GCAGGAAGG CCTGGCAGGC 3540  
TGTTAGCAGG AGCTATGTCC CTTCCTATCG TTTCCGTCCA CTT

Seq ID NO: 352 Protein sequence  
Protein Accession #: NP\_006491.1

60  
65  
70  
75

1 11 21 31 41 51  
GLPRLVCAFL LAACCCCFRV AGVPGEAEQP APELVEVEVG STALLKCGLS QSQGNLSHVD 60  
WFSVKEKRT LIPVRVQQG QSEPGYEYR LSLQDRGATL ALTQVTPQDE RIFLCQGRP 120  
RSQYRIQLR VYKAPREPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIQ VINYKNGRPL 180  
KEEKNRVHIQ SSQTVESSGL YTLQSLKAQ LVKEDKDAQF YCELNYRLPS GNHMKESREV 240  
TVPVFYPTK VWLEVEPVGM LKEGDRVEIR CLADGNPPPH PSISKQNPST REAEETIND 300  
NGVLVLEPAR KEHSGRYEQ AwnLDMISL LSEPQELLVN YVSDVRVSPA APERQEGSSL 360  
TLTCEASSQ DLEFQWREE TDQVLERGEV LQLHDLKREA GGGYRCVASV PSIPGLNRTQ 420  
LVKLAI FGPP WMAFKERKVM VKENMVLNLS CEASGHPRPT ISMNVTAS EODQDPQRL 480  
STLNVLVPE LLETGVECTA SNDLGRNTSI LPLELVNLT LTPDSNTTGT LSTSTASPH 540  
RANSTSTERK LPEPESRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPKR RSGKQBITLP 600  
PSRKTSLVVE VKSDKLPEEM GLLQSSGDK RAPGDQGEKY IDLRH

Seq ID NO: 353 DNA sequence  
Nucleic Acid Accession #: NM\_003183.3  
Coding sequence: 165..2639

80

1 11 21 31 41 51  
TCGAGCCTGG CGGTAGAATC TTCCCACTAG GCGGCGGGG AGGGAAGA GATTGAGGG 60  
CTAGAGCCGG GCGGATCCCG TCCTCCCCG ATGTGAGCAG TTTTCCGAAA CCCCGTCAGG 120  
CGAAGGCTGC CCAGAGAGGT GGAGTCGGTA GCGGGGCGG GAACATGAGG CAGTCTCTCC 180  
TATTCCTGAC CAGCGTGGT CTTTCTGTGC TGGCGCGCG ACCTCCGAT GACCGGGGCT 240  
TCGCCCCCA CCAGAGACTC GAGAAGCTTG ATTCTTTGCT CTCAGACTAC GATATTCTCT 300

5 CTTTATCTAA TATCCAGCAG CATTGCGTAA GAAAAAGAGA TCTACAGACT TCAACACATG 360  
 TAGAAACACT ACTAAGCTTT TCAGCTTTGA AAAGGCATTT TAAATTATAC CTGACATCAA 420  
 GTACTGAAGC TTTTTCACAA AATTTCAAGG TCGTGGTGGT GGATGGTAAA AACGAAAGCG 480  
 AGTACACTGC AAAATGGCAG GACTTCTTCA CTGGACACGT GGTGGTGGAG CCTGACTCTA 540  
 GGGTTCCTAGC CCACATAAGA GATGATGATG TTATAATCAG AATCAACACA GATGGGGCCG 600  
 AATATAACAT AGAGCCACTT TGGAGATTGG TTAATGATAC CAAAGACAAA AGAATGTTAG 660  
 TTTATAAATC TGAAGATATC AAGAATGTTT CACGTTTGCA GTCTCCAAAA GTGTGTGGTT 720  
 ATTTAAAGT GGATAATGAA GAGTTGCTCC CAAAGGGTT AGTAGACAGA GAACCACTG 780  
 10 AAGAGCTTGT TCATCGAGTG AAAAGAAGAG CTGACCCAGA TCCCATGAAG AACACGTGTA 840  
 AATTATTGGT GGTAGCAGAT CATCGCTTCT ACAGATACAT GGGCAGAGGG GAAGAGAGTA 900  
 CAACATACAA TTACTTAATA GAGCTAATTG ACAGAGTTGA TGACATCTAT CGGAACACTT 960  
 CATGGGATAA TGCAGTTTTT AAAGGCTATG GAATACAGAT AGAGCAGATT CGCATTTCTA 1020  
 AGTCTCCACA AGAGGTAAAA CCTGGTGAAG AGCACTACAA CATGGCAAAA AGTTACCCAA 1080  
 15 ATGAAGAAAA GGATGCTTGG GATGTGAAGA TGTGTCTAGA GCAATTTAGC TTTGATATAG 1140  
 CTGAGGAAGC ATCTAAAGTT TGCTTGGCAC ACCTTTTCAC ATACCAAGAT TTTGATATGG 1200  
 GAACTCTTGG ATTAGCTTAT GTTGGCTCTC CCAGAGCAAA CAGCCATGGA GGTGTTTGTG 1260  
 CAAAGGCTTA TTATAGCCCA GTTGGGAAGA AAAATATCTA TTTGAATAGT GGTGTTGACGA 1320  
 GCACAAAGAA TATGGTGAAG ACCATCTTCA CAAAGGAAGC TGACCTGGTT ACAACTCATG 1380  
 20 AATTGGGACA TAAATTTGGA GCAGAACATG ATCCGGATGG TCTAGCAGAA TGTGCCCCGA 1440  
 ATGAGGACCA GGGAGGGAAA TATGTCTATG ATCCCATAGC TGTGAGTGGC GATCACGAGA 1500  
 CAATAAGATG GTTTTCAAAC TGCAGTAAAC AATCAATCTA TAAGACCATT GAAAGTAAGG 1560  
 CCCAGGAGTG TTTTCAAGAA CGCAGCAATA AAGTTTGTGG GAACTCGAGG GTGGATGAAG 1620  
 GAGAAGAGTG TGATCTGGC ATCATGTATC TGAACAACGA CACCTGCTGC AACAGCGACT 1680  
 25 GCACGTTGAA GGAAGGTGTC CAGTGCAGTG ACAGGAACAG TCCTTGCTGT AAAAAGTGTG 1740  
 AGTTTGTAGC TGCCAGGAAG AAGTGCAGAG AGGCGATTAA TGCTACTTGC AAAGCGTGTG 1800  
 CCTACTGACG AGGTAATAGC AGTGAAGTGC CGCTCCAGG AATGCTGTA AATGACACTG 1860  
 TTTGCTTGGG TCTTGGCAAG TGTAAGGATG GGAATATGAT CCCTTCTGCG GAGAGGGGAA 1920  
 AGCAGCTGGA GTCTGTGTCG TGAATGAAA CTGACAACTC CTGCAAGGTG TGTGTCAGGG 1980  
 30 ACCTTTCTGG CCGCTGTGTG CCCTATGTCT ATGCTGAACA AAAGAACTTA TTTTGAAGGA 2040  
 AAGGAAAGCC CTGTACAGTA GGAATTTTGT ACATGAATGG CAAATGTGAG AAACGAGTAC 2100  
 AGGATGTAAAT TGAACGATTT TGGGATTTCG TGGACAGCT GAGCATCAAT ACTTTTGGAA 2160  
 AGTTTTTAGC AGACACATC GTTGGGCTCT TCCTGGTTTT CTCTTGATA TTTTGGATTC 2220  
 CTTTCAGCAT TCTTGTCCAT TGTGTGGATA AGAAATGGA TAAACAGTAT GAATCTCTGT 2280  
 35 CTCTGTTTCA CCCCAGTAAC GTCCAAATGC TGAGCAGCAT GGATCTGCA TCGGTTGCGA 2340  
 TTATCAAAACC CTTTCTCTCG CCCCAGACTC CAGGCGCCCT GCAGCCTGCC CCGTGTGATC 2400  
 CTTGCGCGCC AGCAGCTCCA AAACCTGGAC ACCAGAGAAT GGACACATC CAGGAAGACC 2460  
 CCAGCACAGA CTCCCATATT GACGAGGATG GGTTTGAGAA GGACCCCTTC CCAATATGCA 2520  
 GCACAGCTGC CAAGTCATTT GAGGATCTCA CGGACCATCC GGTGCGCAGA AGTGAAAGG 2580  
 40 CTGCCTCCTT TAACTGTCAG CGTCAGAATC GTGTTAAGAG CAAAGAAACA GAGTGCTAAT 2640  
 TTAGTTCTCA GCTCTCTGCA CTTAAGTGTG CAAAATATTT TTATAGATTT GACCTACAAA 2700  
 TCAATCACAG CTTGTATTTT GTGAAGACTG GGAAGTGACT TAGCAGATGC TGGTCATGTG 2760  
 TTTGAATCTC CTGCAAGTAA ACAGTTCTTG TGTGGTTTGG CCCTTCTCCT TTTGAAAGG 2820  
 TAAGGTGAAA GTGATCTCAT TTATTTTGGG GCTTTCAGGT TTAGTTTCTT AAAATATCTT 2880  
 45 TTGACCTGTG TGCACAAAGC AGAAATACA GCTGGATTGG GTTATGAATA TTTAGCTTTT 2940  
 TGTAAATGAA TCTTTTATAT TGATAACAGC ACTGACTAGG GAAATGATCA GTTTTCTTTT 3000  
 ATACACTGTA ATGAACCGCT GAATATGAAG CATTGGCAT TTATTTGTGA GAAAGTGGGA 3060  
 ATAGTTTTTT TTTTCTTTT TTTTCTTTCG CTTCAACTAA AAACAAAGGA GATAAATTTA 3120  
 GTATACATTG TATCTAATAT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT TTTTATGTAG 3180  
 50 CAGGGAATAAT ATATATCTAA ATTTAGAAAT CATTGGGTTT AATATGGCTC TTCATAATTC 3240  
 TAAGACTAAT GCTCAGAAC TAACCACTAC CTTACAGTGA GGCCTATACA TGGTAGCCAG 3300  
 TGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGTGCGGAGC TTTTCTGTGA 3360  
 TTTTATAGAT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGCTCT AGAAAATTTA 3420  
 CTATTGGCTG GGAGTGGTGG CTCATGCCCTG TAATCCAGC ACTTGGAGAG GCTGAGGTTG 3480  
 CGCCACTACA CTCCAGCCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 354 Protein sequence  
 Protein Accession #: NP\_003174.2

60 1 11 21 31 41 51  
 MRQSLFLTS VVFFVLAPRP PDDPGFGPHQ RLEKLDLSLS DYDILSLNSI QHVSVRKRD 60  
 QSTHVEITLL TFSALKRHEFK LYLTSSSTERF SQNFVVVVVD GKNESEYTAQ WQDFPTGHVV 120  
 GEPDSRLVAH IRDDVVIIRI NTDGAENIE PLWRVNDTK DKRMLVYKSE DIKNVSLRQS 180  
 65 PKVGYLKVVD NEELLPKGLV DREPPPELVH RVKRRADPDF MKNTCKLLVV ADHRFYRYMG 240  
 RGEESTTINY LIELLDVRVD IYRNTSWDNA GFKGYGQIE QIRILKSPQE VKPGEKHYNM 300  
 AKSYPNEEKD AMDVKMLLEQ FSPDIAEAS KVCIAHLFTY QDFDMGTGLL AYVGSPPRANS 360  
 HGGVCPKAYY SPVKKNIYLY NSGLTSTKNY KKTILTKEAD LVTTHELGHN FGAEDHPDGL 420  
 AECAPNEDQG GKVMYPIAV SGDHENNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN 480  
 70 SRVDEGEEDC PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNQCFETA QKKCQEAINA 540  
 TKRGVSYCTG NSSECPPPGN AENDTVCLDL GKCKDGRKIP FCEREQQLS CACNETDNNSC 600  
 KVCCRLDSGR CVPYVDAEQK NLPLRKGPCC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS 660  
 INTFGKFLAD NIVGSVLVFS LIFWIPFSIL VECVDKLDK QYESLSLFHP SNVEMLSMD 720  
 SASVRIIKFP PAPQTGRLQ PAPVIPSAPA APKLDHQMD TIQEDPSTDS HMEDEGPEKD 780  
 PFPNSSTAAR SFEDLTDHPV ARSEKAASPK LQRQNRVNSK ETEC

Seq ID NO: 355 DNA sequence  
 Nucleic Acid Accession #: NM\_021832.1  
 Coding sequence: 164..2248

80 1 11 21 31 41 51  
 TCGAGCCTGG CGGTAGAATC TTCCAGTAGT GCGGCGCGGG AGGAAAAGAG GATTGAGGGG 60  
 CTAGGCCCGG CGGATCCCGT CCTCCCCGA TGTGAGCAGT TTTCCGAAAC CCGTCAGGC 120  
 GAAGGCTGCC CAGAGAGGTG GAGTCGCTAG CCGGCGCGGG AACATGAGGC AGTCTCTCCT 180

5	ATTCTGACC AGCGTGGTTC CTTTCGTGCT GCGCGCGGGA CCTCCGGATG ACCCGGGGCTT 240
	CGGCCCCAC CAGAGACTCG AGAAGCTTGA TTCCTTGGCTC TCAGACTACG ATATTCTCTC 300
	TTTATCTAAT ATCCAGCAGC ATTCCGTAAG AAAAAGAGAT CTACAGACTT CAACACATGT 360
	AGAAACACTA CTAACCTTTT CAGCTTTGAA AAGGCATTTT AAATTATACC TGACATCAAG 420
	TACTGAACGT TTTTCACAAA ATTTCAGGT CGTGGTGGTG GATGGTAAAA ACGAAAGCGA 480
	GTACACTGTA AAATGGCAGG ACTTCTTTCAC TGGACACGTG GTTGGTGAGC CTGACTCTAG 540
	GGTTCTAGCC CACATAAGAG ATGATGATGT TATAATCAGA ATCAACACAG ATGGGGCCGA 600
	ATATAACATA GAGCCACTTT GGAGATTGT TAATGATACC AAAGACAAAA GAATGTTAGT 660
10	TTATAAATCT GAAGATATCA AGAATGTTTC ACGTTTGAG TCTCCAAAAG TGTGTGGTTA 720
	AGAGCTTGTT CATCGAGTGA AAAGAAGAGC TGACCCAGAT CCCATGAAGA ACACGTGTAA 840
	ATTATTGGTG GTAGCAGATC ATCGCTTCTA CAGATACATG GGCAGAGGGG AAGAGAGTAC 900
	AACATACAAAT TACTTAATAG AGCTAATTGA CAGAGTTGAT GACATCTATC GGAACACTTC 960
15	ATGGGATAAT GCAGGTTTTA AAGGCTATGG AATACAGATA GAGCAGATTC GCATTCTCAA 1020
	GTCTCCACAA GAGGTAAAA CTGGTGAAAA GCACTACAAC ATGGCAAAAA GTTACCCAAA 1080
	TGAAGAAAAG GATGCTTGGG ATGTGAAGAT GTTGCTAGAG CAATTAGCTT TTGATATAGC 1140
	TGAGGAAGCA TCTAAAGTTT GCTTGGCACA CTTTTCACA TACCAAGATT TTGATATGGG 1200
	AACCTTTGGA TTAGCTTATG TTGGCTCTCC CAGAGCAAAAC AGCCATGGAG GTGTTTGTCC 1260
20	AAAGGCTTAT TATAGCCAG TTGGGAAGAA AAATATCTAT TTGAATAGTG GTTTGACGAG 1320
	CACAAAGAAT TATGGTAAAA CCATCCTTAC AAAGGAAGCT GACCTGGTTA CAACTCATGA 1380
	ATTGGGACAT AATTTTGGAG CAGAACATGA TCCGATGGT CTAGCAGAAAT GTGCCCGGAA 1440
	TGAGGACCGG GGAGGGGAAAT ATGTCATGTA TCCCATAGCT GTGAGTGGCG ATCAGCAGAA 1500
	CAATAAGATG TTTTCAAACT GCAGTAAACA ATCAATCTAT AAGACCATTG AAAGTAAAGC 1560
25	CCAGGAGTGT TTTCAAGAAC GCAGCAATAA AGTTTGTGGG AACTCGAGGG TGGATGAAGG 1620
	AGAAGAGTGT GATCCTGGCA TCATGTATCT GAACAACGAC ACCTGCTGCA ACAGCGACTG 1680
	CACGTTGAAG GAAAGTGTCC AGTGCAGTGA CAGSAAACAGT CCTTGTCTGA AAACTGTGCA 1740
	GTTTGAGACT GCCCAGAAGA AGTGCCAGGA GCGGATTAAT GCTACTTGCA AAGGCGGTGC 1800
	CTACTGCACA GTGAAATAGCA GTGAGTGGCC GCCTCCAGGA AATGCTGAAG ATGACACTGT 1860
30	TGCTCTGGAT CTTGGCAAGT GTAAGGATGG GAAATGCATC CCTTCTCGCG AGAGGGGAAC 1920
	GCAGCTGGAG TCCTGTGCAT GTAATGAAAC TGACAACTCC TGCAAGGTGT GCTGCAGGGA 1980
	CCTTTCCGGC CGCTGTGTGC CCTATGTCCA TGCTGAACAA AAGAACTTAT TTTTGAGGAA 2040
	AGGAAAGCCC TGACAGTAG GATTTTGTGA CATGAATGGC AAATGTGAGA AACCAGTACA 2100
	GGATGTAATT GAACGATTTT GGGATTTCAT TGACCACTG AGCATCAATA CTTTGGGAAA 2160
35	GTTTTAGCA GACACATCG TTGGGTCTGT CTTGGTTTTC TCCTTGATAT TTTGGATTCC 2220
	TTTCAGCATT CTGTCTCATT GTGTGTAACG TCGAAATGCT GAGCAGCATG GATTCTGCAT 2280
	CGGTTGCGAT TATCAAAACC TTTCTGCGC CCCAGACTCC AGGCCGCGCT CAGCCTGCC 2340
	CTGTGATCCC TTCGCGGCCA GCAGCTCCAA AACTGGACCA CAGAGAAATG GACACCATCC 2400
	AGGAAGACCC CAGCACAGAC TCACATATGG ACGAGGATGG GTTTGAGAAG GACCCCTTCC 2460
40	CAATAGCAG CACAGCTGCC AAGTCAATTG AGGATCTCAC GGACCATCCG GTCACCGAAA 2520
	GTGAAAGGCG TGCCCTCTCT CTCTCTGAC TTAAGTGTGC AAAATATTTT TATAGATTG 2580
	AGTGCTAATT TAGTCTCAG CTCTCTGAC TTAAGTGTGC AAAATATTTT TATAGATTG 2640
	ACCTACAATC AATCAGACT TATATTTTGT GAAGACTGGG AAGTGACTTA GCAGATGCTG 2700
	GTCAATGTTT TGAACCTTCT GCAGGTAAAC AGTTCTTGTG TGGTTTGGCC CTTCTCCTTT 2760
45	TGAAAAGGTA AGGTGAAGGT GAATCTAGCT TATTTTGAAG CTTTCAGGTT TTATGTTTTA 2820
	AAATATCTTT TGACCTGTGG TGCAAAAGCA GAAATACAG CTGGATTGGG TTATGAGTAT 2880
	TTACGTTTTT GTAAATTAAT CTTTTATATT GATAACAGGC ACTGACTAGG GAAATGATCA 2940
	GTTTTTTTTT ATACACTGTA ATGAACCGCT GAATATGAAG CATTTGGCAT TTATTTGTGA 3000
	GAAAAGTGGA ATAGTTTTTT TTTTTTTTTT TTTTCTTGTG CTTCAACTAA AAACAAAGGA 3060
50	GATAAATTTA GTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT 3120
	TTTTATGTAG CAGGGAATAA ATATATCTAA ATTTAGAAAT CATTGGGTTT AATATGGCTC 3180
	TTCAATAATC TAAGACTAAT GCTCAGAAAC TAACCACTAC CTTACAGTGA GGGCTATACA 3240
	TGGTAGCCAG TTGAATTTAT GGAATCTACC AACTGTTTGG GGGCTGATT TGCTGGGCAG 3300
55	TTTTCTGTA TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT 3360
	AGAAAATTC AATTGGCTG GAGTGGTGG CTCATGCTG TAATCCAGC ACTTGGAGAG 3420
	3421 GCTGAGGTG CGCCACTACA CTCAGCCTG GGTGACAG TGAGATCTGC CTC

Seq ID NO: 356 Protein sequence  
Protein Accession #: NP\_068604.1

60	1 11 21 31 41 51
	MRQSLFLTS VVPFVLAPRP PDDPGFGPHQ RLEKLDLSLS DYDILSLNSI QHRSVRKRD 60
	QTSTHVELL TFSALKRHF LYLTSSTERF SQNFKVVVD GKNSEYTVK WQDFFTGHHV 120
65	GEFDSRLAH IRDDVLIIRI NTDGAENIE PLWRFVNDK DKRLVYKSE DIKNVSRQLS 180
	PKVCGYLKVD NEELLPGKLV DREPEELVH RVKRRADPD MKNTCKLLV ADHRFYRYMG 240
	RGEESTTNY LIELIDRVDD IYRNTSWDNA GPKGYGQIE QIRILKSPQE VKPGEKHYNM 300
	AKSYFNEEKD ANDVKMLLEQ PSFDIAEAS KVCLAHFTY QDFDMGTGLL AYVGSFRANS 360
70	HGGVCPKAYY SPVVKKNLYL NSGLTSTKNY GKTILTKEAD LVTTHLGHN FGAHDPDGL 420
	AECAPNEDQG GKVMYPIAV SGDHENNRMF SNCSKQSIYK TIESKAQECF QERSNKVCGN 480
	SRVDBGEEDC PGIMVNLNDT CENSDCLEKE GVQCDRNSP CCKNCQFETA QKKQAEAINA 540
	TCKGVSYCTG NSSECPFPGN AEDDTVCLDL GKCKDKGKIP FCEREQQLS CACNETDNC 600
	KVCCRDLGR CVFVDAEQK NLFRLKGRPC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS 660
	INTFGKFLAD NIVGSLVLPF LIFWIPPSIL VHCV

Seq ID NO: 357 DNA sequence  
Nucleic Acid Accession #: NM\_004994.1  
Coding sequence: 20..2143

80	1 11 21 31 41 51
	AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTG GTCCTGGTGC TCCTGGTGCT 60
	GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA 120
	CTTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGATC GCTATGGTTA 180
	CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCTGCGC TGCTGCTTCT 240

5	CGAGAAGCAA	CTGTCCCTGC	CCGAGACCGG	TGAGCTGGAT	AGCGCCACGC	TGAAGGCCAT	300
	GCGAACCCEA	CGGTGCGGGG	TCCCAGACCT	GGGCGAGATC	CAAACTTTTG	AGGGCGACCT	360
	CAAGTGGCAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGGCGCG	420
	GGCGGTGATT	GACGACGCCT	TTGCCGCGCG	CTTGGCACTG	TGGAGCGCGG	TGACGCGGCT	480
	CACCTTCACT	CGCGTGTACA	GCGGGGACGC	AGACATCGTC	ATCCAGTTTG	GTGTGCGGGA	540
	GCACGGAGAC	GGGTATCCCT	TCGACGGGAA	GGACGGGCTC	CTGGCACAAG	CCTTTCCTCC	600
	TGGCCCGCGC	ATTGAGGGAG	ACGCCCCATT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660
	GGCGGTGCTG	GTTCCTCACT	GGTTTGGAAA	CGCAGATGGC	GGGCGCTGCC	ACTTCCCTTT	720
10	CATCTTCGAG	GGCCGCTCCT	ACTCTGCTGT	CACCACCGAC	GGTGCCTCCG	ACGGCTTGCC	780
	CTGGTGCAGT	ACCACGGCCA	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGOGA	840
	GAGACTCTAC	ACCCGGGAGC	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTTCATCT	900
	CCAAGGCCAA	TCCTACTCCG	CCTGCACCA	GGACGGTCCG	TCCGACGGCT	ACCGCTGGTG	960
	CGCCACCACC	GCCAACTACG	ACCGGGACAA	GCTCTTCGGC	TTCTGCCCGA	CCCCAGCTGA	1020
	CTCGACGGTG	ATGGGGGGCA	ACTCGCGGGG	GGAGCTGTGC	GTCTTCCCTC	TCACTTTCCT	1080
15	GGGTAAGGAG	TACTCGACCT	GTACCAGCGA	GGGCGCGGGA	GATGGGCGCC	TCTGGTGGCG	1140
	TACCACCTCG	AACITTTGACA	GGGACAAGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
	TTTGTCTCTC	GTGGCGCGCG	ATGAGTTCCG	CCACGGGCTG	GGCTTAGATC	ATTCTCTCAGT	1260
	GCGGAGGGCG	CTATGTACCG	CTTCACTGAG	GGGCCCCCTC	TGCATAAGGA	1320	
	CGACGTGAAT	GGCATCCGGC	ACCTCTATGG	TCCTCGCCCT	GAACTTGAGC	CACGGCCTCC	1380
20	AACCACCACC	ACACCGCAGC	CCACGGCTCC	CCGACGGTTC	TGCCCCACCG	GACCCCCCAC	1440
	TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTCAG	CTGGCCCCAC	1500
	AGGTCCCCCC	ACTGCTGGCC	CTTCTACGGC	CACCTACTGTG	CCTTTGAGTC	CGGTGGACGA	1560
	TGCTGCGGCG	GTCGACATCT	TCGACGCCAT	CGCGGAGATT	GGGAACACAG	TGTATTGTGT	1620
25	CAAGGATGGG	AAGTACTGGC	GATTCTCTGA	GGGACGGGGG	AGCCGGCGCG	AGGGCCCCCT	1680
	CCTTATCGCC	GACAGTGGC	CCGCGCTGCC	CCGCAAGCTG	GACTCGGTCT	TTGAGGAGCC	1740
	GCTCTCCCAAG	AAGCTTTTCT	TCCTCTCTGG	GCGCCAGGTG	TGGGTGTACA	CAGGCGGCTC	1800
	GGTGTCTGGG	CGAGGGCGTC	TGGACAAGCT	GGGCGTGGGA	GCCGACGTGG	CCAGGTTGAC	1860
	CGGGCGCTCG	GCGAGTGGCA	GGGGGAAGAT	GCTGCTGTTC	AGCGGGCGCG	GCCTCTGGAG	1920
30	GTTCGACCTG	AAGGCGCAGA	TGGTGGATCC	CCGAGCGCGC	AGCGAGGTGG	ACCGGATGTT	1980
	CCCCGGGGTG	CCTTTGGACA	CGCACGACGT	CTTCCAGTAC	CGAGAGAAAG	CCTATTCTCT	2040
	CCAGGACCGC	TTCTACTGGC	GCGTGAATTC	CCGGAGTGAG	TTGAACCAAG	TGACCAAGT	2100
	GGGCTACGTG	ACCTATGACA	TCCTGCAGTG	CCCTGAGGAC	TAGGGCTCCC	GTCTCTGCTT	2160
	GCACTGCCAT	GTAATATCCC	ACTGGGACCA	ACCCTGGGGA	AGGAGCCAGT	TTGCCGGATA	2220
35	CAAACCTGTA	TTCTGTCTTG	GAGGAAAGGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC	2280
	TCACCTTTGT	TTTTTGTGGG	AGTGTCTTCA	ATAAAGTTGG	ATTCTCTAAC	CTTT	

Seq ID NO: 358 Protein sequence  
Protein Accession #: NP\_004985.1

40	1	11	21	31	41	51	
	MSLWQPLVLV	LLVLGCCFAA	PRQRQSTLVL	PPGDLRLNLT	DRQLAEELY	RYGYTRVAEM	60
	RGESKSLGPA	LLLLQKQLSL	PETGELDSAT	LKAMRTPRCG	VDPDLGRFQTF	EGDLKWHHHN	120
	ITYWIQNYSE	DLPRAVIDDA	PARAFALWSA	VTPLFTTRVY	SRDADIVIQF	GVAEHGDSYF	180
45	PDGKDLLLAH	AFPPGPGIQQ	DAHFDDELW	SLKGVVVVPT	RFGNADGAAC	HFPFIPEGRS	240
	YSACTTDGRS	DGLPWCSTTA	NYDTRDRFPG	CPSERLYTRD	GNADGKPCQF	PFIFQGSYS	300
	ACTTDGRSDG	YRWCAATTANY	DRDKLGFPCP	TRADSTVMGG	NSAGELCVFP	FTFLGKEYST	360
	CTSEGRGDGR	LWCATTNFD	SDKKGWFCPD	QGYSLFLVAA	HEFGHALGLD	HSSVPEALMY	420
	PMYRFTGEPF	LHKDDVNGIR	HLKGRPEPEP	PREPTTTTPQ	PTAPPTVCPT	GPPTVEPSEF	480
50	PTAGTGPSPS	AGPTGPPTAG	PSTATTVPLS	FVDDACNVNI	FDALAEIGNQ	LVLFDGKYW	540
	RFSEGRGSRP	QGFLIADKW	PALPRKLDV	FEEPLSKLFL	FFSGRQVWVY	TGASVLGPRR	600
	LDKLGGLADV	AQVTGALRS	RKMLLPFSGR	RLWRFDVKAQ	MVDPRSASEV	DRMFPGVPLD	660
	THDVFPQREK	AYFQDRFYW	RVSSRSELNQ	VDQVGYVTD	ILQCPED		

Seq ID NO: 359 DNA sequence  
Nucleic Acid Accession #: NM\_000213.1  
Coding sequence: 127..5385

60	1	11	21	31	41	51	
	CGCCCGCGCG	CTGCAGCCCC	ATCTCCTAGC	GGCAGCCCGG	GGCGGAGCGG	AGCGAGTCCG	60
	CCCCGAGGTA	GGTCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	GAGAGGGAGG	120
	AAGAGGATGG	CAGGGCCACG	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
	AGGTCAGGCC	TTCTTGGGAC	CTTGGCAAAC	CGCTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
65	ACGGAGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTCAGGGAC	300
	CGGCGCTGCA	ACACCCAGGC	GGAGCTGTCT	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
	GTCTAGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGGCGC	420
	AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGCTGAGGA	GCGGCATTTT	480
	GAGCTGGAGG	TGTTTGGGCC	ACTGGAGAGC	CCGCTGGACC	TGTACATCCT	CATGGACTTC	540
70	TCCAACCTCA	TGTCGATGA	TCTGGACAAC	CTCAAGAAGA	TGGGGCAGAA	CCTGGCTCGG	600
	GTCTTGAGCC	AGCTCACCA	CGACTACACT	ATTGGATTTC	GCAAGTTTGT	GGACAAAGTC	660
	AGGCTCCCGC	AGACCGACAT	GAGGCGCTAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
	CCCCCTTCT	CCTTCAAGAA	GCTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCCGGAAT	780
	AACTGCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATGCC	840
75	ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGCTGGC	GCCCGGACAG	CACCCACCTG	900
	CTGGTCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	CGTGTGGCT	960
	GGCATCATGA	GCCGCAACGA	TGAACGCTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
	TACAGGACAC	AGGACTACCC	GTCGGTGGCC	ACCCTGGTGC	GCCTGCTCGC	CAAGCACAAC	1080
80	ATCATCCCCA	TCTTGTCTGT	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCACACC	1140
	TATTTCCCTG	TCTCTCACT	GGGGGTGCTG	CAGGAGGACT	OGTCCAACAT	CGTGGAGCTG	1200
	CTGAGGAGG	CCTTCAATCG	GATCGGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCT	1260
	CGAGGCTTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCTTTT	1320
	CACATCGCGC	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
	GATGGGACGC	ACGTGTGCCA	GCTGCGGAG	GACCAAGAAG	GCAACATCCA	TCTGAAACCT	1440



5 TCCTTCTCCG ACCGCCCTCAA GATGGACGCG GGCATCATCT GTGATGTGTG CACCTGCGAG 1500  
 CTGCAAAAAG AGGTGCGGTC AGCTCGCTGC AGCTTCAACG GAGACTTCGT GTGCGGACAG 1560  
 TGTGTGTGCA GCGAGGGCTG GAGTGGCCAG ACCTGCAACT GCTCCACCGG CTCTCTGAGT 1620  
 GACATTACAG CCTGCTGTGG GGAGGGCGAG GACAGCGGT GCTCCGGCCG TGGGGAGTGC 1680  
 CAGTGGCGGG ACTGTGTGTG CTACGGCGAA GGCGGCTAAG AGGGTCAGTT CTGCGAGTAT 1740  
 GACAACTTCC AGTGTCCCG CACTTCCGGG TTCCTCTGCA ATGACCGAGG AOCCTGTCTC 1800  
 ATGGGCCAGT GTGTGTGTGA GCCTGGTTGG ACAGGCCCAA GCTGTGACTG TCCCTCTCAGC 1860  
 AATGCCACCT GCATCGACAG CAATGGGGGC ATCTGTAATG GACGTGGCCA CTGTGAGTGT 1920  
 10 GGCGCTGCC ACTGCCACA GCATCGCTC TACACGGACA CCATCTGCGA GATCAACTAC 1980  
 TCGCGATACC ACCCGGGCCT CTGCGAGGAC CTACGCTCCT GCGTGCAGTG CCAGGCGTGG 2040  
 GGCACCGCG AGAAGAAGGG GCGCACGTGT GAGGAATGCA ACTTCAAGGT CAAGATGGTG 2100  
 GACGAGCTTA AGAGAGCCGA GGAGGTGGTG GTGCGCTGCT CCTTCCGGGA CGAGGATGAC 2160  
 GACTGCACCT ACAGCTACAC CATGGAAGGT GACGGCGCCC CTGGGCCCAA CAGCACTGTC 2220  
 CTGGTGACA AGAAGAAGGA CTGCCCTCCG GGCTCCTTCT GTTGGCTCAT CCCCCTGTCT 2280  
 15 CTCTCTCTCC TGCGCTCTCT GGCCCTGTCTA CTGCTGTCTAT GCTGGAAGTA CTGTGCTGTC 2340  
 TGCAAGGCTC GCCTGGCACT TCTCCCGTGC TGCAACCGAG GTCACATGGT GGGCTTTAAG 2400  
 GAAGACCACT ACATGCTGGG GGAGAACCTG ATGGCTCTG ACCACTTGGG CACGCCCATG 2460  
 CTGCGCAGCG GCAACTCTGA GGGCGGTGAC GTGGTCCGCT GGAAGTGCAC CAACAACATG 2520  
 CAGCGCGCTG GCTTTGCCAC TCATGCCGCG AGCATCAACC CCACAGAGCT GGTGCCCTAC 2580  
 20 GGGCTGTCTT TGCGCTGGC CGCGCTTTGC ACCGAGAACC TGCTGAAGCC TGACACTCGG 2640  
 GAGTGGCGCC AGCTGCGCCA GGAGGTGGAG GAGAACCTGA ACGAGGTCTA CAGGCAGATC 2700  
 TCGGTGTAC ACAAGCTCCA GCAGACCAAG TTCGGCAGC AGCCCAATGC CGGGAAGGAG 2760  
 CAAGACCTAC CCACTTGTGA CACAGTGTCT ATGGCGCCCC GCTCGGCCAA GCGCGCCCTG 2820  
 25 CTGAAGCTTA CAGAGAAGCA GGTGGAACAG AGGGCTTCC ACAGCTCAA GGTGGCCCCC 2880  
 GGCTACTACA CCTCACTGC AGACCAAGGAC GCGCGGGGCA TGGTGGAGTT CCAGGAGGGC 2940  
 GTGGAGCTGG TGGAGCTACG GGTGCCCCCT TTATCCGGC CTGAGGATGA CGACGAGAAG 3000  
 CAGCTGTCTG TGGAGGCTAT CGACGTGCCC GACGGCACTG CCACCTCTGG CCGCGCCTG 3060  
 GTAAACCTCA CCACTATCAA GGAGCAAGCC AGAGACGTGG TGTCTTTGA GCAGCTGAG 3120  
 30 TTCTCGTCA GCGCGGGGA CCAAGTGGCC CGCATCCCTG TCATCCGGCG TGTCTGTGAC 3180  
 GCGGGGAGT CCGAGGTCTC CTACCGCACA CAGGATGGCA CCGCGCAGG CAACCGGGAC 3240  
 TACATCCCCG TGGAGGTGTA GCTGCTGTTC CAGCTGGGG AGGCTGGAA AGAGCTGCAG 3300  
 GTGAAGCTCC TGGAGTGTGA AGAAGTTGAC TCCCTCTGCG GGGGCCGCCA GGTCCGCGT 3360  
 TTCCAGCTCC AGCTCAGCAA CCTTAAGTTT GGGGCCCAAC TGGGCCAGCC CCACTCCACC 3420  
 35 ACCATCATCA TCAGGGACCC AGATGAACTG GACCGGAGCT TCACGAGTCA GATGTTGTCA 3480  
 TCACAGCCAC CCCCCTCAGG CGACCTGGGC GCCCCGAGA ACCCCAATGC TAAGGCGCT 3540  
 GGGTCCAGGA AGATCCATT CAACTGGCTG CCCCCTTCTG GCAAGCCAAT GGGGTACAGG 3600  
 GTAAAGTACT GGATTCAGGG TGAATCCGAA TCCGAAGCCC ACCTGTCTGA CAGCAAGGTG 3660  
 CCCTCACTGG AGCTCAGCAA CCTGTACCG TATTGCGACT ATGAGATGAA GGTGTGCGCC 3720  
 40 TACGGGGCTC AGGGCGAGGG ACCCTACAGC TCCCTGTGTG CTGCGCGCAC CCACAGGAA 3780  
 GTGCCCAGCG AGCCAGGGCG TCTGGCCTTC AATGTCTCTT CCTCCAGGT GACCCAGCTG 3840  
 AGCTGGGCTG AGCGCGCTGA GACCAACGGT GAGATCACAG CCTACGAGGT CTGCTATGGC 3900  
 CTGGTCAAG ATGACAACCG ACCTATTGGG CCAATGAAGA AAGTGTCTGT TGACAACCTT 3960  
 AAGAACCGCA AGCTGCTTAT TGAGAACCTT CGGAGTCCC AGCCCTACCG CTACACGGTG 4020  
 45 AAGGCGGCA ACGGGGCGG CTGGGGGCTT GAGCGGGAGG CCATCATCAA CCGTGGCCAC 4080  
 CAGCCCAAGA GGCCTATGTC CATCCCATC ATCCCTGACA TCCCTATCGT GGAAGCCAG 4140  
 AGCGGGGAGG ACTACGACAG CTTCTTATG TACAGGATG ACGTTCTAG CTCTCCATCG 4200  
 GCGAGCCAGA GGCCTCAGCT CTCGATGAC ACTGAGCACC TGGTGAATGG CCGGATGGAG 4260  
 50 TTTGCTTCC CGGGCAGCAG CAACTCCCTG CACAGGATGA CCAAGCAGG TGCTGTCTGC 4320  
 TATGGCACCC ACCTGAGCCC ACAGTGCCCC CACCGCTGCG TAAGCACATC CTCCACCTTC 4380  
 ACACGGGACT ACAACTCACT GACCGCTCA GAACACTCAC ACTGACACAC ACTGCGGAGG 4440  
 GACTACTCCA CCTCACTC CTCTCTCTCC CAGACTCTC GCCTGACTGC TGGTGTGCCC 4500  
 GACAGCCCCA CCGCGCTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAAGTGG 4560  
 CAGGAGCCCG GTGTGAGCGG GCGCTGCGAG GGCTACAGTG TGGAGTACCA GCTGCTGAAC 4620  
 55 GCGGTGTAGC TGATCGGCT CAACATCCCC AACCTGCCCC AGACCTCGST GGTGGTGGAA 4680  
 GACCTCTGCG CCAACCACTC CTACGTGTTT CCGGTGCGGG CCCAGAGCCA GGAAGGCTGG 4740  
 GCGCGAGAGC GTGAGGGTGT CATCAACATT GAATCCAGG TGCAACCGCA GAGCCCACTG 4800  
 TGTCCCTGCG CAGGCTCCGC CTCACTTTG AGCACTCCCA GTGCCCCAGG CCGCTGGTG 4860  
 TTACTGCTGC TGAGCTCAGA CTGCTGCGAG CTGAGCTGGG AGCGGCCAGG GAGGCCAAT 4920  
 60 GGGATATCG TCGCTACCT GGTGACCTGT GAGATGGCCC AAGGAGGAGG GCCAGCCACC 4980  
 GCATTCCGGG TGGATGGAGA CAGCCCGGAG AGCCGCTGTA CCGTGGCGGG CCTCAGCGAG 5040  
 AACGTGCCCT ACAAGTTCAA GGTGAGGGCC AGGACCACTG AGGGCTTCGG GCCAGAGGCG 5100  
 GAGGGGCTCA TCACCATAGA GTCCAGGAT GGAGGACCTT TCCCGCAGCT GGGCAGCGGT 5160  
 GCGGGGCTCT TCCAGCACCC GCTGCAAGC GAGTACAGCA GCATCACAC CACCCACACC 5220  
 65 AGCGCCACCG AGCCCTTCTT AGTGGATGG CCGACCTGG GGGCCAGCA CCTGGAGGCA 5280  
 GCGCGCTCCC TCACCGGCA TGTGACCCAG GAGTTTGTGA GCGGACACT GACCAACAGC 5340  
 GGAACCTTTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTGACCGCA CCTGCCCCCA 5400  
 CCCCAGCCAT GTCCACTAG GGTCTCTCCC GACTCTCTC CCGAGCGCTC CTCAGTACT 5460  
 CCATCTGTC ACCCTGGGG GCGGAGCCCA CCGCATGCA CAGAGCAGGG GCTAGGTGTC 5520  
 70 TCCTGGGAG CATGAAGGG GCAAGGTCCG TCCTGTGTG GCGCAACCT ATTGTAAAC 5580  
 AAGAGCTGG GAGCAGACA AGGACCCAGC CTTTGTCTG CACTTAATAA ATGTTTGTG 5640  
 TACTG

Seq ID NO: 360 Protein sequence  
 Protein Accession #: NP\_000204.1

75 1 11 21 31 41 51  
 MAGPRPSPWA RLLLAALISV SLSGTILANRC KIPVKSCTE CVRVDKDAY CTDEMFRDRR 60  
 80 CNTQAEALLA GCQRESIVVM ESSPQITEET QIDTTLRSQ MSPQGLRVL RPGEERHFEL 120  
 EVFPELESFV DLYILMDFSN SMSDDLNLK KMGQNLARVL SQLTSDYTIG FGKPFVDKVSU 180  
 PQTDMRPEKL KEFPEFSDPP FSPKRVISLT EDVDEFKRL QGERISGNLD APEGGFDAIL 240  
 QTAUCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLGI MSRNDERCHL DTTGTYYQYR 300  
 TDQYPSFTNL VRLAKENII PIFAVTNSY SYEKLHTYF PVSSGLVQLE DSSNIVELLE 360  
 EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRSEVGIVQV QLRALHVDG 420

5  
10  
15  
20  
25

THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480  
 CSEGWGGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHVCYCEYGR YEQFCEYDN 540  
 FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNNGGIC NGRGHCECGR 600  
 CHCHQQLSYT DTICEINISA IHPGLCEDLR SCVQCQANGT GEKKGRTCEE CNFKVKMVD 660  
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDDG APGNSTVLV HKKDCPPGS FWLIPLLLL 720  
 LLPLALLLLL LCWKYCACCK ACLALLPCCN RGHMVGPKED HYMLRENIMA SDHLDTPMLR 780  
 SGNLKGKRDVW RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840  
 AQLRQVEVEN LNEVYRQISG VHKLQOTKFR QQPNAKKQD HTIVDTVLMA PRSAKPALLK 900  
 LTERQVEEQA PHDLKVAAGY YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDEKQL 960  
 LVEAIDVPAG TATLGRRLVN ITIIKEQARD VVSPEQPEFS VSRGDQVARI PVIRRVLDGG 1020  
 KSQVSYRTQD GTAQGNRDYI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080  
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGLDGP QNFNAKAAGS 1140  
 RKIHFNWLP SGKPMGYRVK YWIQGDESE AHLDSKVPS VELTNLYPYC DYEMKVCAYG 1200  
 AQGESPYSSL VSCRTHQEVF SEPGRFAFNV VSSTVTQLSW AEPAETNGEI TAXEVCYGLV 1260  
 NDDNRPIGPM KKVLDVNFKN RMLLIENLRE SQPYRYTVKA RNGAGWGP ER EAINLATOP 1320  
 KRPMSPPIIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSDDTE HLVNGRMDFA 1380  
 PFGSTNLHR MTTTSAAYG THLSPHVPHR VLSTSSLTTR DYNLSRTRSH SHSTTLPRDY 1440  
 SLTTSVSSHD SRLTAGVPDT PTRLVFSALG PTLRVSWEQ PRCEPLQGY SVEYQLLNGG 1500  
 ELHRLNIPNP AQTSVVVEDL LPNHSYFVRV RAQSQEGWGR EREGVITIES QVHPQSLPCP 1560  
 LPGAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGLVLTCEM AQGGGPATAF 1620  
 RVDGDSPEER LTVPLGSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG 1680  
 LFQHPQLSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEF VSRTLTTSGT 1740  
 LSTHMDQQFF QT

Seq ID NO: 361 DNA sequence  
 Nucleic Acid Accession #: NM\_013332.1  
 Coding sequence: 1..63

30  
35  
40  
45  
50  
55

1 11 21 31 41 51  
 GCACGAGGGC GCTTTGTGCT CCGGTGAGTT TTGTGCGCGG AAGCTTCTGC GCTGGTGCTT 60  
 AGTAACCGAC TTTCCTCCGG ACTCCTGCAC GACCTGCTCC TACAGCCGGC GATCCACTCC 120  
 CGGCTGTTC CCGGAGGGT CCAGAGGCTT TCCAGAGGA GAAGGCAGCT CTGTTTCTCT 180  
 GCAGAGGAGT AGGTCCTTT CAGCCATGAA GCATGTGTG AACCTCTACC TGTTAGGTGT 240  
 GGTACTGACC CTACTCTCCA TCTTCGTTAG AGTGATGGAG TCCCTAGAAG GCTTACTAGA 300  
 GAGCCCATCG CCGGGAGCTT CCTGGACCA CAGAAGCCAA CTAGCCAACA CAGAGCCAC 360  
 CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATA GACCTCTTC CATACTGGCC 420  
 ATATTTTGA ACACCTGACCT AGACATGTCC AGATGGGAGT CCCATTCTTA GCAGACAAGC 480  
 TGAGCAACCT TGTAAACAGA GAACATATAC TAGGCTCTGA AGAACCTGTC TAACTGGATG 540  
 CTCATTGCCT GGGCAAGGCC TGTTTAGGCC GGTGCGGTG GCTCATGCT GTAATCCTAG 600  
 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTGCG 660  
 CAACATGGCG AAACCCCATC TCTACTAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720  
 GGCTCTGAAT CCCAGTTCTT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCCGGGGACG 780  
 GAGGTGCGAG TGAACCGAGA TGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840  
 CATCTCAAAA AAAAAAGAA AAAAAAAGC CTGTTAATG CACAGGTGTG AGTGGATTGC 900  
 TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTG TGCTGTGCTT 960  
 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020  
 TGATATTTT ACCTCTACTT CCTAAACATC TGTCTGGGCT TCCTTTAGTC TTGAATGTCT 1080  
 TATGCTCAAT TATTGTGTGT TGAGCCTCTC TTCCACAAGA GCTCTCCAT GTTTGGATAG 1140  
 CAGTTGAAGA GGTGTGTGTG GTGGGCTGTT GGGAGTGGG ATGGAGTGT CAGTGCCCAT 1200  
 TTCTCATTTT ACATTTTAAA GTCGTTCTCT CAACATAGTG TGTATTGCTC TGAAGGGGGT 1260  
 GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAATGA 1320  
 TTTTCTTAA CTAATAAAGT GGAATATATA TTCAAAAAA AAAAAAATAA AA

Seq ID NO: 362 Protein sequence  
 Protein Accession #: NP\_037464.1

60

1 11 21 31 41 51  
 MKHVLNLYLL GVVLTLISIF VRVMESLEGL LESPSPGTSW TTRSQLANTE PTKLPLDHPS 60  
 RSM

Seq ID NO: 363 DNA sequence  
 Nucleic Acid Accession #: NM\_023915.1  
 Coding sequence: 250..1326

70  
75  
80

1 11 21 31 41 51  
 GGCACGAGGG TTTCTTTTTC ATGCTTTACC AGAAAAATCCA CTTCCTGCC GACCTTAGTT 60  
 TCAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120  
 GTGAATGGAC AGCCAGGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180  
 CCCACGCCCTC AATCGTCCCC AAGTGTITTC TGACACGCAT CTTTGCTTAC AGTGATCATC 240  
 AACTGAAGAA TGGGGTTTCA CTTGACGCTT GCAAAATTAC CAATAACGA GGTGACGGC 300  
 CAAGAGAGTC ACAATTACAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360  
 AATGAATTTG ACACAATTGT CTGCGCGGTG CTTTATCTCA TTATATTGT GGCAAGCATC 420  
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480  
 TTCTATCTCA AAAACATAGT GGTGACGAGC CTCATAATGA CGCTGACAT TCCATTTTCA 540  
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600  
 TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660  
 GATCGCTATC TGAAGGTGGT CAAGCCATTI GGGGACTCTC GGATGTACAG CATAACCTTC 720  
 ACGAAGGTTT TATCTGTTTG TGTGTTGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780  
 ATCTCTGACA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840  
 CCTTTGGGG TCAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900  
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020  
GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAAATCC TTTTACTTTT 1080  
AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAGAA 1140  
ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG 1200  
TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAATA TCAGAACCCAG GAGTGAAAGC 1260  
ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320  
GTGTAGGCTT TTTATTGTTT GTTGGAAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380  
TTCATTATCC TTAATAAAAA AA

Seq ID NO: 364 Protein sequence  
Protein Accession #: NP\_076404

1 11 21 31 41 51  
15 MGFNLTAKL PNNELHQES HNSGNRSDGP GKNTLHNEF DTIVLPVLYL IIFVASILLN 60  
GLAVWIFFHI RNKTSFIPYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL 120  
FYANMYTSIV FLGLISIDRY LKVVPKPGDS RMYSTITPKV LSVCVWVIMA VLSLPNIILT 180  
NGQPTEDNIH DCSKLKSLPG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240  
ISQSSRRKKH NQSIKVVAV FFTCFLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300  
20 FLSACNVCLD PIIFYFMCRS PSRRLFKSN IRTSRSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 365 DNA sequence  
Nucleic Acid Accession #: NM\_005365.1  
Coding sequence: 1..948

1 11 21 31 41 51  
25 ATGTCCTCG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60  
GAGGACTTGG GCCTGATGGG TGACACAGGA CCCACAGCGG AGGAGGAGGA GACTACCTCC 120  
30 TCCTCTGACA GCAGAGGAGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAGAGT 180  
CCTCAGGGAG CGCTTCCTCT CTCCATTTCG GTCTACTACA CTTTATGGAG CCAATTGAT 240  
GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGACCC AGCTCAGCTG 300  
GAGTTTATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360  
35 CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420  
AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAGAGCCT CCGAGTTTCA GCAGGTGATC 480  
TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT 540  
CTTGGCCTCT CGTGCATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCOCGCCCTC 600  
CTGATCATGT TCCTGGGTGT GATCCTAACC AAAGACAAC GCGCCCTGA AGAGTTTATC 660  
40 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAG AGCAGATGTT CTACGGGGAG 720  
CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAACT ACCTGGAGTA CCGGCAGGTG 780  
CCCGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840  
AGCTATGAGA AGGTATATAA TTATTGCTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900  
CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 366 Protein sequence  
Protein Accession #: NP\_005356.1

1 11 21 31 41 51  
50 MSLEQRSPHC KPDELEAQQ EDLGLMGAQE PTGEEETTS SSDSKEEVS AAGSSSPQS 60  
PQGASSSIS VYITLWSQFD EGSSSQESEE PSSSVDPAQL EPMFQALKL KVAELVHPLL 120  
HKYRKEPVT KAEMLSEVIK NYKRYFPVIF GKASEFMQVI FGTDUKEVDP AGHSYILVTA 180  
LGLSCDSMLG DGHSMFKAAL LIIIVLGVILT KNCAPPEVI WEALSVMGVY VGKEHMPYGE 240  
55 PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LMWSKAHAET SYEKVINYL MLNAREPICY 300  
PSLYEEVLGE EQEGV

Seq ID NO: 367 DNA sequence  
Nucleic Acid Accession #: NM\_014400  
Coding sequence: 86..1126

1 11 21 31 41 51  
60 GGTACTCAT CCTGGGCTCA GGTAAGAGGG CCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60  
GAGCCCAAGG GAGCAGGACG GAGCCATGGA CCCGCCAGG AAAGCAGGTG CCCAGGCCAT 120  
65 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180  
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CGAACAAGA TGAAGACAGT 240  
GAAGTGGCGG CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300  
CGGACAATTC TGCGTGGCAG TGCSGGGTG CGGTTGCGGA CTCGCCGCA AGAATGACCG 360  
70 CGGCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420  
CTGCAACGCC AAGCTCAACC TCACTCGCG GCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480  
ATACCCGCC AACCGCGTGG AGTCTACAG CTGTGTGGGC CTGAGCGGG AGGCGTGCCA 540  
GGGTACATCG CCGCGGCTG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600  
CTTGCAGCGC AAGCTCACT TGACGGCAGC TAATGTGACT GTGTCTTTCG CTGTCCGGGG 660  
75 CTGTGCTCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCAGGGT TCACGCTCAG 720  
TGGCTCGATG TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780  
CCCTCGAATC CCACCCCTTG TCCGCTGCC CCTCCAGAG CCAACGACTG TGGCCTCAAC 840  
CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAACCCAT 900  
GCCAGCGCCA ACCAGTCAGA CTCGAGAGCA GGGAGTAGAA CAGAGGCCCT CCGGGGATGA 960  
80 GGAGCCGAGG TTGACTGGAG GCGCGCTGG CCACAGGAC CGCAGCAATT CAGGGCAGTA 1020  
TCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080  
ATTGGCAGCC CTTCGTGTGG CCGTGGCTGC TGGTGTCTTA CTGTAGACTT CTCACCTGG 1140  
AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTGTGT 1200  
CCACCACTG GACTGGGCTG GCCAGCCCC TGTTTTCCA ACATTCCCCA GTATCCCCAG 1260  
CTTCTGCTGC GCTGTTTTCG GCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320

GGGTGTTCTA GCTTTTGGAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380  
 TCCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440  
 AGGATGCTAA GCTTCTTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500  
 GGTGGGACAA TGGCTCCCA CTCTAAGCAC TGCCTCCCT ACTCCCGCA TCTTTGGGGA 1560  
 ATCGSTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620  
 CTTATGTCTG TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680  
 TTGTATAGTG AAAAAAAA

Seq ID NO: 368 Protein sequence  
 Protein Accession #: NP\_055215

1 11 21 31 41 51  
 MDPARKAGAQ AMIWTAGWLL LLLLRRGGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGVUV 60  
 CTEAVGAVET IHGQFSLAVX GGGSLPLGKN DRGLDLHGLL AFILQQAQCA DRCAKLNL 120  
 SRALDPAGNE SAYPPNGVEC YSCVLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVLT 180  
 AANVTSLPV RGCVDDEFT RDGVTGPFT LSGSCCGSR CNSDLRNKTY FSPRIPLVR 240  
 LPPPEPTTVA STTSVTTSTS APVPTSTTK PMPAPTSQTP RQVEHEASR DEEPRLTGGA 300  
 AGHQDRSNS QYPKGGPQQ PHNKGCVAPT AGLAALLAV AAGVLL

Seq ID NO: 369 DNA sequence  
 Nucleic Acid Accession #: NM\_005329.1  
 Coding sequence: 1..1662

1 11 21 31 41 51  
 ATCCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCTGGCA 60  
 GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGAAAAG 120  
 CACTACCTGT CCTTCGGCT GTACGGGCGC ATCTGGGCGC TGCACTGCT CATTGAGAGC 180  
 CTTTTCCTCT TCCTGGAGCA CCGGCGCATG CGACGTGCGC GCCAGGCCCT GAAGCTGCC 240  
 TCCCGCGGCG GGGGCTCGGT GGCACGTGTC ATTGCCGCT ACCAGGAGGA CCCTGACTAC 300  
 TTGCGCAAGT GCCTGCGCTC GGCACGCGC ATCTCCTCC CTGACCTCAA GGTGGTCTG 360  
 GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420  
 GCGGCGACCG AGCAGGCGCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480  
 GGTGAGACGG AGGCGAGCCT GCAGGAGGGC ATGGACCGTG TCGGGAGTGT GGTGCGGGCC 540  
 AGCACCTTCT CGTGCATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTCTAT GTACACGGCC 600  
 TTCAAGGCCCT TCGGCGATTG GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660  
 GATCCAGCCT GCACCATCGA GATGCTCGA GTCTGGAGG AGGATCCCCA AGTAGGGGGA 720  
 GTCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTT CTTGAGCAGC 780  
 GTGCGGTACT GGATGGCCTT CAACGTGGAG CGGGCCTGCC AGTCTACTT TGGCTGTGTG 840  
 CAGTGTAATA GTGGGCGCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900  
 GACTGTGACC ATCAAGAATT CCTAGGCAGC AAGTGCACT TCGGGGATGA CCGGCACCTC 960  
 ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CGCGCGCTC CAAGTGCTCT 1020  
 ACAGAGACCC CCACTAAGTA CCTCGGTGG CTCAACAGC AAACCGCTG GAGCAAGTCT 1080  
 TACTTCCGGG AGTGGCTCTA CACTCTCTG TGGTTCCTA AGCACCCT CTGGATGACC 1140  
 TACGAGTCAG TGGTCAAGGG TTTCTTCCC TTCTCTCCA TTGCCACGGT TATACAGCTT 1200  
 TTCTACCGGG GCGCATCTG GAACATTCTC CTCTCTCTGC TGACGGTGCA GCTGGTGGGC 1260  
 ATTACTAGG CCACTACGG CTGCTTCTT CGGGGCAATG CAGAGATGAT CTTGATGTC 1320  
 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGGCCA AGATCTTGC CATTGCTACC 1380  
 ATCAACAAAT CTGGCTGGGG CACCTCTGGC OGAAAACCA TTGTGGTGAA CTTCTTGGC 1440  
 CTCATTCTG TGTCCATCTG GGTGGCAGT CTCTGGAGG GGCTGGCTA CACAGCTTAT 1500  
 TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCTGT TCTTGGGGC TATCTGTAT 1560  
 GGCTGCTACT GGGTGGCCTT CCTCATGCTA TATCTGGCCA TCATCGCCG GOGATGTGG 1620  
 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 370 Protein sequence  
 Protein Accession #: NP\_005320.1

1 11 21 31 41 51  
 MPVQLTTLAL VVGTSIFALA VLGGILAAV TGYQFIHTEK HYLSPGLYGA ILGLHLIIQS 60  
 LFAPLEHRRR RRAGQALKLP SPRRGVALC IAAYQEDPDY LRKCLRSAQR ISFPDLKVV 120  
 VVDGNRQEDA YMLDIFHEVL GGTGAGPFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180  
 STPSCIMQKW GSKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240  
 VGGDVQILNK YDSWISPLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQGFLE 300  
 DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLW LNQQTRWSKS 360  
 YFREWLNSL WFKHHLWMT YESVVTGFFP FFLIATVIQL PYRGRIWNIL LFLITVLVVG 420  
 IIKATYACFL RGAEMIFMS LYSLLYMSL LPAKIFAIAT INKSGWGTSG RKTIVVNF 480  
 LIPVSIWVAV LLEGLAYTAY QDLFSETEL AFLVSGAILY GYVWALLML YLAILARROG 540  
 KKPEQYSLAP AEV

Seq ID NO: 371 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 148-7095

1 11 21 31 41 51  
 CACACATACG CACGACGAT CTCACTTGA TCTATACCT GGAGGATTAA AACAAACAA 60  
 CAAAAAATC ATTTCTCTCG CTCCCCCTCC CTCTCCACTC TGAGAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CCGCAGACCG TCTGAAATG CGAATCTTAA AGCGTTTCT CGCTTGCATT 180  
 CAGCTCTCTT GTGTTTGGCG CCGGATTTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTGAAG AGATTGGCTG GTCCATATCA GGAGCACTGA ATCAAAAAA TTGGGGAAG 300  
 AAATATCAAC CATGTAATAG CCAAAACAA TCTCTATCA ATATTGATGA AGATCTTCA 360  
 CAAGTAAATG TGAATCTTAA GAACTTAA TTTGAGGTT GGGATAAAC ATCATGGAA 420

AACACATTCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480  
 GTCAGCGGAG GAGTTTCAGA AATGGTGTTC AAAGCAAGCA AGATAACTTT TCACCTGGGA 540  
 AAATGCAATA TGTCTCTGTA TGGATCAGAG CATAGTTTAG AAGGACAAA ATTTCACCTT 600  
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660  
 5 GGAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTGAGG TTGGACAGA AGAAATTTG 720  
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTAGTC GTTTTGGAA GCAGGCTGCT 780  
 TTAGATCCAT TCATCTGTTT GAACCTTCTG CCAACTCAA CTGACAAGTA TTACATTTAC 840  
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900  
 10 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTGTG AAGTCTTAC AATGCAACAA 960  
 TCTGGTTATG TCATGCTGAT GGAATCTTA CAAACAATT TCGAGAGCA ACAGTACAAG 1020  
 TTCTCTAGAG AGGTGTTTTC CTCATACACT GGAAGGAAG AGATTATGA AGCAGTTTGT 1080  
 AGTTCAAGAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTACA 1140  
 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAG 1200  
 15 CAGTTGGATG GAGAGGACCA AACCAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260  
 GGTGCTATTG TCAATAATTT GCTACCCAAT ATGAGTTATG TTTCTCAGAT AGTAGCCATA 1320  
 TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380  
 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAAGT AAGAAATAT CAAGGAGGAG 1440  
 GAAGAGGGA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGTACA 1500  
 20 AACCATACTA GGAAGGAAG ACCCCAGATT TCTACCACA CACTACTCAA TCGCATAGGG 1560  
 ACAGAAATACA ATGAAGCCAA GACTAACCGA TCCCAACAA GAGGAAGTGA ATTCTCTGA 1620  
 AAGGGTATG TTCCCAATAC ATCTTAAAT TCCACTTCCC AACCAGTCA TAAATTAGCC 1680  
 ACAGAAAGAC ATATTTCTCT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740  
 GAAGGTACTT CAGCTCTTGT AAATGATGGC TCTAAAAGT TTTCTAGATC TCCACATATG 1800  
 25 AACTTGTGCG GCACTGCGA ATCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860  
 AGTTTATGTA CCAATTTCAA GCTTGATACT GGAGCTGAAG ATTCTCAGG CTCCAGTCCC 1920  
 GCAACTCTG CTATCCCAT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTCTCTCC 1980  
 GAAACCCAG AGACAATAAC ATATGATGTC CTATATCCAG AATCTGCTAG AAATGCTTCC 2040  
 GAAGATTCAA GTTCATCAGG TTCAGAAGAA TCACTAAGG ATCTCTCTAT GGAGGGAAT 2100  
 30 GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160  
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220  
 TCCCTTTCTG CAGGCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280  
 CATTAATCTA CCTTTGCTCA CTCCCAACT GAGGTAAACAC CTCATGCTTT TACCCATCC 2340  
 TCCAGACAAC AGGATTGCTT CTCCAGGTC AACGTGGTAT ACTCGCAGAC AACCCAAACG 2400  
 35 GTATACAATG GTGAGACACC TCTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460  
 ACCCTTTGTG TGCTTGACAA TCAGATCTCTC AACACTACCC CTGCTGCTC AAGTAGTGAT 2520  
 TCGGCTTGGC ATGCTACGCC TGTATTTCCC AGTGTGATG TGTCTTTGA ATCCATCTG 2580  
 TCTCTCTATG ATGTTGACCC TTGCTTCCA TTTCTCTCTG CTCTCTCAG TAGTGAATTG 2640  
 40 TTTCGCCATC TGCAATACAG TTCTCAATC CTCCACAAG TTACTTCAGC TACCGAGAGT 2700  
 GATAAGGTGC CCTTGATGTC TTCTCTGCCA GTGGCTGGGG GTGATTGCT ATTAGAGCCC 2760  
 AGCCTTGTCT AGTATTCTGA TGTGCTGTCC ACTACTCATG CTGCTTCAGA GAGCTGGAA 2820  
 TTTGTTAGTG AATCTGCTGT TCTTTATAAA ACCTTATGT TTTCTCAAGT TGAACCAACC 2880  
 AGCAGTATG CCAATGATGA TGCAAGTCTC TCAGGCGCTG AACCTTCTTA TGCTTGTCT 2940  
 45 GATAATGAGG GCTCCCAACA CATCTTCACT GTTCTTACA GTTCTGCAAT ACCTGTGCT 3000  
 GATTCTGTG GTGAATCTTA TCAGGTTTCC TTAATTAGCG GCCCTAGCCA TATACCAATA 3060  
 CCTAAGTCTT CGTTAATAAC CCCAAGTGA TCATTACTGC AGCCTACTCA TGCCCTCTCT 3120  
 GGTGATGGGG AATGGTCTGG AGCCTCTCTC GATAGTGAAT TTTCTTTACC TGACACAGAT 3180  
 50 GGGCTGACAG CCCTTAACAT TTCTTCACT GTTCTGTAG CTGAATTTAC ATATACAACA 3240  
 TCTGTGTTG TGCATGATA TAAGGCGCTT TCTAAAAGT AAATAATATA TGGAAATGAG 3300  
 ACTGAAGTGC AAATCTCTTC TTTCAATGAG ATGGTTTACC CTCTGGAAG CACAGTCATG 3360  
 CCCAAGATGT ATGATAATGT AAATAAGTGT AATGCGTCT TACAAGAAAC CTCTGTTTCC 3420  
 55 ATTTCTAGCA CCAAGGCGAT GTTCCAGGG TCCCTTGCTC ATACCACCAC TAAGGTTTTT 3480  
 GATCATGAGA TTAGTCAAGT TCCAGAAAT AACTTTTCTG TTCAACCTAC ACATCTGTCT 3540  
 TCTCAAGCAT CTGGTGACAT TTGCTTAAA CTGTGCTTAA GTGCAAACTC AGAGCCGACA 3600  
 TCTCTGACCC CTGCTTCTAG TGAATGTTA TCTCTTCAA CTCAGCTCTT ATTTATGAG 3660  
 60 ACCTCAGCTT CTTTATGATC TGAAGTATTG CTACAACCTT CCTTTCAGGC TTCTGATGTT 3720  
 GACACCTTGC TTAATACTGT TCTCCAGCT GTGCCAGTG ATCCAATATT GGTGAAACC 3780  
 CCCAAGTTG ATAAATTAG TTCTACAATG TTGCATCTCA TTGTATCAA TTCTGCTTCA 3840  
 AGTGAAACA TGCTGCACTC TACATCTGTA CCAGTTTTG ATGTGTGCGC TACTTCTCAT 3900  
 65 ATGCACCTG CTTCACCTCA AGGTTTGACC ATTTCTATG CAAGTGAGAA ATATGAACCA 3960  
 GTTTTGTAA AAAGTGAAG TTCCCAACAA GTGGTACCTT CTTTGTACAG TAATGATGAG 4020  
 TTGTTCCAAA CGGCCAATT GGAGATTAAC CAGGCCATC CCCCAAAAG AAGGCATGTA 4080  
 TTTGCTACAC CTGTTTATC AATTGATGAA CCATTAAATA CACTAATAAA TAAGCTTATA 4140  
 70 CATTCGATG AAATTTTAA CTCCACCAA AGTTCTGTTA CTGGTAAAGT ATTTGCTGTT 4200  
 ATTCCAACAG TTGCTTCTGA TACATTGTA TCTACTGATC ATTCTGTCC TATAGGAAAT 4260  
 GGGCATGTTG CCATTACAGC TGTCTCTCCC CACAGAGATG GTTCTGTAAC CTCAACAAAG 4320  
 TTGCTGTTTC CTCTAAGGC AACTTCTGAG CTGAGTCATA GTGCCAAATC TGATGCCGGT 4380  
 75 TTAGTGGGTG GTGGTGAAGA TGGTGACACT GATGATGATG GTGATGATGA TGATGATGAC 4440  
 AGAGGTAGTG ATGGCTTATC CATTCATAAG TGTATGTCAT GCTCATCTTA TAGAGAATCA 4500  
 CAGGAAAAGG TAATGAATGA TTCAGACACC CAAGAAAACA GTCTTATGGA TCAGAATAAT 4560  
 CCAATCTCAT ACTCACTATC TGAGAATTCT GAAGAAGATA ATAGAGTCAC AAGTGTATCC 4620  
 80 TCAGACAGTC AAACCTGGAT GGACAGAAGT CCTGGTAAAT CACCATCAGC AAATGGGCTA 4680  
 TCCCAAGAGC ACAAATGATG AAAAGAGGAA AATGACATTC AGACTGGTAG TGCTCTGCTT 4740  
 CCTCTCAGCC CTGAATCTAA AGCATGGGCA GTTCTGACAA GTGATGAAGA AAGTGGATCA 4800  
 GGGCAAGGTA CCTCAGATAG CCTTAATGAG AATGAGACTT CCACAGATT CAGTTTGTGA 4860  
 75 GACACTAATG AAAAGATGC TGATGGGATC CTGGCAGCAG GTGACTCAGA AATAACTCTC 4920  
 GGATTCCTAC AGTCCCAAC ATCATCTGTT ACTAGCAGAG ACTCAGAAGT GTTCCAGCTT 4980  
 TCAGAGGAGC AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGTTG 5040  
 GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 5100  
 80 CTAGTGGTTC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 5160  
 TACTTAGAGG ACAGTACATC CCCTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA 5220  
 ATTTCAAGATG ATGTGCGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 5280  
 CATGCAAGTA GTGGGTTTAC TGAAGAATT GAGACACTGA AAGAGTTTTA CCAGGAAGTG 5340  
 CAGAGCTGTA CTGTGACTT AGGTATTACA GCAGACAGCT CCAACCAACC AGACAACAG 5400  
 CACAAGAATC GATACATAA TATGTTGCC TATGATCATA GCAGGGTTAA GCTAGCAGAG 5460

5 CTTGCTGAAA AGGATGGCAA ACTGACTGAT TATATCAATG CCAATTATGT TGATGGCTAC 5520  
 AACAGACCAA AAGCTTATAT TGCTGCCCAA GGCCCACTGA AATCCACAGC TGAAGATTTC 5580  
 TGGAGATGA TATGGGAACA TAATGTGGAA GTTATTGTCA TGATAACAAA CCTCGTGGAG 5640  
 AAAGGAAGGA GAAATGTGA TCAGTACTGG CCTGCGATG GGAGTGAGGA GTACGGGAAC 5700  
 TTTCTGGTCA CTCAGAAGAG TGTGCAAGTG CTGCGCTATT ATACTGTGAG GAATTTTACT 5760  
 CTAAGAAACA CAAAAATAAA AAAGGGCTCC CAGAAAGGAA GACCCAGTGG ACCTGTGGTC 5820  
 ACACAGTATC ACTACAGCA GTGGGCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 5880  
 CTGACCTTTG TGAGAAAGGC AGCCTATGCC AAGCGCCATG CAGTGGGGCC TGTGTCTGTC 5940  
 10 CACTGCGAGT CTGGAGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAG 6000  
 CAGATTCAAC ACGAAGGAAC TGTCAACATA TTTGGCTTCT TAAACACAT CCGTTCACAA 6060  
 AGAAATTATT TGGTACAAAC TGAGGAGCAA TATGCTTCA TTCATGATAC ACTGGTTGAG 6120  
 GCCATACCTA GTAAAGAAAC TGAGGTGCTG GACAGTCATA TTCATGCCTA TGTTAATGCA 6180  
 CTCCTCATT CTGGACCGAG AGGCAAAACA AAGCTAGAGA AACAAATCCA GCTCCTGAGC 6240  
 15 CAGTCAAAAT TACAGCAGAG TGACTATTCT GCAGCCCTAA AGCAATGCAA CAGGGAAGAG 6300  
 AATCGAAGCTT CTCTATCAT CCCTGTGGAA AGATCAAGGG TTGGCATTTC ATCCCTGAGT 6360  
 GGAGAAGGCA CAGACTACAT CAATGCCTCC TATATCATGG GCTATTACCA GAGCAATGAA 6420  
 TTCACTATTA CCCAGCAGCC CTCTCTCAT ACCATCAAGG ATTCTGGAG GATGATATGG 6480  
 GACCAATAAT CCCAAGCTGT GGTATGATT CCTGATGGCC AAAACATGGC AGAAGATGAA 6540  
 20 TTTGTTTACT GGCCAAATAA AGATGAGCCT ATAAATGTGT AGAGCTTTAA GGTCACTTCT 6600  
 ATGGCTGAAG AACACAAATG TCTATCTAAT GAGGAAAAAC TTATAATTCA GGACTTTATC 6660  
 TTAGAAGCTA CACAGGATGA TTATGTACTT GAAGTGAGGC ACITTCAGTG TCCTAAATGG 6720  
 CCAATCCAG ATAGCCCATC TAGTAAACT TTTGAACCTA TAAGTGTTAT AAAAGAAGAA 6780  
 GCTGCCAATA GGGATGGGCC TATGATTGTT CATGATGAGC ATGGAGGAGT GACGGCAGGA 6840  
 25 ACTTCTGTG CTCTGACAA CTTTATGCAC CAACTAGAAA AAGAAAATTC CGTGGATGTT 6900  
 TACCAGGTAG CCAAGATGAT CAATCTGATG AGGCCAGGAG TCTTTGCTGA CATTGAGCAG 6960  
 TATCAGTTTC TCTACAAAGT GATCCTCAGC CTGTGAGCA CAAGGCAGGA AGAGAATCCA 7020  
 TCCACCTCTC TGACAGTAA TGGTGACAGA TTGCCTGATG GAAATATAGC TGAGAGCTTA 7080  
 GAGTCTTTAG TTTAAACAGC AAAGGGGTGG GGGGACTCAC ATCTGAGCAT TGTTTTCTC 7140  
 30 TTCTAAATAT TAGGCAGGAA AATCAGTCTA GTTCGTGTTT CTGTGATTTC CCCATCACTT 7200  
 GACAGTAATC TTATGACAT AGGATTCTGC GCCCAAATTT ATATCATTA AATTTTACAG 7260  
 CTTTTTGCAA GACTTGAAT TTAATTATTA TGTGTAAGT AAAATGATTG AATTTTACAG 7320  
 TATTTCTAAG AATGGAATTG TGGTATTTT TTCTGTATTG ATTTTAACAG AAAATTTCAA 7380  
 TTTATAGAGG TTAGGAATTC CAAACTACAG AAAATGTTT TTTTGTAGT CAAATTTTAA 7440  
 35 GCTGTATTG TAGCAATTAT CAGGTTTGTG AGAAATATAA CTTTAAATAC AGTAGCCTGT 7500  
 AAATAAAACA CTCTCCATA TGATATTCAC CATTTTACAA CTGCAGTATT CACCTAAAGT 7560  
 AGAAATAATC TGTACTTAT TGTAATACT GCCCTAGTGT CTTCAATGAG CAAATTTATA 7620  
 TTTATAATTG TAGATTTTA TATTTTACTA CTGAGTCAAG TTTTCTAGT CTGTGTAATT 7680  
 GTTTAGTTTA ATGACGTAGT TCATTAGCTG GTCTTACTCT ACCAGTTTTC TGACATTGTA 7740  
 40 TTGTGTTACC TAAGTCATTA ACTTTGTTTC AGCATGTAAT TTTAACTTT GTGGAATAA 7800  
 GAAATACCTT CATTTTGAAA GAAGTTTFTA TGAGAATAAC ACCTTACCAA ACATGTTTCA 7860  
 AATGGTTTTT ATCCAAGGAA TTGCAAAAT AAATATAAAT ATTGCCATTA AAAAAAATA 7920  
 AAAAAAATA AAAAAAATA AAAA

Seq ID NO: 372 Protein sequence:  
 Protein Accession #: built from XP\_031379

1 11 21 31 41 51  
 50 MRILKRFILAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKRWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNKLKL KFGWMDKTSL ENTPIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFHW GKCMNMSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEEAV KKGKLRALS 180  
 ILFEVGTEN LDFKAIIDGV ESVSFRGKQA ALDPFILLNL LNPSTDKYYI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVLMMDY LQNNFREQQY KFSRQVFPSSY 300  
 55 TGKEEIHFAV CSSEPEVQA DPENYTSLLV TWERPRVVD TMIEKFAVLV QQLDGEDQTK 360  
 HEPLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPELDLPE 420  
 LGITEEIIKE EEEGKDIEEG AIVNPRDSA TNQIRKKEPQ ISTTHYNNRI GTKYNEAKTN 480  
 RSPTRGSEFS GKGDVPTSL NTSQPVTKL ATEKDISLS QTVTELEPPT VEGTSASLND 540  
 GSKTVLRSEH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 60 ENISQGYIFS SENPETIITYD VLIPESARNA SEDSTSGSSE ESLKDPSEMG NVWFPSSTDI 660  
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTPAYFP 720  
 TEVTPHAFPT SSRQQLVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVPFL VTPLLLDNQI 780  
 LNTTPAASSS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSE LFRHLHTVSQ 840  
 65 ILPQVTSATE SDKVPILHASL PVAGDILLLE PSLAQYSDVL STTHAASETL EFGSESGVLY 900  
 KILMFQVQEP PSSDAMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG 960  
 SLFSGPSHIP IPKSSLIPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS 1020  
 PVSVAEFTYT TSVPFGDNKA LSKSEIIYGN ETELQIPSPN EMVYPSSEST MPNMYDNVKN 1080  
 LNASLQETSV SISSTKGMFP GSLAHTTKV FDHEISQVPE NNFSVQPTH VSQASGDTSL 1140  
 70 KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200  
 AVPSDPIVLE TPKVDKISST MLHLIVNSA SSENMLHSTS VVPVDSPTS HHSASLQGL 1260  
 TISYASEKEYE PVLLKSESSH QVPSLYSND ELFQTNLEI NQAHPPKGRH VFATFVLSID 1320  
 EPLNTLINKL IHSDEILTST KSSVTGKVA GIPTVASDTF VSDHRSVPFG NGHVAITAVS 1380  
 PHRDGVSST KLLFSPKATS ELSHSAKSDA GLVGGEGDGD TDDGDDDDDD DRGSDGLSIH 1440  
 75 KQMSCSYRE SQEKVWNSD THENSIMDQNP NPIYSLSSEN SEEDNRVTSV SSSDQTGMDR 1500  
 SPKSPSANG LSQKQNDGKE ENDIQTGSAL LPLSPESKAW AVLTSDSESG SQGTSDSL 1560  
 ENETSTDFSP ADTNEKDADG ILAGDSEIT PGFPQSPTSS VTSENSEVPH VSEAEASNSS 1620  
 HESRIGLABG LESEKKAVIP LVIVSALTPI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR 1680  
 80 VISTPPTPIV PISDDVGAIP IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCTVDLGI 1740  
 TADSSNHPDN KHKRYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPRAYIAA 1800  
 QGPLKSTAEF FWRMIWEHNV EVIVMITNLV EKGRKCDQY WPADGSEYQG NFLVTQKSVQ 1860  
 VLAYYTVRNF TLRNTKIKKG SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRKAAAY 1920  
 AKRHAVGPV VHCASAGVRT GTYIVLDSML QQIQHEGTVN IPGFLKHRS QRYNLVQTEE 1980  
 QYVFIHDTLV EAILSKEDEV LDISHIAYVN ALLIPGPAKG TKLEKQFQLL SQSNIQSDPY 2040  
 SAALKQCNRE NKRTSSIIIP ERSRVGISSL SGEPTYDINA SYIMGYQSN EPIITQHPLD 2100  
 HTIKDFWRMI WDHNAQLVVM IPDQGNMAED EFVYWPKNDE PINCESPKVT LMAEHEKCLS 2160

NEEKLIQDF ILEATQDDYV LEVRHFQCPK WPNPDSPIK TFEIISVIKE EAANRDGPMI 2220  
 VHDEHGGVTA GTFCALTTIM HOLEKENSVD VYQVAKMINL MRPGVFADIE QYQFLYKVL 2280  
 SLVSTRQEN PSTSLDSNGA ALPDGNIAES LESLV

5

Seq ID NO: 373 DNA sequence

Nucleic Acid Accession #: built from NM\_002851

Coding sequence: 148-4518

10	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
15	CAGCTCCTCT	GTGTTTGCAG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTTGTGAAG	AGATTGGCTG	GTCTATATCA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAAACAC	TGGGAAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
20	GTGAGCGGAG	GAGTTTCAGA	AATGGTGT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTITCAA	GTITTAGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTGG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTCT	GTITTTGGGA	GCAGGCTGCT	780
25	TTAGATCCAT	TCATACGTGT	GAACCTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAG	CCAGTTGGCT	GTITTTTGTG	AAGTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCACTGCTAG	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCAATG	AGCAGTTTGT	1080
30	AGTTTCAAGC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTATCA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTC	TCAATAATTT	GCTACCCAAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
35	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATATCA	GGAAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCCATAGGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTTCTTGGA	1620
	AAGGGTGATG	TTCCCAATAT	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
40	ACAGAAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACGTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACTG	TTCTTAGATC	TCCATATATG	1800
	AACCTGTGGG	GGAAGTCGGA	ATCCTTAAAT	ACAGTTTCTA	TAAACAGATA	TGAGGAGGAG	1860
	AGTTTATGGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTTCTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTTCTGCTAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
45	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAGAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTCTC	AGACTAATTA	CACGTAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTTCTG	CAGGCCAGGT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
50	CATTATTCTA	CTTTTGCTTA	CTTCCCAACT	GAGGTAAACAC	CTCATGCTTT	TACCCATCTC	2340
	TCCAGACAA	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCACCG	2400
	GTATACAAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAAGAGCG	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
	TGCTAGTGGT	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
55	TTTACTTAG	AGGACAGTAC	ATCCCTTAGA	GTATATCCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTCAG	ATGATGTGGG	AGCAATTTCCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTGGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCCATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
60	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
	TACAACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAAATG	TGATCAGTAC	TGGCCTGCGG	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTTCTGG	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCTT	ATTATACGTG	GAGGAATTTT	3180
65	ACTCTAAGAA	ACACAAAAT	AAAAAGGGC	TCCAGAAAAG	GAAGACCCAG	TGGAAGTGTG	3240
	GTCAACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTGTGC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACCA	GGCACAATATA	TTGTGCTAGA	CAGTATGTTG	3420
70	CAGCAGATCG	AACACGAGG	AACGTGTCAAC	ATATTGGGCT	TCTTAAAAACA	CATCCGTTCA	3480
	CAAAGAAATT	ATTTGTGACA	AACGTAGGAG	CAATATGTCT	TCATTCTATG	TACACTGGTT	3540
	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGTC	ATATTCTATG	CTATGTTAAT	3600
	GCACTCTCTCA	TTCTGGAGCC	AGCAGGCAAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATT	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTTCTAT	CATCCCTGTG	GAAGATCAA	GGGTTGGCAT	TTCACTCCCTG	3780
75	AGTGGAGAAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
	GAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTCTCT	GAGGATGATA	3900
	TGGGACCATTA	ATGCCCACT	GGTGGTTATG	ATTCTGATG	GCCAAAACAT	GGCAGAAGAT	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTATGGCTG	AAGAACAACA	ATGTCTATCT	AATGAGGAAA	AACCTATAAT	TCAGGACTTT	4080
80	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGCTCTAAA	4140
	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAGAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTCATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AAACCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTITACCGCT	TAGCCAGAT	GATCAATCTG	ATGAGGCGAC	GAGTCTTTGC	TGACATTGAG	4380
	CAGTATCAGT	TTCTCTACAA	AGTGATCTCT	AGCCTTGTGA	GCACAAGGCA	GGAAAGAAAT	4440

5 CCATCCACCT CTCTGGACAG TAATGGTGCA GCATTGCCTG ATGGAAATAT AGCTGAGAGC 4500  
 TTAGAGTCTT TAGTTTAAACA CAGAAAGGGG TGGGGGGACT CACATCTGAG CATTGTTTTC 4560  
 CTCTTCTCTAA AATTAGGCAG GAAATCAGT CTAGTCTGT TATCTGTGA TTCCCATCA 4620  
 CCTGACAGTA ACTTTCATGA CATAGGATTC TGCCGCCAAA TTTATATCAT TAACAATGTG 4680  
 TGCCTTTTGG CAAGACTTGT AATTACTTA TTATGTTGA ACTAAATGA TTGAATTTTA 4740  
 CAGTATTCTT AAGAATGGAA TTGTGGTATT TTTTCTGTGA TTGATTTTAA CAGAAATTT 4800  
 CAATTATATAG AGGTTAGGAA TTCCAACTA CAGAAATGT TTGTTTTTAG TGTCAAAATTT 4860  
 10 TTAGCTGTAT TTGTAGCAAT TATCAGGTTT GCTAGAAATA TAACTTTTAA TACAGTAGCC 4920  
 TGTAAATAAA AACTCTCTCC ATATGATATT CAACATTTTA CAATGCACT ATTCACTTAA 4980  
 AGTAGAAATA ATCTGTTACT TATGTAAAT ACTGCCCTAG TGTCTCCATG GACCAAAATTT 5040  
 ATATTTATAA TTGTAGATTT TTATATTTTA CTACTGAGTC AAGTTTTCTA GTTCTGTGTA 5100  
 ATTGTTTAGT TTAATGACGT AGTTCATTAG CTGGTCTTAC TCTACCACTT TTCTGACATT 5160  
 GTATTGTGTT ACCTAAGTCA TTAACCTTGT TTCAGCATGT AATTTTAACT TTGTGGGAAA 5220  
 15 ATAGAAATAC CTTCATTTTG AAAGAAGTTT TTATGAGAAAT AACACCTTAC CAACATTGT 5280  
 TCAATGGTTT TTTATCCAAG GAATTGCAAA AATAAATATA AATATTGCCA TTAATAAAAA 5340  
 AAAAAAANA AAAAAAANA AAAAAA

20 Seq ID NO: 374 Protein sequence:  
 Protein Accession #: built from XP\_031379

1 11 21 31 41 51  
 25 MRILKRFLAC IQLLCVCRLD WANGYYRQR KLVEEIGWSY TGALEQKMWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNKKL KFGWDKTSI ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFHW GKNMSSDGS EHSLEGQKFP LEMQIYCPDA DRFSSPEBAV KGKGLRLALS 180  
 ILFEVGTEN LDFKAIIDGV ESVSFQKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISEQL AVFCEVLTMQ QSGYVLMMDY LQNNFREQQY KFSRQVPSSY 300  
 30 TGKEIEHEAV CSSEPENVOA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360  
 HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPDLDFPE 420  
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPO ISTTHYNRI GTKVNEAKTN 480  
 RSPTRGSEFS GKGDVNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPTT VEGTSASLND 540  
 35 GSKTVLRSPH MNLSTGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 ENISQGYIFS SENPETITVD VLIPESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSSTDI 660  
 TAQPDVGSGR ESFLQNTYTE IRVDESEKIT KSFSAGPVMS QGPSVTDLEM PHYSTFAFFP 720  
 TEVTPHAFPT SSRQDLVST VNVVYSQTTQ PVYNAEASNS SHESRIGLAE GLESEKKAVI 780  
 PLVIVSALTF ICLVVLVGLL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDDVGAI 840  
 PIKHFFKHVA DLHASSGFTE EFETLKEFYQ EVQSCVDLG ITADSSNHPD NKHKRNYINI 900  
 40 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
 VEIVIMITNL VEKGRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020  
 GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFRKAA YAKRRAVGPV VVHCAGVGR 1080  
 TGTIYVLDSM LQIQIHEGTV NIPGFLKHIR SQRYNLVQTE EQYVFIDTL VEAILSKETE 1140  
 VLDSHIAHYV NALLIPGPAG KTKLEKQFQL LSQSNIIQSD YSAALKQCNR EKNRTSSIIP 1200  
 45 VERSRVGISL LSGETDYIN ASYIMGYQS NEFLITQHPL LHTIKDFWRM IWDHNAQLVV 1260  
 MIPDQGNMAE DEFVYWNKO EPINCESFKV TLMAEHEKCL SNEEKLIQD FILEATQDDY 1320  
 VLEVRFHQPC KWNPDSPIS KTFELISVIK EBAANRGPMP IVHDEHGGVT AGTFCALITL 1380  
 MHQLEKENSV DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440  
 AALPDGNIAE SLESVLV

50 Seq ID NO: 375 DNA sequence  
 Nucleic Acid Accession #: EOS sequence  
 Coding sequence: 148-4494

1 11 21 31 41 51  
 55 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA ACAAACAAA 60  
 CAAAAAACA ATTTCTCTCG CTCCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGCGGAGGGG CGCAGACOG TCTGAAATG CGAATCCTAA AGCGTTTCTT CGCTTGCAAT 180  
 60 CAGCTCTCTT GTGTTTCCCG CTTGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTTGAAG AGATTGGCTG TCTCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAG 300  
 AAATATCCAA CATGTAATAG CCCAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA 360  
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTGAGGTTT GGGATAAAAC ATCATTGGAA 420  
 AACACATTCA TTCATAACAC TGGGAAAAA GTGGAAATTA ATCTCACTAA TGACTACCGT 480  
 65 GTCAGCGGAG GAGTTTCAGA AATGGTGTIT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540  
 AAATGCAATA TGTCTATCGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600  
 GAGATGCAAA TCTACTGCTT TGATGCAGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAA 660  
 GGAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAAG TTGGGACAGA AGAAAATTTG 720  
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTAGTC GTTTTGGGAA GCAGGCTGCT 780  
 70 TTAGATCCAT TCATCTGTTT GAACCTCTG CCAAACTCAA CTGACAAGTA TTACATTAC 840  
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900  
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTGTGTG AAGTCTTAC AATGCAACAA 960  
 TCTGTTATG TCTATGCTAT GGACTACTTA CAAAACAATT TTGAGAGCA ACAGTACAA 1020  
 TTCTCTAGAC AGGTGTTTTC CTCTATACAT GGAAAGGAAG AGATTCATGA AGCAGTTTGT 1080  
 75 AGTTCTAGAC CAGAAAATGT TCAGGCTGAC CCAGAGAAAT ATACCAGCTT TCTTGTTACA 1140  
 TGGGAAGAC CTCGAGTCTT TTATGATACC ATGATTGAGA AGTTTGAGT TTTGTACAG 1200  
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260  
 GGTGCTATTG TCAATAATT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320  
 80 TGGCAATAG GCTTATATGG AAAATACAGC GACCAACTGA TTGTGCATG GCCTACTGAT 1380  
 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAACAG AAGAAATAT CAAGGAGGAG 1440  
 GAAGAGGGAA AAGACATTGA AGAAGSGCCT ATTGTGAATC CTGTTAGAGA CAGTGCTACA 1500  
 AACCATAATCA GGAAGAGGA ACCCCAGATT TCTACCACAA CACACTACAA TCGATAGGG 1560  
 ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620  
 AAGGGTATG TTCCCAATAC ATCTTTAAAT TCCACTCCC AACCACTCAC TAAATTAGCC 1680  
 ACAGAAAAAG ATATTTCCTT GACTCTCTAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740



5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60

GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAACTG TTCTTAGATC TCCACATATG 1800  
 AACTTGTGGG GGAAGTGCAG ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860  
 AGTTTATTGA CCAAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920  
 GCAACTCTCG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCTCTC 1980  
 GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040  
 GAAGATTCAA CTTCATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT 2100  
 GTGTGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTGTGGATC AGGCAGAGAG 2160  
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGTATG AATCTGAGAA GACAAACCAAG 2220  
 TCCTTTCTCG CAGGCCCACT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280  
 CATTATTCTA CCTTTGCCTA CTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340  
 TCCAGACAAC AGGATTGGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCAAACG 2400  
 GTATACAATG AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGGTTG 2460  
 GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 2520  
 CTAGTGGTTC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 2580  
 TACTTAGAGG ACAGTACATC CCTTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA 2640  
 ATTTAGATG ATGTGCGAGC AATTCGAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 2700  
 CATGCAAGTA GTGGGTTTAC TGAAGAATTT GAGGAAGTGC AGAGCTGTAT GTTGTACTTA 2760  
 GGTATTACAG CACACAGCTC CAACCAACCA GACAACAAGC ACAAGAATCG ATACATAAAT 2820  
 ATCGTGCCT ATGATCATAG CAGGGTTAAG CTAGCACAGC TTGCTGAAA GGATGGCAAA 2880  
 CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA ACAGACCAAA AGCTTATATT 2940  
 GCTGCCAAG GCCCACTGAA ATCCACAGCT GAAGATTCTT GGAGAATGAT ATGGGAACAT 3000  
 AATGTGAAGA TTATTGTATC GATAACAAAC CTCGTGGAGA AAGGAAGGAG AAAATGTGAT 3060  
 CAGTACTGCG CTGCCGATGG GAGTGAGGAG TACGGGAAC TTCTGGTCAC TCAGAAGAGT 3120  
 GTGCAAGTGC TTGCTTATTA TACTGTGAGG AATTTTACTC TAAGAAACAC AAAATAAAAA 3180  
 AAGGGCTCCC AGAAGGAAG ACCCAGTGGG CGTGTGGTCA CACAGTATCA CTACACGAG 3240  
 TGGCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC TGACCTTTGT GAGAAAGGCA 3300  
 GCCTATGCCA AGCGCCATGC AGTGGGGCTT GTTGTGCTCC ACTGCAGTGC TGGAGTTGGA 3360  
 AGAACAGGCA CATATATTGT GCTAGACAGT ATGTTGCAGC AGATTCAACA CGAAGGAAC 3420  
 GTCAACATAT TTGGCTTCTT AAAACACATC CGTTCACAAA GAAATTTATT GGTACAAACT 3480  
 GAGGAGCAAT ATGCTTCTAT TCATGATACA CTGGTTGAGG CCATCTTAG TAAAGAACT 3540  
 GAGGTGCTGG ACAGTCATAT TCATGCCTAT GTTAATGCAC TCCTCATTCG TGGACCAGCA 3600  
 GGCAAAACAA AGCTAGAGAA ACAATTCAGC CTCTGAGCC AGTCAAATAT ACAGCAGAGT 3660  
 GACTATTCTG CAGCCCTAAA GCAATGCAAC AGGGAAGAGA ATCGAATCTT TTCTATCATC 3720  
 CCTGTGAAA GATCAAGGGT TGGCATTCA TCCTGAGTG GAGAAGGCAC AGACTACATC 3780  
 AATGCCCTCT ATATCATGGG CTATTACCAG AGCAATGAAT TCATCATAC CCAGCACCTC 3840  
 CTCCTTCATA CCATCAAGGA TTTCTGGAGG ATGATATGGG ACCATAATGC CCAACTGGTG 3900  
 GTTATGATTC CTGATGGCCA AAACATGGCA GAAGATGAAT TTGTTTACTG GCCAAATAAA 3960  
 GATGAGGCTA TAAATTGTGA GAGCTTTAAG GTCACTCTTA TGGCTGAAGA ACACAAATGT 4020  
 CTATCTAATG AGGAAAACT TATAATTGAG GACTTTATCT TAGAAGCTAC ACAGGATGAT 4080  
 TATGTACTTG AAGTGGGCA CTTCAGTGT CCTAAATGGC CAAATCCAGA TAGCCCAT 4140  
 AGTAAACTTT TTGAACCTAT AAGTGTATA AAAGAAGAAG CTGCCAATAG GGATGGGCT 4200  
 ATGATTTGTC ATGATGAGCA TGGAGGAGTG ACCGCAGGAA CTCTGTGTG TCTGACAAAC 4260  
 CTATGCAACC AACTGAAAAA AGAAATTTCC GTGGATGTT ACCAGGTAGC CAAGATGATC 4320  
 AATCTGATGA GGCACAGGAG CTGTGCTGAC ATTGAGCAGT ATCAGTTTCT CTACAAAGTG 4380  
 ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCCAT CCACCTCTCT GGACAGTAAT 4440  
 GGTGAGCAT TGCTGATGG AATATAGCT GAGAGCTTAG AGTCTTAGT TTAACACAGA 4500  
 AAGGGTGGG GGGACTCACA TCTGAGCATT GTTTTCTCT TCCTAAATIT AGGCAGGAAA 4560  
 ATCAGTCTAT TTCTGTTATC TGTTGATTTT CCATCACTGT ACAGTAACIT TCATGACATA 4620  
 GGATTCCTGC GCCAATTTA TATCATTAAC AATGTGTGCC TTTTGTCAAG ACTTGTAAAT 4680  
 TACTTATTAT GTTTGAACATA AATGATTGA ATTITACAGT ATTTCTAAGA ATGGAATTGT 4740  
 GGTATTTTTC TCTGATTGA TTTTAACAGA AAATTTCAAT TTATAGAGGT TAGGAATTC 4800  
 AAACACAGA AAATGTTTGT TTTTAGTGT AAATTTTITAG CTGATTTGT AGCAATTATC 4860  
 AGTTTGTCTA GAAATATAAC TTTTAATACA GTAGCCTGTA AATAAAACAC TCTTCCATAT 4920  
 GATATTCAAC ATTTTCAAC TGCAATATC ACCTAAAGTA GAAATAATCT GTTACTTATT 4980  
 GTAAATACTG CCTAGTGTCC TCCATGGACC AAATTTATAT TTATAATGT AGATTTTTAT 5040  
 ATTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATTG TTAGTTTAA TGACGTAGTT 5100  
 CATTAGCTGG TCTTACTCTA CCAGTTTCT GACATTGTAT TGTGTTACCT AAGTCATTAA 5160  
 CTTTGTTTCA GCATGTAAAT TTAACTTTGT TGGAAAAATG AAATACCTTC ATTTTGAAG 5220  
 AAGTTTAT GAGATAACA CCTTACCAA CATTGTTCAA ATGTTTITA TCCAAGGAAT 5280  
 TCCAAAAATA AATATAATA TTGCCATTAA AAAAAA AAAA AAAA 5340  
 AAA

Seq ID NO: 376 Protein sequence:  
 Protein Accession #: EOS sequence:

65  
70  
75  
80

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRID WANGYYRQR KLVBEIGWSY TGAHQKQWNG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKLL KFGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKLRALS 180  
 ILFEVGTEN LDFKAIIDGV ESVSRPGKQA ALDPFILLNL LPNSTDKYVI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVLMMDY LQNNFREQQY KFSRQVFSSY 300  
 TGKEIHEAV CSSEPNVQA DPENYTSLLV TWERPRVVD TMIEKFAVLV QQLDGEDQTK 360  
 HEFLTDGQD LGAILNLNLLP NMSYVLQIVA ICTINGLYGKY SDQLIVDMPT DNPDLPLPE 420  
 LIGTEIIEKE EEEGKIDIEG AIVNPGRDSA TNQIRKKEPY ISTTHYNRI GTKYNEAKTN 480  
 RSPTRGSEFS KGKDVNTSL NSTSQPVTKL ATEKDISLTS QTVTELPHT VEGTSASLND 540  
 GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 ENISQGYIFS SENPETITYD VLPESARNA SEDSTSSGSE ESLKPSMEG NVWFPSSTDI 660  
 TAQPDVGSGR SSKQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 720  
 TEVTPHAFPT CLVVVLGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 780  
 LIVSALITFI CLVVVLGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840  
 IKHPHGVAD LHASGFTTE FEEVQSCTVD LGITADSSNH PDNIGKIRYI NIVAYDHSRV 900  
 KLAQLAEKDG KLTIDYINANY VDGYNRPKAY IAAQGLKST AEDFWRMIWE HNVEIVMIT 960  
 NLVEKGRRC DQYWPADGSE EYGNFLVTQK SVQVLATYTV RNFTLRNTKI KGSQKGRPS 1020

GRVVTQHYHT QWPDGMVPEY SLPVLTFRK AAYAKRHAVG PVVHCSAGV GRTGTIIVLD 1080  
 SMLQQIQHEG TVNIFGPLEKH IRSQRNYLVQ TEEQYVFIHD TLVEAILSKE TEVLDSHIHA 1140  
 YVNALIPGP AGKTKLEKQF QLLSQSNIQQ SDYSAALKQC NREKNRTSSI IPVERSRVGI 1200  
 SSSLGEGTDY INASYIMGYQ QSNFIIIOH PLLHTIKDFW RMIWDHNAQL VVMIPDQNM 1260  
 AEDEFVYWN KDEPINCESF KVTLMAEHKK CLSNEEKLI QDFILEATQD DYVLEVRHFQ 1320  
 CPKWPNDSP ISKTFELISV IKEEAANRDG PMIVHDEHGG VTAGTFCALT TLMHQLKEN 1380  
 SVDVYQAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRO EENPSTSLDS NGALPDGNI 1440  
 AESLESIV

Seq ID NO: 377 DNA sequence  
 Nucleic Acid Accession #: EOS sequence  
 Coding sequence: 501-4514

15 1 11 21 31 41 51  
 CACACATACG CACGCAOGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAAC ATTTCTCTCG CTCCTCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCTC CGCTTGCAAT 180  
 20 CAGCTCTCTCT GTGTTTCCCG CCGGATTGGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTGTGTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAAT TGGGGAAAGA 300  
 AATATCCAAC ATGTAATAGC CCAAAACAAT CTCCTATCAA TATTGATGAA GATCTTACAC 360  
 AAGTAAATGT GAATCTTAAG AACTTAAAT TTCAGGGTTG GGATAAAACA TCATTGGAAA 420  
 ACACATTTCAT TCATAACACT GGGAAACAG TGGAAATTA TCTCACTAAT GACTACCGTG 480  
 25 TCAGCGGAGG AGTTTCAGAA ATGGTGTFTA AAGCAAGCAA GATAACTTTT CACTGGGGAA 540  
 AATGCAATAT GTCATCTGAT GGATCAGAGC ATAGTTTAGA AGGACAAAAA TTTCACCTTG 600  
 AGATGCAAAAT CTACTGCTTT GATGCGGACC GATTTCAGG TTTTGAGGAA CGAGTCAAAG 660  
 GAAAAGGGAA GTTAAGAGCT TTATCCATTT TGTGTGAGGT TGGGACAGAA GAAAATTGG 720  
 ATTTCAAAGC GATTATTGAT GGAGTCGAAA GTGTAGTTCG TTTTGGGAAG CAGGCTGCTT 780  
 30 TAGATCCATT CATACTGTG AACTTCTGTC CAAACTCAAC TGACAAGTAT TACATTACA 840  
 ATGGCTCATT GACATCTCCT CCTGTCACAG ACACAGTTGA CTGGATTGTT TTTAAAGATA 900  
 CAGTTAGCAT CTCTGAAAGC CAGTTGGCTG TTTTGTGTA AGTTCTTACA ATGCAACAAT 960  
 CTGGTTATGT CATGCTGATG GACTACTTAC AAAACAATT TCGAGAGCAA CAGTACAAGT 1020  
 TCTCTAGACA GGTGTTTCC TCATACACTG GAAAGGAAGA GATTCAAGAA CGAGTTTGTA 1080  
 35 GTTCAGAAC AGAAAATGTT CAGGCTGACC CAGAGAATTA TACCAGCCTT CTGTTCAT 1140  
 GGGAAAGACC TCGAGTCGTT TATGATACCA TGATTGAGAA GTTTGCAGTT TTGTACCAGC 1200  
 AGTTGGATGG AGAGGACCAA ACCAAGCATG AATTTTGTAC AGATGGCTAT CAAGACTTGG 1260  
 GTGCTATTCT CAATTAATTG CTACCCAATA TGAGTTATGT TCTTCAGATA GTAGCCATAT 1320  
 40 GCCTAATGG CTTATATGGA AAATACAGCG ACCAAGTATG TGTGACATG CCTACTGATA 1380  
 ATCTGAAGT TGATCTTTTC CCTGAATTA TGGAACTGA AGAAATAATC AAGGAGGAGG 1440  
 AAGAGGGAAA AGACATTGAA GAAGGCGCTA TTGTGAATCC TGGTAGAGAC AGTGCTACAA 1500  
 ACCAAATCAG GAAAAGGAAA CCCCAGATTT CTACCAACAC ACTACTCAAT CGCATAGGGA 1560  
 CGAAATACAA TGAAGCCAG ACTAACCGAT CCCCACAAG AGGAAGTGA TTTCTGGAA 1620  
 45 AGGGTGATGT TCCCAATACA TCTTAAAT CCACTTCCCA ACCAGTCACT AAATTAGCCA 1680  
 CAGAAAAGA TATTTCTTG ACTTCTCAGA CTGTGACTGA ACTGCCACT CACACTGTGG 1740  
 AAGGTACTTC AGCTCTTTTA AATGATGGCT CTAAACTGT TCTTAGATCT CCACATATGA 1800  
 ACTTGTGCGG GACTGACGAA TCCTTAAATA CAGTTTCTAT AACAGAAAT GAGGAGGAGA 1860  
 50 GTTTATTCAG CAGTTTCAAG CTGATACTG GAGCTGAAGA TTCTTCAGGC TCCAGTCCCG 1920  
 CAACTTCTGC TATCCATTC ATCTCTGAGA ACATATCCCA AGGGTATATA TTTTCTCCG 1980  
 AAAACCCAGA GACAAATACA TATGATGCC TTATACCAGA ATCTGCTAGA AATGCTTCCG 2040  
 AAGATTCAAC TTCATCAGGT TCAGAAGAAT CACTAAAGGA TCCTTCTATG GAGGGAATG 2100  
 TGTGGTTTCC TAGCTCTACA GACATAACAG CACAGCCCGA TGTGTGATCA GGCAGAGAGA 2160  
 GCTTTCTTCA GACTAATTAC ACTGAGATAC GTGTGATGA ATCTGAGAAG ACAACCAAGT 2220  
 55 CCTTTTCTGC AGGCCAGTG ATGTCAAGG GTCCCTCAGT TACAGATCTG GAAATGCCAC 2280  
 ATTATTCTAC CTTTGCCTAC TTCCCAACTG AGGTAACACC TCATGCTTTT ACCCATCCT 2340  
 CCAGACAACA GGATTGGTC TCCAGGTC ACGTGGTATA CTGCGAGACA ACCCAACCGG 2400  
 TATACATGA GGCCAGTAAT AGTAGCCATG AGTCTGATG TGTGTAGCT GAGGGGTGG 2460  
 AATCGAGAA GAAGGCAAT ATACCCCTTG TGATGCTGTC AGCCCTGACT TTTATCTGTC 2520  
 60 TAGTGGTTCT TGTGGGTATT CTATCTACT GGAGGAAATG CTTCCAGACT GCACACTTTT 2580  
 ACTTAGAGGA CAGTACATCC CTTAGAGTTA TATCCACACC TCCAACACT ATCTTTCCAA 2640  
 TTTCAATGA TGTGAGGACA ATTCCAATAA AGCACTTCC AAAGCATGTT GCAGATTAC 2700  
 ATGCAAGTAG TGGGTTTACT GAAGAATTG AGACACTGAA AGAGTTTAC CAGGAAGTGC 2760  
 AGAGCTGTAC TGTGACTTA GGTATTACAG CAGACAGCTC CAACCAACCA GACAAACAGC 2820  
 65 ACAAGAATCG ATACATAAAT ATGTTGCCT ATGATCATAG CAGGGTTAAG CTAGCACAGC 2880  
 TTGCTGAAAA GGATGGCAAA CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA 2940  
 ACAGACCAAA AGCTTATATT GCTGCCAAG GCCCACTGAA ATCCACAGCT GAAGATTCT 3000  
 GGAGAATGAT ATGGGAACAT AATGTGGAAG TTATTGTCTAT GATAACAAAC CTCGTGGAGA 3060  
 AAGGAAGGAG AAAATGTGAT CAGTACTGCG CTGCGGATGG GAGTGAGGAG TACGGGAAT 3120  
 70 TTCTGGTCA CCAAGAGT GTGCAAGTGC TTGCTATTA TACTGTGAGG AATTTTACTC 3180  
 TAAGAAACAC AAAAATAAAA AAGGGCTCCC AGAAAGGAG ACCCACTGGA CGTGTGGTCA 3240  
 CACAGTATCA CTACAGCAG TGGCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC 3300  
 TGACCTTTGT GAGAAAGGCA GCCTATGCCA AGCGCCATGC AGTGGGCTC GTTGTCTGCC 3360  
 ACTGCAAGT TGGAGTTGGA AGAACAGGCA CATATATTGT GCTAGACAGT ATGTTGAGC 3420  
 75 AGATTCAACA CGAAGGAAT GTCAACATAT TTGCTTCTT AAAACATC CGTTCAACAA 3480  
 GAAATTTATT GGTACAACT GAGGAGCAAT ATGCTTCTAT TCATGATACA CTGGTTGAGG 3540  
 CCATCTTAG TAAAGAACT GAGGTGCTGG ACAGTCTAT TCATGCCTAT GTTAATGCAC 3600  
 TCCTCATTC TGGACAGCA GGCAAAACAA AGCTAGAGAA ACAATTCAG CTCCTGAGCC 3660  
 AGTCATATAT ACAGCAGAT GACTATTCTG CAGCCCTAAA GCAATGCAAC AGGGAAGA 3720  
 80 ATGCAACTTC TTCTATCATC CCTGTGAAA GATCAAGGGT TGGCATTTCA TCCTGAGTG 3780  
 GAGAAGGCAC AGACTACATC AATGCCCTCT ATATCATGGG CTATTACCAG AGCAATGAAT 3840  
 TCTCATTAC CCAGCACCTC CTCCTTCTA CCATCAAGGA TTTCTGAGG ATGATATGGG 3900  
 ACCATATGC CCAACTGGT GTTATGATTC CTGATGGCCA AAACATGSCA GAAGATGAAT 3960  
 TTGTTTACTG GCCAAATAAA GATGAGCCTA TAAATTGTGA GAGCTTTAAG GTCACCTTCA 4020  
 TGGCTGAGA ACACAAATGT CTATCTAATG AGGAAAACT TATAATTCAG GACTTTATCT 4080

5  
10  
15  
20  
25

TAGAAGCTAC ACAGGATGAT TATGTACTTG AAGTGAGGCA CTTTCAGTGT CCTAAATGGC 4140  
 CAAATCCAGA TAGCCCCATT AGTAAACTT TTGAACCTAT AAGTGTTATA AAAGAAGGAG 4200  
 CTGCCAATAG GGAATGGGCTT ATGATTGTTC ATGATGAGCA TGGAGGAGTG ACGGCAGGAA 4260  
 CTTTCTGTGC TTGACAAACC CTTATGCACC AACTAGAAAA AGAAAAATCC GTGGATGTTT 4320  
 ACCAGGTAGC CAAAGATGATC AATCTGATGA GGCCAGGAGT CTTTGCTGAC ATTGAGCAGT 4380  
 ATCAGTTTCT CTACAAAGTG ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCCAT 4440  
 CCACCTCTCT GGACAGTAAT GGTGCAGCAT TGCCTGATGG AAATATAGCT GAGAGCTTAG 4500  
 AGTCTTTAGT TTAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCAIT GTTTCTCTCT 4560  
 TCCTAAAAAT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TGTGATTTC CCATCACCTG 4620  
 ACAGTAATCT TCATGACATA GGATTCTGCC GCCAAATTTA TATCATTAAAC AATGTGTGCC 4680  
 TTTTGTCAAG ACTTGTAAAT TACTTATTAT GTTTGAACTA AAATGATTGA ATTTTACAGT 4740  
 ATTTCTAAGA ATGGAATGTG GGTATTTTTT TCTGTATTGA TTTTAACAGA AAATTTCAAT 4800  
 TTATAGAGGT TAGGAATTC AACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTAG 4860  
 CTGTATTGT AGCAATTATC AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTGTA 4920  
 AATAAACAC TCTTCCATAT GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA 4980  
 GAAATACTCT GTTAACTACTG CCCTAGTGTG TCCATGGACC AAATTTATAT 5040  
 TTATAATGT AGATTTTAT ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATTG 5100  
 TTTAGTTTAA TGACGTACTT CATTAGCTGG TCITACTCTA CCAGTTTCT GACATGTAT 5160  
 TGTGTTACCT AAGTCATTAA CTTTGTITCA GCATGTAATT TTAACTTTGT TGGAAAATAG 5220  
 AAATACCTTC ATTTTGAAAG AAGTTTITAT GAGAATAACA CCTTACCATA CATTTGTTCA 5280  
 ATGGTTTATA TCCAAGGAAT TGCAAAAAATA AATATAAATA TTGCCATTAA AAAAAAATA 5340  
 AAAAAAATA AAAAAAATA AAA

Seq ID NO: 378 Protein sequence:  
 Protein Accession #: EOS sequence

1 11 21 31 41 51  
 30 MVFKASKITP HWGKCNMSSD GSEHSLEGQK FPLEMQIYCP DADRFSSFEE AVKKGKGLRA 60  
 LSILFEVGTG ENLDFKAIID GVESVSRFGK QAALDPFILL NLLPNSTDYK YIYNGSLTSP 120  
 PCTDVTDMIV FKDTVSISES QLAVFCEVLT MQQSGYVLM DLQNNFREQ QYKFSRQVFS 180  
 SYTGKEEIEH AVCSSPENPV QADPENYTSI LVTNERPRVV YDTMLEKFAV LYQQLDGEDQ 240  
 TKHEFLTGY QDLGAILNML LPMNSYVLQI VAICTNGLYG KYSDQLIVDM PTDNPELDF 300  
 35 PELIGTERII KEEEGKDIE EGAIVNPGRD SATNQIRKKE PQISTTTHYN RIGTKYNEAK 360  
 TNRSPTRGSE FSGKGDVPNT SLNSTSQPVT KLATEKDIL TSQVTLEPP HTVEGTSASL 420  
 NDGSKTVLRS PHMNLGGTAE SLNTVSITEY EESLLTSFK LDTGAEDSSG SSPATSAIPP 480  
 ISENISQGYI FSSNPEITIT YDVLIPESAR NASEDSTSSG SEESLKDPSM EGNVWFPSST 540  
 DITAQPDVGS GRESPLQITNY TEIRVDESEK TTKSFSAGPV MSQGPSVTDL EMPHYSTFAY 600  
 40 FPEVTPHAP TPSSRQDQDLV STVNVVYSQT TQPVYNEASN SSHESTRIGLA EGLESEKKAV 660  
 IPLVIVSALT FICLVVLVGI LIYWRKCFQT AHFYLEDSTS PRVISTPPTP IFFISDDVGA 720  
 IPIKHFPKEV ADLHASSGFT EEFETLKEFY QEVQSCVTDL GITADSSNHP DNKHKRYIN 780  
 IVAYDSHRVK LAQLAEKDGK LTDYINANYV DGYNRPKAYI AAQGPLKSTA EDFWRMIWEH 840  
 NVEVIVMITN LVEKGRKCD QYWPADGSEB YGNFLVTQKS VQVLAITYVR NFTLRNTKIK 900  
 45 KGSQKGRPSG RVVTQYHYTQ WPDMGVPEYS LPVLTFRKA AYAKRHAVGP VVHCSAGVG 960  
 RTGTYIVLDS MLQIQIHEGT VNIQFLKHI RSQRNYLVQT EEQYVFIDHT LVEAILSKET 1020  
 EVLDSHIAH VNALILPGPA GKTLEKQFO LLSQSNIQSS DYSALKQCN REKNRTSSII 1080  
 PVERSRVGIS SLSEGTDYI NASYIMGYO SNEFIITQHP LLEHTIKDWR MINDHNAQLV 1140  
 VMIPDQGNMA EDEFVYWFNK DEPINCESFK VTLMAEHEK LSNEEKLIQ DFLEATQDD 1200  
 50 YVLEVRHFQC PKWPNPSPSI SKTFELISVI KEEAANRDP MIHVDHGGV TAGTFCALIT 1260  
 LMHLEKENS VDVIQVAKMI NLMRPGVFAD IEQYQFLYK ILSLVSTRQE ENPSTSLDSN 1320  
 GAALPDGNIA ESLESIV

Seq ID NO: 379 DNA sequence  
 Nucleic Acid Accession #: EOS sequence  
 Coding sequence: 148-4632

1 11 21 31 41 51  
 60 CACACATAG CAGCAGCAT CTAACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAAC ATTTCTCTCG CTCCTCCCTCC CTCCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AACGTTTCTC CGCTTGCAAT 180  
 CAGCTCCTCT GTGTTTGCGG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTTGAGA AGATTGGCTG GTCCATACA GGAGCACTGA ATCAAAAAA TTGGGGAAG 300  
 65 AAATATCCAA CATGTAATAG CCCAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA 360  
 CAAGTAAATG TGAATCTTAA GAAACTTAA TTTCAGGGT GGGATAAAC ATCATTGSA 420  
 AACACATTCA TTCATAACAC TGGGAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480  
 GTCAGCGGAG GAGTTTCAGA AATGGTGTGTT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540  
 AAATGCAATA GTTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600  
 70 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAA 660  
 GGAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAAATTG 720  
 GATTTCAAAG CATATTATGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA CGAGGCTGCT 780  
 TTAGATCCAT TCATATGTTT GAACTTCTG CCAAACTCAA CTGACAGTA TTACATTTAC 840  
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900  
 75 ACAGTTAGCA TCTCTGAAAG CCAAGTTGGCT GTTTTGTGTG AAGTTCITAC AATGCAACAA 960  
 TCTGGTTATG TCATGCTGAT GGACTACTTA CAAACAAATT TTCGAGAGCA ACAGTACAAG 1020  
 TCTCTAGAC AGGTGTTTTC CTCATACACT GGAAAGGAAG AGATTATGA AGCAGTTTGT 1080  
 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACAGCCT TCTGTGTACA 1140  
 80 TGGGAAAGAC CTCAGTCGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAT 1200  
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260  
 GGTGCTATTC TCAATAATT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATG 1320  
 TGCACTAATG GCTTATATG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380  
 AATCCTGAAC TTGATCTTTT CCTGAAATTA ATTGGAACAG AAGAAATAAT CAGGAGGAG 1440  
 GAAGAGGGA AAGACATTGA AGAAGGCGCT ATTTGGAATC CTGGTAGAGA CAGTGCTACA 1500  
 AACCAATCA GGAAAAAGGA ACCCCAGATT TCTACCACAA CACACTACAA TGCATAGG 1560

	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAG	ATATTTCCIT	GACTTCTCAG	ACTGTGACTG	AACGGCCACC	TCACACTGTG	1740
5	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACGT	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGAGCTGCAG	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAIT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAGACCCAG	AGACATAAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
10	GAAGATTCAA	CTTCATCAGG	TTCAGAAAG	TCACATAAAG	ATCCTTCTAT	GGAGGGAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACACCAAG	2220
	TCCTTTCTG	CAGGCCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
15	TCCAGACAAC	AGGATTITGGT	CTCCAGCGTC	AACGTGGTAT	ACTCGCAGAC	AACCCCAACG	2400
	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGTTTG	2460
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	2580
20	TACTTAGAGG	ACAGTACATA	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
	ATTTCCAGATG	ATGTCCGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTAA	CCAGGAAGTG	2760
	CAGAGCTGTA	CTGTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAAACAG	2820
	CACAAGAAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTAA	GCTAGCAGAG	2880
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
25	AACAGACCAA	AAGCTTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	3000
	TGGGAATGA	TATGGGAACA	TAATGTGGAA	GTATTGTCA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	GAAATGTGTA	TCAGTACTGG	CCTGCGGATG	GGAGTGAGGA	GTACGGGAAC	3120
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCTTATT	ATACTGTGAG	GAATTTTACT	3180
	CTAAGAAACA	CAAAAATATA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	3240
	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
30	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTC	3360
	CAGTGCAGTG	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	3420
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGCTTCTT	TAAACACAT	CCGTTACAAA	3480
	AGAAATATT	TGATACAAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	3540
35	GCCATACITTA	GTAAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCCTA	TGTTAATGCA	3600
	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GGTCTCACT	3660
	CTGTACCCA	GGCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCTCTCCCT	3720
	GGCTTAACCTG	ATCCTCTCTG	CTCAGCCTCC	CGAGTGGCTG	GGACTATACT	CCTGAGCCAG	3780
	TCAATATAC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAGAAT	3840
40	CGAACTTCTT	CTATCATCCC	TGTGGAAGA	TCAAGGGTTG	GCAATTTCATC	CCTGAGTGGG	3900
	GAAGGCACAG	ACTACATCAA	TGCCCTCTAT	ATCATGGGCT	ATTACCAAG	CAATGAATTC	3960
	ATCATTACCC	AGCACCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
	CATAATGCCC	AACGTGGTGT	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAATAAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTCTATG	4140
45	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAACTTA	TAATTGAGGA	CTTTATCTTA	4200
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCAC	TTCAAGTCTC	TAAATGGCCA	4260
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACCTATA	GTGTTATAAA	AGAAGAAGCT	4320
	GCCAAATAGG	ATGGGCTCT	GATTGTTTCT	GATGAGCATG	GAGGAGTGAC	GGCAGGAAC	4380
	TTCTGTGCTC	TGACAAACCT	TATGCAACAA	CTAGAAAAAG	AAAATTCCGT	GGATGTTTAC	4440
50	CAGGTAGCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	4500
	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	GTGGGCACAA	GGCAGGAAGA	GAATCCATCC	4560
	ACCTCTCTGG	ACAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
	TCTTTAGTTT	AACACAGAAA	GGGTGGGGGG	GACTCACATC	TGAGCAATTG	TTTCTCTCTC	4680
	CTAAATTTAG	GCAGAAATAT	CAGTCTAGTT	CTGTATCTG	TTGATTTCCC	ATCACTGAC	4740
55	AGTAACITTC	ATGACATAGG	ATTCTGCCGC	CAAAATTATA	TCATTAACAA	TGTGTGCCCT	4800
	TTTGCAAGAC	TTGTAATTTA	CTTATATGTT	TTGAACATA	ATGATTGAAT	TTTACAGTAT	4860
	TTCTAAGAA	GGAAATGTGG	TATTTTCTT	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	4920
	ATAGAGGTTA	GGAAATCCAA	ACTACAGAAA	ATGTTTGT	TTAGTGTCAA	ATTTTATAGT	4980
	GTATTTGTAG	CAATTATCAG	GTTTGCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	5040
60	TAAACACTC	TTCCATATGA	TATTCACAT	TTTCAACTG	CAGTATTCAC	CTAAAGTAGA	5100
	AATAATCTGT	TACTTATGTT	AAATCTGCC	CTAGTGTCTC	CATGACCCAA	ATTTATATTT	5160
	ATAATGTAG	ATTTTATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTCTG	TGTAATGTT	5220
	TAGTTTAAATG	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTGCA	CATTGTATTG	5280
	TGTTACCTAA	TGCTAATACT	TTGTTTCAGC	ATGTAATTTT	AACTTTGTG	GAAAAAGAAA	5340
65	ATACCTTCAT	TTTGAAAGAA	GTTTATGTA	GAATAACACC	TTACCAACAA	TGTTCAAAAT	5400
	GGTTTTATC	CAAGGAATTG	CAAAAATAAA	TATAAATATT	GCCATTAATA	AAAAAATAAA	5460
	AAAAAAAAAA	AAAAAAAAAA	A				

Seq ID NO: 380 Protein sequence:  
Protein Accession #: EOS sequence

70	1	11	21	31	41	51	
	MRILKRLFLAC	IQLLCVCRLD	WANGYYRQOR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNPK	60
	QSPINIDEDL	TQNVNVLKXL	KPQGWKDTSL	ENTFHNHNGK	TVEINLNDY	RVSQGVSEMV	120
75	FKASKITFWH	GKQNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRPSSFEEAV	KGKGLRLALS	180
	ILFEVGTENN	LDPKAIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPFC	240
	TDVDWIVFK	DTVSISESQ	AVFCEVLTMO	QSGYVLMNDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEBIHQAD	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEPLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYKGY	SDQLIVDMPT	DNPELDLPE	420
80	LIGTEEIIKE	BEEGKDIIEG	ATVNPGRDSA	TNQRKKEPQ	ISTTTHYRNI	GTYNEAKTN	480
	RSPTRGSEFS	KGKDVNTSL	NSTSPQVTKL	ATEKDISLTS	QIVTELPHPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAEISL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITIDY	VLIPESARNA	SEDSTSSGSE	ESLKDFSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSGAPVMS	QGPSVTDLEM	PHYSTFAYFP	720

5	TEVTPHAFTP SSRQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAIVP 780
	LVIVSALTFI CLVVVLGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
	IKHFPKHVAD LHASSGFTEE FETLKEYQOE VQSCTVDLGI TADSSNHPDN KHKNRYINIV 900
	AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAEF FWRMIWEHNV 960
	EVIVMITNLV EKGRRKCDQY WPAAGSEEEG NFLVTQKSVQ VLAYYTVRNF TLNRTIKIKKG 1020
	SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRVKAAY AKRHAUVGVV VHCSAGVGRT 1080
	GTIVVLDSML QQIQHEGTVN IFGLFKHIRS QRNYLVQTEE QYVFIHDTLV EAILSKEDEV 1140
10	LDSHIHAYVN ALLIPGPAKG TKLEKQFQGL TSPRLRCRG TISAHCNLP LGLTDPPTSA 1200
	SRVAGTILLS QSNIOQSDYS AALKQCNREK NRTSSIIPEV RSRVGISLS GEGTDYINAS 1260
	YIMGYQSNF FIITQHLLH TIKDFWRMIW DHNAQLVMI PDGQNAEDE FVYWPNDKDEP 1320
	INCESFKVTL MAESHKCLSN EEKLIQDFI LEATQDDYVL EVRHQPCPKW PNFDSPISKT 1380
	FELISVKEE AANRDGPMIV HDEHGGVITAG TFCALTLMH QLEKENSVDV YQVARMINLM 1440
	RPGVFADIEQ YQFLYKVLIS LVGTRQENP STSLDSNGAA LPDGNIAESL ESLV
15	Seq ID NO: 381 DNA sequence
	Nucleic Acid Accession #: NM_002851.1
	Coding sequence: 148..7092
20	1 11 21 31 41 51
	CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
	CAAAAACAAAC ATTTCCCTCG CTCCTCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
25	CGGCGAGGGG CGGCAGACCG TCTGGAAATG CSAATCCTAA AGCGTTTCCT CGCTTGCAAT 180
	CAGCTCCTCT GTGTTTGCCG CTTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
	CTTGTGGAAG AGATTGGCTG GTCCCTATACA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG 300
	AAATATCCAA CATGTAATAG CCAAAACAAA TCTCCTATCA ATATTGATGA AGATCTTACA 360
	CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420
30	AACACATTCA TTCATAACAC TGGGAAACAA GTGGAAATTA ATCTCACTAA TGACTACCGT 480
	GTCACGCGAG GAGTTTCAGA AATGGTGTIT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
	AAATGCAATA TGTATCTCTG TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600
	GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTCCTA GTTTTGAGGA AGCAGTCAAA 660
	GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTGG 720
	GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTATGTC GTTTTGAGGA GCAGGCTGCT 780
35	TTAGATCCAT TCATACCTGT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTAC 840
	AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
	ACAGTTAGCA TCTCTGAAAG CCAAGTTGGCT GTTTTTTGAG AAGTTCTTAC AATGCAACAA 960
	TCTGTGTTATG TGAATCTGAT GGACTACTTA CAAACAAATT TTGAGAGCA ACAGTACAAG 1020
40	TTCTCTAGAC AGGTGTTTTT CTCATACACT GGAAGGAAG AGATTCTAGA AGCAGTTTGT 1080
	AGTTCTAGAA CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTATCA 1140
	TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAG 1200
	CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
	GGTGCTATTC TCAATAATTG GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
	TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTGAGCAT GCCTACTGAT 1380
45	AATCCTGAAC TTGATCTTTT CCTGAATTA ATTGGAACAG AAGAAATAAT CAAGAGGAG 1440
	GAAGAGGGAA AAGACATTGA AGAAGCGCGT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500
	AACCAATCA GGAAGAAAGGA ACCCCAGATT TCTACCAAA CACACTACAA TCGCATAGGG 1560
	ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620
50	AAGGGTGATG TTCCCAATAC ATCTTAAAT TCCACTTCCC AACAGTCAC TAAATTAGCC 1680
	ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
	GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAAACCTG TTCTTAGATC TCCACATATG 1800
	AACCTTGCGG GGACTGCGA ATCTCTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860
	AGTTTATTGA CAGATTCTAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCAGTCCC 1920
55	GCAACTTCTG CTATCCCAT TATCTCTGAG AACATATCCC AAGGGTATAT ATTTCTCTCC 1980
	GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040
	GAAGATTCAA CTTTCATCAGG TTCAGAAGAA TCACTAAAGC ATCTTCTAT GGAGGGAAT 2100
	GTGTGGTTCC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160
	AGCTTTCTCC AGACTTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220
60	TCCTTTTCTG CAGSCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280
	CATTATCTTA CCTTTGCCTA CTTCCTCACT GAGGTAAAC ACCTGCTAT ACTGCAGAC AACCCAACC 2340
	TCCAGACAAC AGGATTGGT CTCCAGGTC AACGTGGTAT ACTGCAGAC AACCCAACC 2400
	GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460
	ACCCCTTGTG TGTGAGACAA TCAGATCCTC AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520
65	TCGGCCTTGC ATGCTACGCC TGTATTCCC AGTGTGATG TGTCAATTGA ATCCATCTG 2580
	TTCTCTATG ATGCTGACC TTTGCTTCCA TTTCTCTG CTCTCTCAG TAGTGAATTG 2640
	TTTGGCCATC TGATACAGT TTCTCAAATC CTTCCACAAG TTACTTCAGC TACGAGAGT 2700
	GATAAGGTGC CCTTGATGCT TTCTCTGCCA GTGGCTGGGG GTGATTGTCT ATTAGAGCCC 2760
	AGCCTTGCTC AGTATTCTGA TGTGCTGTCC ACTACTCATG CTGCTTCAGA GACGCTGGA 2820
70	TTTGGTAGTG AATCTGGTGT TCTTTATAAA AGCCTTATGT TTCTCAAGT TGAACCAACC 2880
	AGCAGTGATG CCAATGATGA TGCACGTTCT TCAGGCGCTG AACCTTCTTA TGCCTGTGCT 2940
	GATAATGAGG GCTCCCAACA CATCTTCACT GTTCTTACA GTTCTGCAAT ACCTGTGCAT 3000
	GATTCTGTGG GTGTAACCTA TCAGGGTTCC TTATTTAGCG GCCCTAGCCA TATACCAATA 3060
	CCTAAGTCTT GCTTAATAAC CCAACTGCA TCATTACTGC AGCCTACTCA TGCCCTCTCT 3120
75	GGTGATGGGG AATGCTCTGG AGCCTCTTCT GATAGTGAAT TTCTTTTACC TGACACAGAT 3180
	GGGCTGACAG CCCTTAATAT TTCTTCACTT GTTCTGTAG CTGAATTTAC ATATACAACA 3240
	TCTGTGTTTG GTGATGATAA TAAGCGCTT TCTAAAAGTG AATAATATA TGAATAGAG 3300
	ACTGAAGTGC AATTTCTTCT TTTCAATGAG ATGGTTTACC CTCTGTAAG CACAGTCATG 3360
80	CCCAACAGT ATGATAATGT AAATAAGTTG AATGCGTCTT TACAAGAAAC CTCTGTTTCC 3420
	ATTCTAGCA CCAAGGCGAT GTTCCAGGG TCCCTTGTCT ATACCACCA TAAGGTTTTT 3480
	GATCATGAGA TTAGTCAAGT TCCAGAAAT AACCTTTCAG TTCAACCTAC ACATACTGTC 3540
	TCTCAAGCAT CTGCTGACAC TTGCTTAAA CCTGTGCTTA GTGCAAACTC AGAGCCAGCA 3600
	TCTCTGACC CTGCTCTAG TGAATATGTA TCTCTTCAA CTCAGCTCTT ATTTTATGAG 3660
	ACCTCAGCTT CTTTATGATC TGAAGTATTG CTACAACTT CTTTTCAGGC TTCTGATGT 3720
	GACACCTTGC TTAACACTGT TCTTCCAGCT GTGCCAGTG ATCAATATT GGTGTAAACC 3780

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70

```

CCCAAAGTTG ATAAAATTAG TTCTACAATG TTGCATCTCA TTGTATCAA TTCTGCTTCA 3840
AGTGA AAAACA TGCTGCACCTC TACATCTGTA CCAGTTTTTG ATGTGTCGCC TACTTCTCAT 3900
ATGCACCTCG CTTCACCTCA AGGTTTGACC ATTTCTATG CAAGTGAGAA ATATGAACCA 3960
GTTTTGTAA AAGGTGAAG TTCCACCAA GTGGTACCTT CTTGTACAG TAATGATGAG 4020
TTGTTCCAAA CGGCCAATTT GGAGATTAAC CAGGCCCATC CCCC AAAAGG AAGGCATGTA 4080
TTTGCTACAC CTGTTTATC AATTGATGAA CCATTAAATA CACTAATAAA TAAGCTTATA 4140
CATTCGATG AATTTTAAAC CTCACCAA AGTTCGTGTA CTGGTAAGGT ATTTGCTGGT 4200
ATTCCAACAG TTGCTTCTGA TACATTGTGA TCTACTGATC ATTCTGTTCC TATAGGAAAT 4260
GGGCA GTTG CCATTACAGC TGTTCTCCC CACAGAGATG GTTCTGTAA CTAACCAAAG 4320
TTGCTGTTTC CTCTAAGGC AACTCTGAG CTGAGTCATA GTGCCAATC TGATGCOGGT 4380
TTAGTGGGTG GTGGTGAAGA TGGTGACACT GATGATGATG GTGATGATGA TGATGACAGA 4440
GATAGTGATG GCTTATCCAT TCATAAGTGT ATGTGATGCT CATCCTATAG AGAATCACAG 4500
GAAAAGGTAA TGAATGATTC AGACACCCAC GAAAACAGTC TTATGGATCA GAATAATCCA 4560
ATCTCATACT CACTATCTGA GAATCTGAA GAAGATAATA GAGTCACAAG TGTATCCTCA 4620
GACAGTCAA CTGGTATGGA CAGAAGTCTT GGTAAATCAC CATCAGCAA TGGGCTATCC 4680
CAAAAGCACA ATGATGGAAA AGAGGAAAAT GACATTGAGA CTGGTAGTGC TCTGCTTCTC 4740
CTCAGCCCTG AATCTAAAGC ATGGGCAGTT CTGACAAGTG ATGAAGAAAG TGGATCAGGG 4800
CAAGGTACTC CAGATAGCCT TAATGAGAAT GAGACTTCCA CAGATTTTCA TTTTGACAGC 4860
ACTAATGAAA AAGATGCTGA TGGGATCCTG GCAGCAGGTG ACTCAGAAAT AACTCCTGGA 4920
TTCCACAGT CCCCACATC ATCTGTTACT AGCGAGAACT CAGAAGTGT CCACGTTTCA 4980
GAGGCGAGGG CCAGTAATAG TAGCCATGAG TCTCGTATTG GTCTAGCTGA GGGGTGGA 5040
TCCGAGAAGA AGGCAGTTAT ACCCCTGTGT ATCGTGTGAG CCTGACTTT TATCTGTCTA 5100
GTGGTCTCTG TGGGTATTCT CATCTACTGG AGGAAATGCT TCCAGACTGC ACACITTTAC 5160
TTAGAGGACA GTACATCCCC TAGAGTTATA TCCACACCTC CAACACCTAT CTTTCCAATT 5220
TCAGATGATG TCGGAGCAAT TCCAATAAAG CACTTTCCAA AGCATGTTGC AGATTTACAT 5280
GCAAGTAGTG GGTTTACTGA AGAATTTGAG ACCTGAAAG AGTTTATCCA GGAAGTGCAG 5340
AGCTGTACTG TTGACTTAGG TATTACAGCA GACAGCTCCA ACCACCAGA CAACAAGCAG 5400
AAGAACTCCT ACATAAATAT CGTTGCCTAT GATCATAGCA GGGTTAAGCT AGCACAGCTT 5460
GCTGAAAAGG ATGGCAACT GACTGATTAT ATCAATGCCA ATTATGTGA TGGCTACAAC 5520
AGACCAAAG CTATATTGCG TGCCCAAGGC CCACTGAAAT CCACAGCTGA AGATTTCTGG 5580
AGAATGATAT GGGAACTAAA TGTGGAAGTT ATGTGTCATGA TAACAAACCT CGTGAGAAA 5640
GGAAGGAGAA AATGTGATCA GTACTGGCCT GCCGATGGGA GTGAGGAGTA CCGGAACCTT 5700
CTGGTCACTC AGAAGAGTGT GCAAGTGCTT GCCTATTATA CTGTGAGGAA TTTTACTCTA 5760
AGAAACACAA AATAAAAAA GGGCTCCAG AAAGGAAGAC CCAAGTGGAG TGTGTCACA 5820
CAGTATCACT ACACGCACTG GCCTGACATG GGAGTACCAG AGTACTCCTC GCCAGTCTG 5880
ACCTTTGTGA GAAAGGCAGC CTATGCCAAG CGCCATGCAG TGGGGCTCTG TGTGCTCCAC 5940
TGCACTGCTG GAGTTGGAAG AACAGGCACA TATATTGTGC TAGACAGTAT GTTGACGACG 6000
ATTCAACAG AGGAAGCTGT CAACATATTT GGCTTCTTAA AACACATCCG TTCACAAAGA 6060
AATTATTGGG TACAACATGA GGAGCAATAT GTCTTCACTC ATGATACACT GGTGTAGGCC 6120
ATACTTAGTA AAGAACTGA GGTGCTGGAC AGTCATATTC ATGCTATGT TAATGCACTC 6180
CTCATTCTCG GACCAGCAGG CAAAACAAAG CTAGAGAAAC AATTCCAGCT CCTGAGCCAG 6240
TCAATATATC AGCAGATGGA CTATTCTGCA GCCCTAAAGC AATGCAACAG GGAAGAAGAT 6300
CGAATCTTCT CTATCATCCC TGTGGAAGA TCAAGGGTTG GCATTTATC CCTGAGTGGG 6360
GAAGGCACAG ACTACATCAA TGCTCTCTAT ATCATGGGCT ATTACCAGAG CAATGAATTC 6420
ATCATTACCC AGCACCCCTC CCTTCATACC ATCAAGGATT TCTGGAGGAT GATATGGGAC 6480
CATAATGCCC AACTGGTGGT TATGATTCTC GATGGCCAAA ACATGGCAGA AGATGAATTT 6540
GTTTACTGGC CAAATAAAGA TGAGCCTATA AATTGTGAGA GCTTTAAGGT CACTCTTATG 6600
GCTGAAGAAC ACAATGTCT ATCTAATGAG GAAAACTTA TAATTACGGA CTTTATCTTA 6660
GAAGCTACAC AGGATGATTA TGTACTTGAA GTGAGGCACT TTCAGTGTCC TAAATGGCCA 6720
AATCCAGATA GCCCCATTAG TAAAACITTT GAACITATAA GTGTTATAAA AGAAGAAGCT 6780
GCCAATAGGG ATGGGCTAT GATTGTTTAT GATGAGCATG GAGGAGTGC GGCAGGAAT 6840
TTCTGTGCTC TGACAACCCCT TATGCACCAA CTAGAAAAAG AAAATTCGT GGATGTTTAC 6900
CAGGTAGCCA AGATGATCAA TCTGATGAGG CCAGGAGTCT TTGCTGACAT TGAGCAGTAT 6960
CAGTTTCTCT ACAAGTGAT CCTCAGCCTT GTGAGCAGAA GGCAGGAAGA GAATCCATCC 7020
ACCTCTCTCG ACAGTAATGG TGCAGCATG CCTGATGGAA ATATAGCTGA GAGCTTAGAG 7080
TCTTTAGTTT AACACAGAAA GGGGTGGGG GACTCACATC TGAGCATGT TTTCTCTTTC 7140
CTAAATATAG GCAGGAAAAT CAGCTAGATT CTGTATCTG TTGATTTCCC ATCAGCTGAC 7200
AGTAACITTC ATGACATAGG ATTCTGCCGC CAAATTTATA TCATTAAACA TGTGTGCCCT 7260
TTTGCAAGAC TTGTAATTTA CTTATTATGT TTGAACATAA ATGATTGAAT TTTACAGTAT 7320
TTCTAAGAA GGAATGTGG TATTTTCTTC TGTATTGATT TTAACAGAAA ATTTCAATTT 7380
ATAGAGGTTA GGAATTCCAA ACTACAGAAA ATGTTTGTIT TTAGTGTCAA ATTTTAGCT 7440
GTATTTAGT CAATTATCAG GTTTGCTAGA AATATAACTT TTAATACAGT AGCCTGTAAA 7500
TAAACACTC TTCCATATGA TATTCAACAT TTTACAACCT CAGTATTAC CTAAAGTAGA 7560
AATAATCTGT TACTTATGT AATACTGCC CTAGTGTCTC CATGACCAA ATTTATATTT 7620
ATAATTGTAG ATTTTATAT TTTACTACTG AGTCAAGTTT TCTAGTCTG TGTAAATTGT 7680
TAGTTTAATG ACGTAGTTCA TTAGCTGGTC TTAGCTTACC AGTTTCTGA CATGTATTG 7740
TGTTACCTAA GTCATTAACT TTGTTTCAGC ATGTAATTTT AACTTTTGTG GAAAATAGAA 7800
ATACCTTCAT TTTGAAAGAA GTTTTATGA GAATAACACC TTACCAACA TGTTCAAAT 7860
GGTTTTATC CAAGGAATTG CAAAATAAA TATAAATAT GCCATTAAAA AAAAAAAA 7920
AAAAAAA A
  
```

Seq ID NO: 382 Protein sequence  
 Protein Accession #: NP\_002842.1

75  
 80

```

1 11 21 31 41 51
| | | | |
MRILKRFLAC IQLLCVCRLD WANGYYRQR KLVEEIGHSY TGA LNQKNWG KKYPTCNSPK 60
QSPINIDEDL TOYVNVLKRL KFGWDKTSI ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFW KGNMSSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEEAV KKGKLRALS 180
ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
TDTVDNIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLNDY LQNNFRBOQY KFSRQVFSKY 300
TGKEEIEHAV CSSEPNVQA DPNYTSLLV TWERPRVVDY TMIEKFAVLV QQLDGEDQTK 360
HEFLTGYDQ LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNFELDLFPE 420
LIGTEBIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTHYNRI GTKYNEAKTN 480
  
```

	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPH	VEGTSASLND	540
	GSKTVLRSRH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSTDI	660
	TAQPDVSGSR	ESFIQNTYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLE	PHYSTFAYFP	720
5	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSE	LEFRLHVTVSQ	840
	ILPQVTSATE	SDKVPLHASL	PVAGDLLLLL	PSLAQYSDVL	STTHAASETL	EPGSESGVLY	900
	KTLMFSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVITYQG	960
10	SLFSGPSHIP	IPKSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVAEFTYT	TSVFGDDNKA	LSKSEIYGN	ETELQIPSN	EMVYPSESTV	MPNMYDNVNK	1080
	LNASLQETSV	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	NNFSVQPTH	VSOASGDTSL	1140
	KPVLANSSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLKTVLP	1200
	AVPSDPIIVE	TKVDKISST	MLHLIVNSNA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
15	TISYASEKEY	PVLLKSESSH	QVVPISLYND	ELFQTANLEI	NQAPHPKGRH	VFATPVLSID	1320
	EPLNTLINK	IHSDEILTST	KSSVTGKVFA	GIPTVASDTF	VSTDHSPVIG	NGHVAITAVS	1380
	PHRDGVTST	KLLFPKATS	ELSHSAKSDA	GLVGGGEDGD	TDDGDGDDDD	RDSGLSIHK	1440
	CMSCSSYRES	QEKVMDSDT	HENSMDQNN	PIYSLSSENS	EEDNRVTSVS	SDSQTMGDRS	1500
	PKSFSANGL	SKHNDGKEE	NDIQTGSALL	PLSPESKAWA	VLTSDSESGS	GQGTSDSLNE	1560
20	NETSTDFSPA	DINEKADAGI	LAAGDSEITP	GFPQSPSTSV	TSENSEVFHV	SEAEASNSSH	1620
	ESRIGLAEG	ESEKKAIVPL	VIVSALTFFC	LVLVGLIY	WRKCFQTAHF	YLEDSTSPRV	1680
	ISTPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGPTTEF	ETLKEFYQEV	QSCITVDLIT	1740
	ADSSNHPNK	HKNRYINIVA	YDSRVKLAQ	LAEKDGKLT	YINANYVDGY	NRPKAYIAAQ	1800
	GPLKSTAEFL	WKMIHNEHVE	VIVMITNLVE	KGRKCDQYV	PADGSEBYGN	FLVTQKSVQV	1860
25	LAYTVTRNFT	LRNTKIKKGS	QKGRPSGRVV	TOYHYTQWPD	MGVPEYSLPV	LTFVRKAAVA	1920
	KRHAVGPFVV	HCSAGVGRTG	TYIVLDSMLQ	QIQHEGTVNI	FGLKHLRSQ	RNYLVQTEEQ	1980
	YVFIHDTLVE	ALLSKETEVL	DSHIHAYVNA	LLIPGPAGKT	KLEKQFQLLS	QSNIQQSDYS	2040
	AALKQCNREK	NRTSSIIIVE	RSRVGISSLS	GEGTDYINAS	YIMGYQSNES	FIITQHPLH	2100
	TIKDFWRMIW	DHNAQLVVM	PDGQNMMAED	FVYWPKNODEP	INCESPKVLT	MAEEHKCLSN	2160
30	EELKIIQDFI	LEATQDDVVL	EVRHFQCPKW	PNPDSPISK	FELISVIKEE	AANRDGPMIV	2220
	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINIM	RPGVFADIEQ	YQFLYKVILS	2280
	LVSTRQENEP	STSLDSNGAA	LPGDNIAESL	ESLV			

Seq ID NO: 383 DNA sequence

Nucleic Acid Accession #: NM\_005688.1

Coding sequence: 126..4439

	1	11	21	31	41	51	
40	CCGGGCGAGT	GGCTCATGCT	CGGAGCGGTG	GTTGAGCGGC	TGGCGCGGTT	GTCCTGGAGC	60
	AGGGGCGCAG	GAATTCGTAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCGCTCAG	120
	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	CGGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTGGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCGAGGGGCC	300
	TCTCTCTTGA	TGCCCTCCATG	CATTCTCAGC	TCAGAAATCCT	GGATGAGGAG	CATCCCAAGG	360
45	GAAAGTACCA	TCATGGCTTG	AGTGCCTCTG	AGCCCATCCG	GACTACTTCC	AAACACCCAG	420
	ACCCAGTGGG	CAATGCTGGG	CTTTTCTCCT	GTATGACTTT	TTCTGCTGCT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	AGAGTCTCTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
50	AAGTTGGGCC	AGACGCTGCT	TCCTCGCGAA	GGGTGTGTGT	GATCTTCTGC	CGCACCCAGG	660
	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCCAGCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTTAGT	GCTGGGCTCT	CTCTGACCG	AAATCGTGGC	GTCTTGGTGG	CTTGCACTGA	840
	CTTGGGCACT	GAATACCGA	ACCGGTGTCC	GCTTGGGGGG	GGCCATCTTA	ACCATGGCAT	900
55	TTAAGAAGAT	CCTTAAGTTA	AAGAACAATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGCTCCAA	CGATGGGCAG	AGAAATGTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATCTCT	GGACCAACAG	1080
	GCTTCTCTGG	ATCAGCTGTT	TTTATCTCT	TTTACCAGC	AATGATGTTT	GCATCACGCG	1140
	TCACAGACTA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
60	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTICA	AAAAATCCGC	GAGGAGGAGC	GTCGGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTATAT	GACCCCTGGC	TTCCGATCTG	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCCTTCAATC	CATGACTTTT	GCTTTGAAAG	TAACACOGTT	TTCAGTAAAG	TCCCTCTCAG	1500
65	AAGCCTCAGT	GGCTGTTGAC	AGATTTAAGA	GTTTGTCTCT	AATGGAAGAG	GTTTCAATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCSC	ACTGAGCATC	1740
	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCTCTCTGGA	CAGTGAACGAG	CGGCCCATGC	1800
70	COGAAGAGGA	AGAGGCCAAG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGGAGATC	CAAGAGGGA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCTCT	AATGCTACTC	2040
	TGAGAGACAA	CATCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGGAGATTG	2160
75	GAGAGGAGG	AGCCAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTT	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGTATACC	GGAAACATCT	CAAGTCCAA	ACAGTTCTGT	2340
	TGTTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
80	CCATTTTAA	TAACTGTGTT	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCACTGG	TTCAACAGAAG	AAGTCAACAAG	ACAAGGCTCC	TAAACAGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGCGAGG	2640
	GTTCACTGCC	CTGGTCAGTA	TATGTTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCTCGTTAT	TATGCCCTTT	TTCATGCTGA	ATGTAGGCAG	CACCGCTTCT	AGCACTGGT	2760



5  
10  
15  
20  
25  
30  
35  
40  
45  
50

GGTGTAGTTA CTGGATCAAG CAAGGAAGCG GGAACACCAC TGTGACTCGA GGGAAACGAGA 2820  
 CCTCGGTAG TGACAGCATG AAGGACAATC CTCATATGCA GTACTATGCC AGCATCTACG 2880  
 CCTCTCCAT GGCAGTCATG CTGATCCTGA AAGCCATTGG AGGAGTTGTC TTTGTCAAGG 2940  
 GCAGCTGCG AGCTTCTCCTC CGGCTGCATG ACGAGCTTTT CGAAGGATC CTTCGAAGCC 3000  
 CTATGAAGTT TTTTGACACG ACCCCACAG GGAGGATTCT CAACAGGTTT TCCAAAGACA 3060  
 TGGATGAAGT TGACGTGCGG CTGCGGTTCC AGGCGAGAT GTTCATCCAG AACGTTATCC 3120  
 TGGTGTCTCT CTGTGTGGGA ATGATCGCAG GAGTCTTCCC GTGGTTCCTT GTGGCAGTGG 3180  
 GGCCCTCTGT CATCTCTTT TCAGTCTGCG ACATTGTCTC CAGGTCCTG ATTCCGGAGC 3240  
 TGAAGCGTCT GGACAATATC ACGCAGTCAC CTTTCTCTC CCACATCAG TCCAGCATAC 3300  
 AGGGCCTTGC CACCATCCAC GCCTACAATA AAGGGCAGGA GTTCTGACAG ATATACCAGG 3360  
 AGCTGCTGGA TGACAAACAA GCTCCTTTTT TTTGTTTAC GTGTGCGATG CGGTGGCTGG 3420  
 CTGTGCGGCT GGACCTCATC AGCATCGCCC TCATCACCAC CACGGGCTG ATGATCGTTC 3480  
 TTATGACCGG GCAGATTGCG CCAGCCTATG CCGGTCTGCG CATCTCTTAT GCTGTCCAGT 3540  
 TAACGGGCT GTTCCAGTTT ACGGTCAGAC TGGCATCTGA GACAGAAGCT CGATTCACT 3600  
 CGGTGGAGAG GATCAATCAC TACATTAAGA CTCTGTCCTT GGAAGCACCT GCCAGAATTA 3660  
 AGAACAGGCT TCCCTCCCTT GACTGGCCCC AGGAGGAGA GGTGACCTTT GAGAACGCGAG 3720  
 AGATAGAGTA CGAGAAAAC CTCCCTCTTG TCCTAAAGAA AGTATCCTTC ACGATCAAAAC 3780  
 CTAAAGAGAA GATTGGCATT GTGGGGCGGA CAGGATCAGG GAAGTCTCG CTGGGATGG 3840  
 CCTCTCTCG TCTGTGGAG TTATCTGGAG GCTGCATCAA GATTGATGA GTGAGAATCA 3900  
 GTGATATTGG CCTTGGCGAC CTCGGAAGCA AACTCTCTAT CATTCTCTCA GAGCCGGTGC 3960  
 TGTTCAGTGG CACTGTGAGA TCAAAATTTG ACCCTTCAA CCAGTACACT GAAGACCAGA 4020  
 TTTGGGATGG CTTGGAGAGG ACACACATGA AAGAAATGAT TGCTCAGCTA CCTCTGAAAC 4080  
 TTGAATCTGA AGTATGAGG AATGGGGATA ACTTCTCAGT GGGGGAACGG CAGCTCTTGT 4140  
 GCATAGCTAG AGCCCTGCTC CGCCACTGTA AGATTCTGAT TTAGATGAA GCCACAGCTG 4200  
 CCATGGACAC AGAGACAGAC TTATTGATTG AAGAGACCAT CCGAGAAGCA TTTGCAGACT 4260  
 GTACCATGCT GACCATTTGCC CATGCGCTGC ACACGGTTCT AGGCTCCGAT AGGATTATGG 4320  
 TGCTGGCCCA GGGACAGGTG GTGGAGTTTG ACACCCCATC GGTCTTCTG TCCAAACGACA 4380  
 GTTCCGGATT CTATGCCATG TTTGCTGCTG CAGAGAACAA GGTGCTGTC AAGGGCTGAC 4440  
 TCCTCCCTGT TGACGAAGTC TCITTTCTTT AGAGCATTGC CATTCCCTGC CTGGGGCGGG 4500  
 CCCTCATCG CGTCTCTCTA CCGAAACCTT GCCTTCTCG ATTTTATCTT TCGCACAGCA 4560  
 GTTCCGGATT GGCCTGTGTG TTTCACTTTT AGGAGAGATC ATATTTTGTAT TATTGTATT 4620  
 ATTCCATTAT CATGTAACAA AAATTTAGTT TTTGTTCTTA ATTGCACCTT AAAAGGTTCA 4680  
 GGGAAACGTT ATTATTAATTG TATCAGAGGC CTATAATGAA GCTTTATACG TGTAGCTATA 4740  
 TCTATATATA ATTCTGTACA TAGCCTATAT TTACAGTAA AATGTAAGCT GTTTATTTTA 4800  
 TATTAAATA AGCACTGTGC TAATAACAGT GCATATTCCT TTCTATCATT TTTGTACAGT 4860  
 TTGCTGTACT AGAGATCTGG TTTTGTCTAT AGACTGTAGG AAGAGTAGCA TTTCACTCTT 4920  
 CTCTAGCTGG TGTGTTTACG GTGCCAGGTT TTCTGGGTGT CCAAGGAAG ACGTGTGGCA 4980  
 ATAGTGGGCT CTCGACAGCG CCCCTCTGCC GCCTCCCATC AGCCGCTCCA GGGGTGGCTG 5040  
 GAGACGGGTG GCGCGCTGGA GACCATGCAG AGCGCGTGA GTTCTCAGG CTCTGCTCTT 5100  
 CTGTCTGTGT GTCACTTACT GTTCTGTGCA GGAGAGCAGC GGGCGGAAGC CCAGGCCCTT 5160  
 TTTCACTCCC TCCATCAAGA ATGGGATCA CAGAGACATT CTTCCGAGCC GGGGAGTTTC 5220  
 TTTCTGCTCT TCTCTTTT GCTGTTGTTT CTAACACAGA ATCAGTCTAT CCACAGAGAG 5280  
 TCCCACTGCC TCAGGTTCTT ATGGCTGGCC ACTGCACAGA GCTCTCCAGC TCCAGACCTT 5340  
 GTTGTGTTCA AGCCCTGAG CCAACTGCTG CTTTGTGAGG TGGCACTTT TCAATTGCTT 5400  
 ATTCACACAC CTCACAGTT CAGTGGCAGG GCTCAGGATT TGTGGGTCT GTTTTCTTTT 5460  
 CTCACGCGAG TCGTCGCACA GTCCTCTCT CTCTCTCCC TCAAAGTCTG CAACCTTAAG 5520  
 CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT 5580  
 ACCTCAGTGC TCTGTTGCT GTGTGTTTGG GTGTGTTTCC GCAACCCCTT TTTGTGCTGT 5640  
 GGGGCTGTA GCTCAGGTGG GCGTGTGCTG TGCTGTATC AGTTGAATGG TCAGCGTTGC 5700  
 ATGTGCTGAC CAACTAGACA TTCTGTGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760  
 CAAAAATCTG AAAATGTGAA TAAATTTATT TTGATTTTG TAAAAAATA AAAAAAATA 5820  
 AAAAAAATA AAAAAAATA

Seq ID NO: 384 Protein sequence  
 Protein Accession #: NP\_005679.1

55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRF TRPLEQDAL ETAARAEGLS 60  
 LDASHMSQLR ILDEEHPKKG YHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120  
 VAHKKGELSM EDVWLSKHE SSDVNCRRLE RLWQBELNEV GPDAASLRV VWIFCRTLRI 180  
 LSIVCLMITQ LAGFSGPAPM VKHLLLEYTA TESNLQYSL LVLGLLLEI VRSWSLALTW 240  
 ALNYRTGVRL RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300  
 PUVAILGMIY NVILIGTGF LGSAVFILFY PAMMFASRLT AYFRKCVAA TDERVQKMNE 360  
 VLTYIKFIKM YAWVKAFQS VQKIREBER ILEKAGYPQG ITVGVAPIVV VIASVVTFSV 420  
 HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PFSVKLSLEA SVAVDRFKSL PLMEEVHMIK 480  
 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKDK RASRGKKEV RQLQRTENQA 540  
 VLAQKHELL LDSDERPSPE EEBGKHILG HRLQRTLHS IDLEIQEGL VGIOGVSVGG 600  
 KTSLSAILG QMTLLEGSIA ISGTFAVVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660  
 CCLRPDLAIL PSSDLTEIGE RANLSGGQR QRISLARALY SDRSIVILDD PLSALDAHVG 720  
 NHIFNSAIRK HLKSKTVLFV THQLQYLVD C DEVIPKKEG ITERGTHEEL MNLNGDYATI 780  
 FNLLIGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840  
 VPNSVGVYI QAAGGLAPLF VIMALFMLNV GSTAFSTWML SYWIKQSGN TTVTRGNETS 900  
 VSDSMKDNPH MQYASIALY SMAVMLILKA IRGVVVFVKT LRASSRLHDE LFRRLILRSPM 960  
 KFPDTPPTGR ILNRFKSDMD EVDVRLPFQA EMFIQNVILV PFCVGMIAV PFWFLVAVGP 1020  
 LVILFVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEPLHRYQEL 1080  
 LDONQAPFL FTCAMNLA V RLDLISIALI TTTGLMIVLM HQQIPPAYAG LAISYAVQLT 1140  
 GLFOFTVRLA SETEARTSV ERINHYIKTL SLEAPARIKN KAPSPDPQE GEVTFENAEM 1200  
 RYRENPLVL KKVSTFIKPK EKIGIVGRTG SGKSSLMGAL FRLVELSGGC IKIDGVRISD 1260  
 IGLADLRSLK SIIPQEPVLF SGTVRNLDLP FNQYTEDQIW DALERTHME CIAQLPLELE 1320  
 SEVMENDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIIQ TIREAPADCT 1380  
 MLTIAHLRHT VLGS DRIMVL AQGGVVEFDT PSVLLSNDSS RPYAMPAAAE NKVAVKG



Seq ID NO: 385 DNA sequence  
Nucleic Acid Accession #: NM\_001327.1  
Coding sequence: 89..631

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
      AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
      CTGAGAGCOG GGCAGAGGCT CCGAGGCCAT GCAGGCCGAA GGCOCGGGCA CAGGGGGTTC 120
      GACGGGGCAT GCTGATGGCC CAGGAGGCCCT TGGCATTCTCT GATGGCCAG GGGCAATGC 180
10     TGGCGGCCCA GGAGAGGGCG GTGCCACGGG CCGCAGAGGT CCGCGGGCG CAGGGGCAGC 240
      AAGGGCCTCG GGGCGGGGAG GAGGCGCCCG GCGGGGTCOG CATGGCGGCG CGGCTTCAGG 300
      GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGAG AGCCGCTGCG TTGAGTTCTA 360
      CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
      GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGTG TGTCCGGCAA 480
15     CATACTGACT ATCCGACTGA CTGCTCAGA CCACCCCAA CTGCAGCTCT CCATCAGCTC 540
      CTGTCTCAG CAGCTTTCCT TGTGATGTG GATCAGCAG TGCTTTCTGC CCGTGTITTT 600
      GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCAGCCT GGGCCCTTCT CTAAGTTCAT 660
      GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
20     GTTTGTCTCT GGAGGAGGAC GGCTTACATG TTTGTTCTG TAGAAAATAA AACTGAGCTA
```

Seq ID NO: 386 Protein sequence  
Protein Accession #: NP\_001318.1

```
25     1      11      21      31      41      51
      |      |      |      |      |      |
      MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
      PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLPVPQ 120
      VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCFLEVF LAQPPSGQRR
```

30 Seq ID NO: 387 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 52..459

```
35     1      11      21      31      41      51
      |      |      |      |      |      |
      CCTCGTGGGC CTGACCTTC TCTCTGAGAG CCGGGCAGAG GTCCTGGAGC CATGCAGGCC 60
      GAAGGCCAGG GCACAGGGGG TTGACAGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
      CTGATGGCCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CCGGTGCCAC GGGCGGCAGA 180
      GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGCCGA GAGGAGGCGC CCGCGGGGT 240
40     CCGCATGGCG GTGCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCGC 300
      GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAAT CTGAGCTCTCC 360
      ATCAGCTCCT GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGAGTG CTCTTCTGCC 420
      GTGTTTGTGG CTGAGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCTTCC 480
45     TAGGTCAATG CTCTCCCTT AGGGAATGGT CCCAGCAGA GTGCCAGTT CATTTGTTGG 540
      GCCTGATTGT TTGTGCTGG AGGAGGACGG CTTACATGTT TGTTTCTGTA GAAAATAAAG 600
      CTGAGCTA
```

Seq ID NO: 388 Protein sequence  
Protein Accession #: Eos sequence

```
50     1      11      21      31      41      51
      |      |      |      |      |      |
      MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
55     PRGPHGGAAS AQDGRCPGCA RRPDSRLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
      FLPVFLAQAP SGQRR
```

Seq ID NO: 389 DNA sequence  
Nucleic Acid Accession #: NM\_005562.1  
Coding sequence: 90..3671

```
60     1      11      21      31      41      51
      |      |      |      |      |      |
      ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCG GGCAGCGACC CTGCAGCGG 60
      AGACAGAGAC TGAGCGGCC GGCACCGCA TGCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
65     GCTTCTCGCT CCTCTGCCG GCAGCCCGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
      ATGGGAAGTC CAGGCAGTGT ATCTTGATC GGAAGCTTCA CAGACAACT GGTAAATGGAT 240
      TCCGCTGCCT CAATGCAAT GACAACACTG ATGGCATTCA CTGOGAGAAG TGCAAGAATG 300
      GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTGCCTCG CAATTGTAAC TCCAAAGGTT 360
      CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACAGGT GTGACAGGAG 420
70     CCAGATGCGA CCGATGTCTG CCGAGCTTCC ACATGCTCAC GGATGCGGG TGCAACCAAG 480
      ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAG TGCCATGCGA GGGCCCTGTG 540
      ACGCGGGCGG CTGTGTCTGC AAGCCAGCTG TTAGTGGAGA ACCTGTGAT AGGTGTGAT 600
      CAGGTTACTA TAACTCTGAT GGGGGGAACC CTGAGGCGTG TACCCAGTGT TTCTGCTATG 660
      GGCATTGAGC CAGCTGCCCG AGCTCTGAG AATACAGTGT CCATAAGATC ACCTTACCT 720
75     TTATCAAGA TGTGTATGGC TGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
      AATGGTCACA GCGCCATCAA GATGTGTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840
      TTGTGGCTCC TGCCAAATTT CTTGGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCTT 900
      TTGACTACCG TGTGACAGCA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATCTGGAAG 960
      GTGCTGTCT ACAGATCACA GCTCCCTGA TGCCACTTGG CAAGACACTG CCTTGTGGG 1020
80     TCACCAAGAC TTACACATTG AGGTTAATG AGCATCCAAG CAATAATTGG AGCCCCAGC 1080
      TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCCG ATCCGAGCTA 1140
      TATCTGGAGC ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTC GCGCGCCCTG 1200
      TCCTGTGGG ACCAGCACCC TGGGTTGAAC AGTGTATATG TCCTGTGGG TACAGGGGCG 1260
      AATTCTGCCA GGATTGTGCT TCTGGCTACA AGAGAGATTG AGCGAGACTG GGGCCTTTTG 1320
```

GCACCTGTAT TCCTTGTAAC TGTCAAGGGG GAGGGGCCCTG TGATCCAGAC ACAGGAGATT 1380  
 GTTATTACAGG GGATGAGAAT CCTGACATTG AGTGTGCTGA CTGCCCAATT GGTTCCTACA 1440  
 ACGATCCGCA CGACCCCGCG AGCTGCAAGC CATGTCCCTG TCATAACGGG TTCAGCTGCT 1500  
 CAGTGATGCC GGAGACGGAG GAGGTGGTGT GCAATAACTG CCTCCCGGGG GTACCCGGTG 1560  
 CCCGCTGTGA GCTCTGTGCT CAATGCAACA ACAATGTGGA CCCAGTGCC TCTGGGAATT 1620  
 TGAGGCCCTG TCAGCCCTGT CAATGCAACA ACAATGTGGA CCCAGTGCC TCTGGGAATT 1680  
 GTGACCGGCT GACAGGCGAG TGTTTGAAGT GTATCCACAA CACAGCCGGC ATCTACTGCG 1740  
 ACCAGTGCAA AGCAGGCTAC TTCGGGGACC CATTTGGCTCC CAACCCAGCA GACAAGTGTC 1800  
 GAGCTTGCAA CTGTAACCCC ATGGGCTCAG AGCCTGTAGG ATGTGGAAGT GATGGCACCT 1860  
 GTGTTTGCAA GCCAGGATTT GGTGGCCCCA ACTGTGAGCA TGGAGCATT AGCTGTCCAG 1920  
 CTTGCTATAA TCAAGTGAAG ATTGAGATGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG 1980  
 AGGCCCTGAT TTCAAAGGCT CAGGGTGGTG ATGGAGTAGT ACCTGATACA GAGCTGGAAG 2040  
 GCAGGATGCA GCAGGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTCAG 2100  
 AAGGTGCTAG CAGATCCCTT GGTCTCCAGT TGGCCAAGST GAGGAGCCAA GAGAACAGCT 2160  
 ACCAGAGCCG CCTGGATGAC CTCAGATGA CTGTGGAAG AGTTCCGGCT CTGGGAAGTC 2220  
 AGTACCGAGG CCGAGTTCCG GATACTCACA GGCTCATCAC TCAGATGCAG CTGAGCCTGG 2280  
 CAGAAAGTGA AGCTTCTCTG GGAACACTA ACATTCTGCT CTGAGACCAC TACGTGGGGC 2340  
 CAAATGGCTT TAAAGTCTG GCTCAGGAG CCACAAGATT AGCAGAAAGC CAGTTGAGT 2400  
 CAGCCAGTAA CATGGAGCAA CTGACAAGG AACTGAGGA CTATTCCAAA CAGGCCCTCT 2460  
 CACTGGTGCG CAAGGCCCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG 2520  
 CTGTGGTGCA AGGGCTTGTG GAAAAATTGG AGAAAAACCA GTCCTTGGCC CAGCAGTTGA 2580  
 CAAGGGAGGC CACTCAAGCG GAAATTGAAG CAGATAGGTC TTATCAGCAC AGTCTCCGCC 2640  
 TCTGGATTCT AGTGTCTGAG CTTGAGGAG TCAGTGATCA GTCTTTTCAG GTGGAAGAAG 2700  
 CAAAGAGGAT CAAACAAAAA GCGGATTAC TCTCAACGCT GGTAAACAGG CATATGGATG 2760  
 AGTTCAAGCG TACACAAAAA AATCTGGGAA ACTGGAAGA AGAAGCACAG CAGCTCTTAC 2820  
 AGAATGGAAA AAGTGGGAGA GAGAAATCAG ATCAGCTGCT TCCCGTGCC AATCTTGCTA 2880  
 AAGCAGAGC ACAAGAAGCA CTGAGTATGG GCAATGCCAC TTTTATGAA GTTGAGAGCA 2940  
 TCCTTAAAAA CCTCAGAGAG TTTGACCTGC AGGTGGACAA CAGAAAAGCA GAAGCTGAAG 3000  
 AAGCCATGAA GAGACTCTCC TACATCAGCC AGAAGTTTTC AGATGCCAGT GACAAGACCC 3060  
 AGCAAGCAGA AAGAGCCCTG GGGAGCCCTG CTGCTGATGC ACAGAGGGCA AAGAATGGGG 3120  
 CCGGGGAGGC CCTGGAAATC TCCAGTGAGA TTGAACAGGA GATTGGGAGT CTGAACCTGG 3180  
 AAGCCATGAT GAGCAGAGAT GGAGCCTTGG CCATGGAAAA GGGACTGGCC TCTCTGAAGA 3240  
 GTGAGATGAG GGAAGTGGAA GGAGAGCTGG AAAGGAAGGA GCTGGAGTTT GACACGAATA 3300  
 TGGATGCACT ACAGATGGTG ATTACAGAAG CCCAGAAGST TGATACAGCA GCCAAGAAGC 3360  
 CTGGGGTATC AATCCAGAC ACACTCAACA CATTAGACGG CCTCCTGCAT CTGATGGACC 3420  
 AGCCTCTCAG TGTAGATGAA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCCGAGCCA 3480  
 AGACCCAGAT CAACAGCCAA CTGCGGCCCA TGATGTGAGA GCTGGAAGAG AGGGCAGCTC 3540  
 AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATCTGT GCTGATGTGA 3600  
 AGAAGTGGGA GAACATTAGG GACAACCTGC CCCAGGCTG CTACAATACC CAGGCTCTTG 3660  
 AGCAACAGTG AAGCTGCCAT AAATATTCTT CAACAGAGT TCTTGGGATA CAGATCTCAG 3720  
 GGCTCGGGAG CCATGTCATG TGAGTGGGTG GGATGGGGAC ATTTGAACAT GTTTAATGGG 3780  
 TATGCTCAGG TCAACTGACC TGACCCCATC CTGATGCCCA TGGCCAGGTG GTTGTCTTAT 3840  
 TGCAACATG TCCTTGCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA 3900  
 ATGATCAAGG ATCTGGACCC CAAAGAATAG ACTGGATGGA AAGACAAACT GCACAGGCAG 3960  
 ATGTTTGCCCT CATATATGTC GTAAGTGGAG TCCTGGAATT TGGACAAGTG CTGTTGGGAT 4020  
 ATAGTCAACT TATTCTTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCAGGC 4080  
 ATGAAATCTT TCCTAATGTC AGAAGCAGAGT GCAACCCAGT CACACTGTGG CCACTAAAAAT 4140  
 ACTATTGCTT CATATTGCTC TCTGCAAGCT TCTTGTGAT CAGAGTTTCT CTTACTTACA 4200  
 ACCCAGGGTG TGAACATGTT CTCCATTTC AAGCTGGAAG AAGTGAGCAG TGTGGAGTG 4260  
 AGGACCTGTA AGGCAGGCCC ATTGAGAGCT ATGCTGCTTG CTGGTGCTTG CCACCTTCAA 4320  
 GTTCTGGACC TGGGCATGAC ATCCCTTCTT TTAATGATGC CATGGCACTT TAGAGATTGC 4380  
 ATTTTATTA AAGCATTTC TACCAGCAAA GCAAAATGTT GGAAGATATT TACTTTTTCG 4440  
 GTTCAAGAT GATAGAAAAG TGTGGCTTGG GCATTGAAAG AGGTAAAAAT CTCTAGATT 4500  
 ATTAGTCTTA ATTCAATCCT ACTTTTCGAA CACCAAAAT GATGCGCATC AATGTATTTT 4560  
 ATCTTATTTT CTCATCTCC TCTCTCTTC CTCCACCCAT AATAAGAGAA TGTTCCTACT 4620  
 CACACTTCAG CTGGGTACCA TCCATCCCTC CATTATCCT TCCATCCATC TTTCCATCCA 4680  
 TTACCTCCAT CCATCTTCC AACATATATT TATTGAGTAC TACTGTGTG CCAGGGGGCTG 4740  
 GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA 4800  
 AGCATTTTTA AAAAATAAAT TAAACTTAC AACTTTGTT TGTCAACAGT GGTGTTTATT 4860  
 GCAATAACCG CTTGGTTTGC AACCTCTTG CTCAACAGAA CATATGTTGC AAGACCTCC 4920  
 CATGGGGGCA CTTGAGTTT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTCTTGTG 4980  
 CATTCCAGCT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040  
 TAACCCAGT GGAATTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGGAAGACTA 5100  
 TGGTGCTGCC TTGCTCTGT ATTTCTTGG ATTTCTCTGA AAGTGTTTTT AAATAAGAA 5160  
 CAATTGTTAG ATGCC

Seq ID NO: 390 Protein sequence  
 Protein Accession #: NP\_005553.1

70 1 11 21 31 41 51  
 MPALNLGCLL CFSLLLPAAAR ATSRREVDCD NGKSRQCIFD RELHRQTGNG FRCLNCDNDT 60  
 DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCPKPGVTG ARCDRLPGF 120  
 HMLTDAGCTQ DQRLDLSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYINLDGGN 180  
 75 PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVGWKA VQRNGSPAKL QNSQRHQDVF 240  
 SSAQRIDPVY FVAPAKFLGN QQVSYGQSLF FDYRVDGRGR HPSAHDVILE GAGLRITAPY 300  
 MPLGKTLPCG LTKTYTFRIN EHPNNWSPQ LSYFEYRLL RNLTALRIRA TYGEYSTGYI 360  
 DNVTLISARP VSGAPAPWVE QCICFVGKYG QFCQDCASGY KRDSARLGPP GTCLPCNCQG 420  
 80 GGACDPDGD CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCNGFSC SVMPETEVEV 480  
 CNNCPGPGVTG ARCELADGY FGDPPGERGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK 540  
 CHERTAGIYC DQCKAGYFGD PLAPNPADKC RACNCPMGS EPVGCSDGT CVCKPFGGPP 600  
 NCHGAFSPC ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAQEL 660  
 QDILRDAQIS EGASRSISLQ LAKVRSQENS YQSRLLDLKM TVERVALGS YQNRVRDTH 720  
 RLITQMLSL AESEASLGNT NIPASDHYVG PNGPKSLAQE ATRLAESHVE SASNMEQLTR 780

5  
10  
ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL ETKSLAQQL TREATQAEIE 840  
ADRSYQHSRLR LLDVSRLQGG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG 900  
NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEAISM GNATFYEVES ILKNLREFDL 960  
QVDNRKAEAE EAMKRLSYIS QKVSADSKT QQAERALGSA AADAQRAKNG AGEALEISSE 1020  
IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDN MDAVQMVITE 1080  
AQKVDTRAKN AGVTIQDTLN TLDGLLHMD QPLSVDEEGL VLLLEQLSRA KTQINSQLRP 1140  
MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ

Seq ID NO: 391 DNA sequence  
Nucleic Acid Accession #: AF101051.1  
Coding sequence: 221.856

15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80  
1  
11  
21  
31  
41  
51  
GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCCGCC CCGGGCCGGG ACCCCAACCC 60  
CGACCCAGAG CTCTCCAGC GCGGCGCAG CGAGCAGGGC TCCCGCCCTT AACTTCTCTC 120  
GCGGGGCCCA GCCACCTCG GAGTCCGGG TTGCCCACTT CCAAACTCTC CGCTTCTGCG 180  
ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAAG CGGGGCTGCA 240  
GCTGTGGGCG TTCATTCTCG CCTTCTCGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300  
CGCCCACTGG AGGATTACT CCTATGCCG CGACAACATC GTGACCGCCC AGGCCATGTA 360  
CGAGGGGCTG TGGATGTCT GCGTGTGCA GAGCACCAGG CAGATCCAGT GCAAAGCTTT 420  
TGACTCCTTG CTGAATCTGA CGACACATC GCAAGCAACC CGTCCCTTGA TGTGGTGTG 480  
CATCTCCTCG GGAGTGATAG CAATCTTGT GGCACCCGTT GGCATGAAGT GTATGAAGTG 540  
CTTGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTCT 600  
TCTTGCAAGT CTGGCTATT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660  
ATCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTGGTTCAGG CTCTCTTAC 720  
TGGCTGGGCT GCTGCTTCT TCTGCTTCT GGGAGGTGCC CTACTTTGCT GTTCTGTTC 780  
CCGAAACAAAC ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCAGCGG 840  
GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAATCA TGGTGAACA AACCGAAAAT 900  
GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTGGGTATT GTAATCTGAA 960  
GTATGGTATT ACAAACAAAC CAAACAAACA AAAACCCAT GGTGTAATAA ACTCAGTGCT 1020  
AAACATGGCT TAATCTTATT TTATCTTCT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080  
TGTATTACT GCTTCCCATT GAGTAATCAT ACTCAATGG GGGAGGGGT GCTCCTTAA 1140  
TATATATAGA TATGTATATA TACATGTTT TCTATTAAA ATAGACAGTA AAATACTATT 1200  
CTCATATTGT TGATACTAGC ATACTTAAA TATCTTAAA ATAGGTAAAT GTATTAAAT 1260  
CCATATTGAT GAAGATGTTT ATTGTATAT TTCTTTTTC GTCTTATAT ACATATGTAA 1320  
CAGTCAATA TCATTACTC TTCTTCAAT GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380  
CTAATTACTC AAGGATGATT TCTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT 1440  
TTATTTTTTA CCATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTGTG 1500  
TTTCATTGGT CTCTATCTCC TGAATCTAAC ACATTTTATA GCCTACATTT TAGTTTCTAA 1560  
AGCCAGAGAG AATTATTATC AAATCAGAAC TTGGGAGGCA AATCTTTCTG CATGACCAAA 1620  
GTGATAAATT CCGTGTGACC TTCCACACA ATCCCTGTAC TCTGACCCAT AGCACTCTTG 1680  
TTTGCTTTGA AATATTATTG CCAATTGAGT AGCTGCATGC TGTTCGCCCA GGTGTTGTAA 1740  
CACAACTTTA TTGATTGAAT TTTAAGCTA CTATTATATA GTTTTATATC CCCCTAAAAT 1800  
ACCTTTTGTG TCCCATTTCC TTAATTGTAT TGTTTTCCCA AGTGTAAAT TCAATGCTTT 1860  
TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTCTCGGAGT 1920  
GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAAGA AGTCATTTAA TCTTTCTACC 1980  
TCTTTTCTCT ATCTGCCAAA TTGAGATAAT GATACTTAA CAGTTAGAAG AGGTAGTGTG 2040  
AATATTAATT AGTTTATATT ACTCTCATT TTTGAACATG AACTATGCTT ATGTAGTGTG 2100  
TTTATTGTCT CAGCTGGCTG AGCACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC 2160  
CTTCATGTA TTCACTGCTT TCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220  
ACACATACCT TCATGTGGTT CAGTGCTTCT CTCTCTCTAC CAGTCTATTT CCACTGAACA 2280  
AAACCTAGCG ACATACCTTC ATGTGGCTCA GTGCCCTTCT CTCTCTACCA GTCTATTTC 2340  
ATTCTTTTCA CTGTGTCTGA CATGTTGTG CTCTGTTCCT TTTTAAACAC TGCTCTTACT 2400  
TTTCCAGTCT GTACAGAATG CTATTTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460  
GCACTGGTGT CTGGAGACCT GGATTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTG 2520  
AGCAAGGCTT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580  
CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640  
GTGGTTTTGT AATTGAAAA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAACGTGATA 2700  
OGTTTTGGTG TTGCTTTTCA AATGTTTGA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760  
GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACGAAT 2820  
AAGATTCTGA GGAAGTCTTA TCTTCTGAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880  
ACAGATGTAA TGGGAAGAAA TAAAGCCTA CGTGTGTTGTA AATCCAACAG CAAGGGAGAT 2940  
TTTTGAATCA TAATAACTCA TAAGTGCTA TCTGTTTCA GATGCCCTCA GAGCTCTTGC 3000  
TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060  
CTACACAAGG AAGTCTAGCC ACCGTGCTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120  
TGCCCTTCAA ACCTGAGAA ATATGCTTTT GGAAGTTAAA ATTTAAATGG CTTTGGCCAC 3180  
ATACATAGAT TCTCATGATG TGTGAGTGA ATTCCATGTG GATATCAGTT ACCAAACATT 3240  
ACAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATGT TACAATAGAA TTTATCCAAT 3300  
TTTGATCTTT TTATATTCTT CTACCACACC TGAAAAACA CCAATAGACA TTTTGGGGTT 3360  
TTATAATGGG AATTGTGATA AAGCATTACT CTTTTCAT AAATGTTTTT TTAATTTAAA 3420  
AAAAAGAAAA AAAAAA AAA

Seq ID NO: 392 Protein sequence  
Protein Accession #: AAD16433.1

80  
1  
11  
21  
31  
41  
51  
MANAGLQLLG FILAPLWIG AIUSTALPW RIYSYAGDNI VTAQAMYEGE WMSCVSQSTG 60  
QIQCKVFDLS LNLSSLTQAT RALMVVIGLL GVIAIFVATV GMKMKCLEDE DEVQKRMMAV 120  
IGGAIFLLAG LAILVATAWY GNRIVQEPYD FMTFVNARYE FGQALPTGWA AASLCLLGA 180  
LLCCSCPRKT TSYPTPRYP KPAPSSGKDY V

Seq ID NO: 393 DNA sequence  
Nucleic Acid Accession #: NM\_006180.1  
Coding sequence: 352..2820

```
5 1 11 21 31 41 51
| | | | |
CCCCATTG CATCTAACAA GGAATCTGCG CCCAGAGAG TCCCGGACGC CGCCGGTCCG 60
TGCCCGGCGC GCCGGGCCAT GCAGCGACGG CCGCCGCGGA GCTCGAGCA GCGGTAGGCG 120
CCCCCTGTAA AGCGGTTCGC TATGCGGGGA CCATGTGAA CCCTGCCGCC TGCCGGAACA 180
CTCTTCGCTC CGGACCACTG CAGCCTCTGA TAAGCTGGAC TCGGCACGCC CGCAACAAGC 240
ACCGAGAGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCTTC CCGGCACGGG TGGGGGAAAG 300
CGGCCGGTGC AGCCGCGGGA CAGGCACTCG GGCTGGCACT GGCTGCTAGG GATGTCGTCC 360
TGGATAAGGT GGCATGGACC CGCATGGCG CGGCTCTGGG GCTTCTGCTG GCTGGTTGTG 420
GGCTTCTGGA GGGCGGCTTT CGCCTGTCCC AGTCTCTGCA AATGCAGTGC CTCTGGATC 480
15 TGGTGCAGCG ACCCTTCTCC TGGCATCGTG GCATTTCCGA GATTGGAGCC TAACAGTGTG 540
GATCCTGAGA ACATCACCGA AATTTTCATC GCARACCAGA AAAGGTTAGA AATCATCAAC 600
GAAGATGATG TTGAAGCTTA TGTGGGACTG AGAAATCTGA CAATTGTGGA TTCTGGATTA 660
AAATTTGTGG CTGATAAGAC ATTTCTGAAA AACAGCAACC TGCAGCACAT CAATTTTACC 720
CGAAACAAAC TGACAGGTTT GTCTAGGAAA CATTTCCGTC ACCTTGACTT GTCTGAACTG 780
20 ATCCTGGTGG GCAATCCATT TACATGCTCC TGTGACATTA TGTGGATCAA GACTCTCCAA 840
GAGGCTAAAT CCAGTCCAGA CACTCAGGAT TTGTACTGCG TGAATGAAAG CAGCAAGAAT 900
ATTCCCCTGG CAACCTGCA GATACCCAAT TGTGGTTTGC CATCTGCAAA TCTGGCCGCA 960
CTAACTTCTG CTGTGGAGCA AGGAAAGTCT ATCACAATTAT CCTGTAGTGT GGCAGGTGAT 1020
CGGTTTCTTA ATATGTATTG GGATGTTGGT AACCTGGTTT CCAACATAT GAATGAAACA 1080
25 AGCCACACAC AGGGCTCCTT AAGGATAACT AACATTTTAT CCGATGACAG TGGGAAGCAG 1140
ATCTCTGTGG TGGCGGAAAA TCTTGTAGGA GAAGATCAAG ATTCTGTCAA CCTCACTGTG 1200
CAATTTGCAC CAATCATCAC ATTTCTCGAA TCTCCAACT CAGACCACCA CTGGTGCATT 1260
CCATTCTACT TGAAAGGACA CCCCACCA GCGCTTCAGT GGTCTATATA CGGGGCAATA 1320
TGAAATGAGT CCAATACAT CTGTACTAAA ATACATGTTA CCAATCACAC GGAGTACCAC 1380
30 GGCTGCTTCC AGCTGGATA TCCCACTCAC ATGAACAATG GGGACTACAC TCTAATAGCC 1440
AAGAATGAGT ATGGGAAGGA TGAGAAACAG ATTTCTGCTC ACTTCATGGG CTGGCCTGGA 1500
ATTGACGATG GTGCAAAACC AAATATCTCT GATGTAATTT ATGAAGATTA TGGAACTGCA 1560
CGGAATGACA TCGGGGACAC CACGAACAGA AGTAATGAAA TCCCTTCAC AGACGTCAT 1620
GATAAAACCG GTCCGGAACA TCTCTCGTCT TATGCTGTGG TGGTGTATGC GTCTGTGGTG 1680
35 GGAATTTGCC TTTTGGTAAT GCTGTTTCTG CTTAAGTTGG CAAGACATC CAAGTTTGGC 1740
ATGAAAGGCC TCTTGGTGGT TATCAGCAAT GATGATGACT CTGCCAGCCC ACTCCATCAC 1800
ATCTCCAATG GGAGTAACAC TCCATCTTCT TCGGAAGGTG GCCCAGATGC TGTCTATTAT 1860
GGAATGACCA AGATCCCTG CATTGAAAAT CCCCAGTACT TTGGCATCAC CAACAGTCAG 1920
CTCAAGCCAG ACACATTGTT TCAGCACATC AAGCGACATA ACATTGTTCT GAAAGGGAG 1980
40 CTAGGCGAAG GAGCCTTTGG AAAAGTGTTC CTAGCTGAAT GCTATAACCT CTGTCCTGAG 2040
CAGGACAAGA TCTTGGTGGC AGTGAAGACC CTGAAGGATG CCAGTGACAA TGCAACGAAG 2100
GACTTCCACC GTGAGGCCGA GCTCCTGACC AACCTCCAGC ATGAGCACAT CGTCAAGTTC 2160
TATGGCGTCT GCGTGGAGGG GACCCCTCTC ATCATGGTCT TTGAGTACAT GAAGCATGGG 2220
45 GACCTCAACA AGTTCTCTAG GGCAACGGCC CTGATGCCCG TGCTGATGGC TGAGGGCAAC 2280
CCGCCCAAGG AACTGACGCA GTGCGAGATG CTGCATATAG CCCAGCAGAT CGCCGCGGGC 2340
ATGGTCTACC TGGCGTCCCA GCACCTCGTG CACCGCGATT TGGCCACCAG GAACTGCCTG 2400
GTCCGGGAGA ACTTGTCTGT GAAAATGGGG GACTTTGGGA TGTCCCGGGA CGTGTACAGC 2460
ACTGACTACT ACAGGGTGGG TGGCCACACA ATGCTGCCCA TTGCTGGAT GCCTCCAGAT 2520
50 AGCATCATGT ACAGGAAATT CACGACGGA AGCGAGCTCT GGAGCCTGGG GGTGTTGTG 2580
TGGGAGATTT TCACCTATGG CAAACAGCCC TGGTACCAGC TGTCAAAACA TGAGGTGATA 2640
GAGTGTATCA TCTAGGGCCG AGTCCCTGAG GACCCCGCA CGTGCCCAAG GGAGGTGTAT 2700
GAGCTGATGC TGGGGTGTCT GCAGCGAGAG CCCCAATGGA GGAAGAACAT CAAGGGCATC 2760
CATACCCCTC TTCAGAACTT GGCCAAGGCA TCTCCGGTCT ACCTGGACAT TCTAGGCTAG 2820
55 GGCCCTTTTC CCCAGACCGA TCCCTCCCAA CGTACTCCTC AGACGGGCTG AGAGGATGAA 2880
CATCTTTTAA CTGCCGCTGG AGGCCACCAA GCTGCTCTCC TTCCTCTGA CAGTATTAA 2940
ATCAAGACTC CCAAGAGCTC CTGAGGGGAA CAGATGTGTA CTTCTTATC CATAGACACA 3000
GTATTGACTT CTTTGTGGCA TTATCTCTTT CTCTCTTCC ATCTCCCTTG GTTGTCTCT 3060
TTTCTTTTCT TAAATTTTCT TTTTCTTCT TTTTCTGCT TCCCTGCTT CACGATTCTT 3120
60 ACCCTTCTCT TTGAATCAAT CTGGCTCTG CATTAATATT AACTCTGCAT AGACAAGGC 3180
CTTAACAAC GTAATTTGTT ATATCAGCAG ACACCTCAGT TGGCCACCA CAACTAACAA 3240
TGCTTGTGTT TATCTCTGCC TTTGATGTGG ATGAAAAAAA GGGAAACAA ATATTTCAT 3300
TAAACTTTGT CACTCTGCT GTACAGATAT CGAGAGTTTC TATGGATTCA CTTCTATTTA 3360
TTTATTATTA TTAATGTTCT TATGTTTTT GGATGGCTTA AGCCTGTGTA TAAAAAGAA 3420
65 AACTGTGTTT CAATCTGTGA AGCCTTTATC TATGGGAGAT TAAACACGA GAGAAAGAG 3480
ATTTATTATG AACCGCAATA TGGGAGGAAC AAAGACAACC ACTGGGATCA GCTGGTGTCA 3540
GTCCCTACTT AGGAAATACT CAGCAACTGT TAGCTGGGAA GAATGTATTTC GGCACCTTCC 3600
CCTGAGGACC TTTCTGAGGA GTAAAGAGAC TACTGGCCTC TGTGCCATGG ATGATTCTTT 3660
TCCCATCACC AGAAATGATA GCGTGCACTA GAGAGCAAAG ATGGCTT
```

Seq ID NO: 394 Protein sequence  
Protein Accession #: NP\_006171.1

```
75 1 11 21 31 41 51
| | | | |
MSSWIRWHPG AMARLWGFCH LVVGFWRAPF ACPTSCKCSA SRIWCSDESP GIVAFPRLEP 60
NSVDPENITE IFIANQKRLB IINEDDVEAY VGLRNLITVD SGLKPVAKHA FLKNSNLQHI 120
NFRNKLKLSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TDLYCLNES 180
SKNPLANLQ IPNCGLPSAN LAAPNLVVEE GKSITLSCSV AGDPVPVPMYV DVGNLVSKHM 240
NETSHTQGLS RITNISDDDS GKQISCVAEV LVGEDQDSVN LTVHFAPFIT FLESPTSDHH 300
80 WCIPTFVKGN EKPAQWFFYN GAILNESKYL CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
LIARNEYGRD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVN LFLKLARHS KFGMRGPASV ISNDDDSASP 480
LHHSISGNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDFTFV QHKRHNIVL 540
KRELGEAGFG KVFLAECYNL CPEDQKILVA VKTLKQASDN ARKDFHREAS LLTNLQHEHI 600
```

VKPYGVCEVG DPLIMVFYEM KHGDLNKFRLR AHGPDAVLMA EGNPPELTQ SQMLHIAQQI 660  
AAGMVLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVVG GHTMLPIRMM 720  
PPESIMYRKF TTESDVWSLG VVLWEIFTYG KQPHYQLSNN EVIECITQGR VLQRPRTCPQ 780  
EYVELMLGCV QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG

Seq ID NO: 395 DNA sequence  
Nucleic Acid Accession #: AF410899  
Coding sequence: 483..2999

10 1 11 21 31 41 51  
GGGAGCAGGA GCCTCGCTGG CTGCTTCGCT CGCGCTCTAC GCGCTCAGTC CCGGGCGGTA 60  
GCAGGAGCCT GGACCCAGGC GCCGGCGGCG GCGGTGAGGC GCCGGAGCCC GGCTCGAGG 120  
TGCATACCGG ACCCCCATTC GCATCTAACA AGGAATCTGC GCCCCAGAGA GTCCCGGACG 180  
15 CCGCGCGTGG GTGCCCGGCG CGCCGGGCCA TGCAGCGACG CCGCGCGGCG AGCTCCGAGC 240  
AGCGGTAGCG CCCCCCTGTA AAGCGGTTCT CTATGCGGGG ACCACTGTGA ACCCTGCGCG 300  
CTGCGGGAAC ACTCTTCGCT CCGGACCAGC TCAGCCTCTG ATAAGCTGGA CTCGCGCACG 360  
CCGCAACAA GACCGAGGAG TTAAGAGAGC CGCAAGCGCA GGGAAAGGCT CCGCGCACGG 420  
GTGGGGGAAA GCGCGCGGTG CAGCGCGGGG ACAGGCACCT GGGCTGGCAC TGGCTGCTAG 480  
20 GGATGTGCTG CTGGATAAGG TGGCATGGAC CCGCCATGGC GCGCTCTGG GGCTCTGCT 540  
GGCTGGTTGT GGGCTTCTGG AGGGCCGCTT TCGCCTGTCC CACGTCTCTG AATGTCAGTG 600  
CCTCTCGGAT CTGGTGACAG GACCCTTCTC CTGCGATCGT GGCATTTCGG AGATTGGAGC 660  
CTAACAGTGT AGATCTGAG AACATCACCG AAATTTTCAT CGCAAAACCG AAAAGGTTAG 720  
AAATCATCAA CGAAGATGAT GTTGAAGCTT ATGTGGGACT GAGAAATCTG ACAATTGTGG 780  
25 ATTCTGGATT AAAATTTGTG GCTCATAAAG CATTCTGAA AAACAGCAAC CTGCAGCACA 840  
TCAATTTTAC CGGAAACAAA CTGACGAGTT TGTCTAGGAA ACATTTCCGT CACCTTGACT 900  
TGTCTGAATC GATCCTGGTG GGCATCCAT TACATGCTCT CTGTGACATT ATGTGGATCA 960  
AGACTCTCCA AGAGGCTAAA TCCAGTCCAG ACACCTCAGG TTTGTACTCG CTGAATGAAA 1020  
GCAGCAAGAA TATTCCTCTG GCAAACTCTG AGATACCCAA TTGTGGTTTG CCATCTGCAG 1080  
30 ATCTGGCCCG ACCTAACCTC ACTGTGGAGG AAGGAAAGTC TATCACATTA TCCTGTAGTG 1140  
TGGCAGGTGA TCCGGTTCTT AATATGTATT GGGATGTTGG TAACCTGGTT TCCAAACATA 1200  
TGAATGAAAC AAGCCACACA CAGGGCTCCT TAAGGATAAC TAACATTTCA TCCGATGACA 1260  
GTGGGAAGCA GATCTCTTGT GTGGCGGAAA ATCTGTAGG AGAAGATCAA GATTCTGTCA 1320  
ACCTCACTGT GCATTTTGCA CCAACTATCA CATTTCGGA ATCTCCAACC TCAGACCAAC 1380  
35 ACTGGTGCAAT TCCATTCATC GTGAAAGGCA ACCCAAAACC AGCGCTTCAG TGGTTCTATA 1440  
ACGGGGCAAT ATTGAATGAG TCCAAATACA TCTGTACTAA AATACATGTT ACCAATCACA 1500  
CGGAGTACCA CCGCTGCTCT CAGCTGGATA ATCCCACTCA CATGAACAAT GGGGACTACA 1560  
CTCTAATAGC CAAGAATGAG TATGGGAAGG ATGAGAAACA GATTCTGCT CACTTCATGG 1620  
GCTGGCTCGG AATTGAGCAT GGTGCAAAAC CAAATTATCC TGATGTAATT TATGAAGATT 1680  
40 ATGGAAGTGC AGCGAATGAC ATCGGGGACA CCACGAACAG AAGTAATGAA ATCCCTTCCA 1740  
CAGAAGTACG TGATAAAACC GGTGGGGAAC ATCTCTCGGT CTATGCTGTG GTGGTGATTG 1800  
CGTCTGTGTT GGGATTTTGC CTTTGTGTAA TGCTGTTTCT GCTTAAGTTG GCAAGACACT 1860  
CCAAAGTTGG CATGAAGATG TTCTCATGGT TTGGATTGGG GAAAGTAAAA TCAAGACAAAG 1920  
GTGTGGCCCC AGCCTCCGTT ATCAGCAATG ATGATGACTC TGCCAGCCCA CTCATCACA 1980  
45 TCTCCAATGG GAGTAACACT CCATCTTCTT CGGAAGGTGG CCCAGATGCT GTCATTATTG 2040  
GAATGACCAA GATCCCTGTC ATTGAAAATC CCCAGTACTT TGGCATCACC AACAGTCAGC 2100  
TCAAGCCAGA CACATTTGTT CAGCACATCA AGCGACATAA CATTGTTCTG AAAAGGGAGC 2160  
TAGGCGAAGG AGCCTTTGGA AAAGTGTTC TAGCTGAATG CTATAACCTC TGTCTGAGC 2220  
AGGACAAGAT CTTGTGTGCA GTGAAGACCC TGAAGGATGC CAGTGACAAT GCACGCAAGG 2280  
50 ACTTCCACCG TGAGGCCGAG CTCCTGACCA ACCTCCAGCA TGAGCACATC GTCAAGTTCT 2340  
ATGGGCTCTG CGTGAGGGGC GACCCCTCA TCAATGCTT TGAGTACATG AAGCATGGGG 2400  
ACCTCAACAA GTTCTCTCAG GCACACGGCC CTGATGCGGT GCTGATGGCT GAGGGCAACC 2460  
CGCCCAAGGA ACTGACGAGC TCGCATATGC TGCAATATGC CCAGCAGATC CCGCGGGGCA 2520  
TGGTCTACCT GGGCTCCGAG CACTTCGTGC ACCGCGATT GGCACACAGG AACTGCTGCG 2580  
55 TOGGGGAGAA CTTGCTGGTG AAAATCGGGG ACTTTGGGAT GTCCCGGGAC GTGTACAGCA 2640  
CTGACTACTA CAGGGTCTGT GGCACACAA TGCTGCCCAT TCGCTGGATG CCTCCAGAGA 2700  
GCATCATGTA CAGGAAATTC ACGACGGAAG GCGACGCTG GAGCCTGGGG GTGCTGTTGT 2760  
GGGAGATTTT CACCTATGGC AAACAGCCCT GGTACCACT GTCAAACAAT GAGGTGATAG 2820  
AGTGATACAC TCAGGGCCGA GTCTGCAGC GACCCCGCAC GTGCCCCACG GAGGTGATG 2880  
60 AGCTGATGCT GGGGTGCTGG CAGCGAGAGC CCCACATGAG GAAGAATATC AAGGGCATCC 2940  
ATACCCCTCT TCAGAACTTG GCCAAGGCAT CTCGGTCTTA CCTGGACATT CTAGGCTAGG 3000  
GCCCTTTTCC CCAGACCGAT CCTTCCCAAC GTACTCTCTA GAGCGGCTGA GAGGATGAAC 3060  
ATCTTTTAA TCGCGCTGGA GGCCACCAAG CTGCTCTCCT TCACTCTGAC AGTATTAAAC 3120  
TCAAAGACTC CGAAGAGCTC TCGAGGGAAG CAGTGTGTAC TTCTTCATCC ATAGACACAG 3180  
65 TATTGACTTC TTTTGGCAT TATCTCTTTC TCTCTTCCA TCTCCCTTGG TTGTTCTTTT 3240  
TTCTTTTCTT AAATTTTCTT TTTCTTCTT TTTTGTCTT TCCCTGCTTC ACGATTCTTA 3300  
CCCTTCTTCT TGAATCAATC TGGCTTCTGC ATTACTATTA ACTCTGCATA GACAAAGGCC 3360  
TTAAACAAAG TAATTTGTTA TATCAGCAGA CACTCCAGTT TGCCCAACAC AACTAACAT 3420  
GCCTGTGTGT ATTCTGCTCT TTGATGTGGA TGAATAAAGG GGAATAAACA TATTTCACTT 3480  
70 AAACITTTGTC ACTTCTGCTG TACAGATATC GAGAGTTTCT ATGGATTAC TTTCTATTAT 3540  
TTATTATTAT TACTGTCTCT ATTGTTTTTG GATGGCTTAA GCCTGTGTAT AAAAAGGAAA 3600  
ACTTGTGTGC AATCTGTGAA GCCTTTATCT ATGGGAGATT AAAACAGAG AGAAGAGAGA 3660  
TTTATTATAG ACCGCAATAT GGGAGGAACA AAGACACCA CTGGGATCAG CTGGTGTGAG 3720  
75 TCCTACTTAA GGAATACTC AGCAACTGTT AGCTGGGAAG AATGATTTCC GCACCTTCCC 3780  
CTGAGGACCT TCTGAGGAG TAAAAAGACT ACTGGCCTCT GTGCCATGGA TGATTCTTTT 3840  
CCCATCACA GAAATGATAG CGTGCACTAG AGAGCAAGA TGGCTTCCGT GAGACACAAG 3900  
ATGGCGCATA GTGTGCTCGG ACACAGTTT GTCTTCGTAG GTTGTGATGA TAGCACTGGT 3960  
80 TTGTTCTCA AGCGCTATCC ACAGAACCTT TGTCAACTTC AGTTGAAAAG AGGTGGATTG 4020  
ATGTCCAGAG CTCATTTCGG GTCAAGTGG GAAAGCC

Seq ID NO: 396 Protein sequence  
Protein Accession #: AAL67965.1

1 11 21 31 41 51

5 MSSWIRWHGP AMARLWGFCH LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60  
NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120  
NFRNKLTL SL SRKHFRHLDL SELILVGNPF TCSCDIMNIK TLQEAKESSPD TQDLYCLNES 180  
SKNIPLANLQ IPNCGPLSAN LAAPNLVTEE KXSITLSCSV AGDPVFNMYW DVGNLVSKHM 240  
NETSHTQSSL RITNISSDDS GKQISCVAEV LVGEDQDSVN LTVHFAPIT FLESPTSDHH 300  
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIRVTNHT EYHGCLQLDN PTHMNGDYT 360  
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKDFSWF GFGKVKSRQG 480  
10 VGPAFVISND DDSASPLHHI SNGSNTPSSS EGGPDVAIIG MTKIPVIENP QYFGITNSQL 540  
KPDFTVQHAK RHNIIVLKREL GEGAFKQVFL AECCYNLCPEQ DKILVAVKTL KDASDNARKD 600  
FHREAEELLN LQHEHIVKFY GVCVBGDPLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP 660  
PTELTSQSQL HIAQQAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720  
15 DYYRVGGHTM LPIRMPPES IMYRKPTTES DVWSLGVVLW EIFTYKQFW YQLSNNEVIE 780  
CITQGRVLQR PRTCPQEVYE LMLGCHQREP HMRKNKIGIH TLLQNLAKAS PVYLDILG

Seq ID NO: 397 DNA sequence  
Nucleic Acid Accession #: AB052906  
Coding sequence: 74..814

20 1 11 21 31 41 51  
AAAACCTTGA GGTGATTGAT CTTCCAGGCT CTCCTTCCAT CAAGTCTCTC CTCCTTAGCG 60  
CTCTGGGTCC TTAATGGCAG CAGCGGCCGC TACCAAGATC CTCTGTGTC TCCCGCTTCT 120  
25 GCTCGGTGCT TCGGGCTGCT CCGGGCTGCG GCGAGCCGAC CCTCACTCTC TTTGCTATGA 180  
CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGCTGG TGTGCGGTTC AAGGCCAGGT 240  
GGATGAAAG ACITTTCTTC ACTATGACTG TGGCAACAG ACAGTCAAC CTGTGCTGTC 300  
CCTGGGGAAG AACTCAATG TCACAACGGC CTGGAAGCA CAGAACCCAG TACTGAGAGA 360  
30 GGTGGTGAGC ATACTTACAG AGCAACTGCG TGACATTGAG CTGGAGAATT ACACACCCAA 420  
GGAACCCCTC ACCCTGAGG CCGAGATGTC TTGTGAGCAG AAAGCTGAAG GACACAGCAG 480  
TGGATCTTGG CAGTTGAGT TCGATGGGCA GATCTTCTC CTCTTGTACT CAGAGAAGAG 540  
AATGTGGACA ACGGTTGATC CTGGAGCCAG AAAGATGAAA GAAAAGTGGG AGAATGACAA 600  
GGTTGTGGCC ATGTCTCTTC ATTACTTCTC AATGGGAGAC TGTATAGGAT GGCITGAGGA 660  
35 CTCTTGTATG GGCATGGACA GCACCTGGA GCCAAGTGCA GGAGCACCAC TCGCCATGTC 720  
CTCAGGCACA ACCCACTCA GGGCCACAGC CACCACCTC ATCCTTTGCT GCCTCCTCAT 780  
CATCTCCCTC TGCTTCATCC TCCCTGGCAT CTGAGGAGAG TCCTTTAGAG TGACAGGTTA 840  
AAGCTGATAC CAAGAGGCTC CTGTGAGCAC GGTCTTGATC AAATCGCCCT TTCTGTCTGG 900  
CCAGCTGCC ACGACCTAGC GTGTATGTCC AGTGGCCTCC AGCAGATCAT GATGACATCA 960  
40 TGGACCCAAAT AGCTCATTCA CTGCCTTGAT TCCTTTTGCC AACAAATTTA CCAGCAGTTA 1020  
TACTTAACAT ATTAATGCAAT TTCTCTTGG TGCTACCTGA TGGAAATCCT GCACCTAAAG 1080  
TCTGCTGAGA CTAACAAGAA TATATCATTT TCTTTCTTCT CTTTTGTGTT GGAAATCAAA 1140  
GTACTTCTTT GAATGATGAT CTCTTTCTTG CAAATGATAT TGTCAAGTAA ATAATCAAGT 1200  
TAGACTTCAG ACCTCTGGGG ATTCTTTCCG TGTCTGAAA GAGAATTTT AAATTATTTA 1260  
45 ATAGAAAAA ATTTATATTA ATGATTGTTT CCTTAGTAA TTTATTGTTT TGTACTGATA 1320  
TTTAAATAAA GAGTTCATT TCCCAAAAAA AAAAAAAAAA AA

Seq ID NO: 398 Protein sequence  
Protein Accession #: BAB61048.1

50 1 11 21 31 41 51  
MAAAATKIL LCLPLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGGVDEKT 60  
FLHYDCGNKT VTPVSPGLKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT 120  
55 LQARMSCEBK ABGHSSGSWQ FSPDQIFLL FDSEKRMWTT VHGARKMKE KWENDKVVAM 180  
SFHYPSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC 240  
FILPGI

Seq ID NO: 399 DNA sequence  
Nucleic Acid Accession #: NM\_001898.1  
Coding sequence: 57..482

60 1 11 21 31 41 51  
GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCCTCTGAG GAGACCATGG 60  
65 CCCAGTATCT GAGTACCCTG CTGCTCTGCT TGGCCACCCT AGCTGTGGCC CTGGCCTGGA 120  
GCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180  
AGTGGGTACA GCGTCCCTTT CACTTCGCGA TCAGCGAGTA TAACAGGCGC ACCAAGATG 240  
ACTACTACAG ACGTCCGCTG CCGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300  
70 ATTACTTCTT CGACGTAGAG GTGGGCGGCA CCATATGTAC CAAGTCCCAG CCCAAGTTGG 360  
ACACCTGTGC CTTCATGAA CAGCCAGAAC TGCAGAGGAA ACAGTTGTGC TCITTCGAGA 420  
TCTACGAAGT TCCTGGGAG AACAGAGGT CCTGGTGAA ATCCAGGTGT CAAGAATCCT 480  
AGGATCTGTT GCCAGGCCAT TCGCACCAGC CACCAACCCAC TCCACCCCCC TGTAAGTCTC 540  
CCACCCCTGG ACTGGTGGCC CCCACCTGCG GGGAGGCTC CCAATGTGCC TGCCCAAGA 600  
75 GACAGACAGA GAAGGCTGCA GGAGTCTTT GTTGCTCAGC AGGGCGCTCT GCCCTCCTC 660  
CTTCTCTCTT GCTTCTAATA GCCCTGGTAC ATGGTACACA CCCCCCACC TCTGCAATT 720  
AACAGTAGC ATGCC

Seq ID NO: 400 Protein sequence  
Protein Accession #: NP\_001889.1

80 1 11 21 31 41 51  
MAQYLSTLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWQORALHF AISEYNKATK 60  
DDYYRRLRV LRARQTVGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120

EIVEVPWENR RSLVKSRCQE S

Seq ID NO: 401 DNA sequence  
Nucleic Acid Accession #: NM\_003976.2  
Coding sequence: 299..961

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
CTCTGAGCTT CTCTGAGCCT TGTITGCTCA TCTGGAAGAA GGGGATTAAA CCATTACCT 60  
CATGGAGTTG TGAAGAATA GCTGCAAGC ACCTAACACA TAGTAAGTT CCCAGTGCAG 120  
CTACTTCTGC TGGGTGAGT CTAGCTGTGT AGGCCCTCTG TTCCTCACCT GGAGAACTG 180  
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTTCGAA GCTGCCTCAA 240  
CAGGAGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTGTGTGT TGATAGAGAT 300  
GGAACCTGGA CTGAGAGGCC TCTCCACGCT GTCCACTGCG CCCTGGCTTA GCGGCGAGCC 360  
TGCCCTGTGG CCCACCTTGG CCGCTCTGGC TGTGCTGAGC AGCGTCGCG AGGCTCCCT 420  
GGGCTCCGCG CCGCGCAGCC CTGCCCCCG CGAAGGCCCC CCGCTGTCC TGGCGTCCCC 480  
CGCGCGGCGC CTGCGGGGGG GACGCAACGCG CCGCTGTGCG AGTGAAGAG CCGGCGGGCC 540  
GCCGCGGCGC CTTTCTCGGC CCGCGCCCC GCGGCTGCA CCCCCATCTG CTCTTCCCG 600  
CGGGGGCGCG GCGGCGCGGG CTGGGGGCC GGGCAGCGCG GCTCGGGCAG CGGGGGCGCG 660  
GGGTGCGCGC CTGCGCTGCG AGCTGGTGCC GGTGCGCGCG CTGCGCTGG GCGACGCTC 720  
CGACGAGCTG GTGCGTTTCC GCTTCTGCG CCGCTCTGCG CGCGGCGCG GCTCTCCACA 780  
CGACCTCAGC CTGGCGAGCC TACTGGGCGC CCGGGGCCCTG CGACCGCCCC CGGGCTCCCG 840  
CGCGCTCAGC CAGCCTCTGT CCGACCCAC GCGCTACGAA CGGCTCTCT TCTGGAGCT 900  
CAACAGCACC TGGAGAAGCG TGGACCGCT CTCCGCCACC GCTTGGGCT GCTTGGGCTG 960  
AGGGCTCGCT CCAGGCTTT GCAGACTGGA CCGTTACCG TGGCTCTTC TGGCTGGGAC 1020  
CTTCCGCGAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCT CAAAGCTGAG 1080  
AGGCCCTTAC CGGTGGGTGA TGGATATCAT CCGCGAACAG GTGAAGGAG AACTGACTAG 1140  
CAGCCCCAGA CGCCTCAGC TGGGATCCC AGCCTAAAG ACACAGAGA CCTCAGTAT 1200  
GGAGCCCTTC GGACCCACT CTACAGACT CTGGCACTGG CCAGGCTCG AACCTGGGAC 1260  
CCCTCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGGCCGAG CCCTGTAGG 1320  
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCCTGTG CTGGAACCTG 1380  
CCTGTACTCA CTATGGGAG CTGGCCCC

Seq ID NO: 402 Protein sequence  
Protein Accession #: NP\_003967.1

40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
MELGLGLST LSHCPWRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPFVLAS 60  
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAGA 120  
RGCLRLSLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180  
RPVSPQCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 403 DNA sequence  
Nucleic Acid Accession #: NM\_057091.1  
Coding sequence: 783..1445

50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60  
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCA CCGCAGGACC GGCCTACCCC 120  
TCGCTCCCGC CCTCACTCA CTCTTCCCG CCTCGGCC CCGCTCCAG CTCTCTACTT 180  
CGCGTGTCTA CAACTCAAC TCCCGTTTC CGTGCTCTC CACCGCTCGA GTTCTCTACT 240  
CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCT CCAACCTCG GGGACCTAGC 300  
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAGGTGGGG 360  
CGGGGACGGG GCGCTCCAG CCCCACCCG GGTCTGGTG ACGCTGGGC TGGAAATTGA 420  
CACCGGACGG CTGCGGGGCG GGGCAGGAG CTGCTGAGG ATGGAGTTGG GCCCGGCC 480  
CAGACAAGGC CCGGGGGCTC CGCCAGCAG AGGTCCCTCG GGGCCAGCC CTGCTGCCA 540  
CCCGGGCTG GAGCCCAACA CCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTGGC 600  
TAAAGAGGC ACTGCCAGT GTACAGTCTT GGCATGCGC TGTITGAGCT TCGGGGAGA 660  
GCCAGCACT GGTCCCGGA AAGGTGCCA GAAGAACAAG GTGCAGGACC CCGTCTGCC 720  
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GCGCTCTCT GTGTGTATAG 780  
AGATGGAAC TGGACTTGA GGCCTCTCA CGCTGTCCA CTGCCCTGC CTAGGCGGC 840  
AGCCTGCCCT GTGCCACCC CTGCGCGCT TGGCTCTGCT GAGCAGGCTC GCAGAGGCT 900  
CCCTGGGCTC GCGCGCCCG AGCCCTGCC CCGCGGAAG CCCCCGCT GTCTGGGT 960  
CCCCCGCGG CCACTGCGG GGGGACGCA GGGCCGCTG GTGCAGTGA AGAGCCGGC 1020  
GGCGCGCGC GAGCCTCT CTGCGCGCG CCGCGCGCC TGCACCCCA TCTGCTCTT 1080  
CCCGCGGGG CCGCGCGCG GGGCTGGG GCGCGGCG CCGCTCGG GCAGCGGGG 1140  
CGCGGGGCT CCGCTGCG CTGCGCTCT TCGCGGTG GCGCTCGG CTGGGCCACC 1200  
GCTCCGACA GCTGGTGGT TTCCGCTCT GCAGCGGCT CTGCGCGCG GCGGCTCTC 1260  
CACACGACT CAGCTGGCC AGCCTACTG GCGCGGGGC CCGTGCAGC CCGCGGGCT 1320  
CCCGGCCGT CAGCGAGCC TGCTGCCAG CACCGGCTA CGAAGCGGT TCCTTCATG 1380  
ACGTCAACAG CACTGGAGA ACCGTGGAC GCGCTCCGC CACCGCTCG GCGTGGCTG 1440  
GCTGAGGGCT CGCTCCAGG CTTGCGAGC TGGACCTTA CCGGTGGCT TTCTGCTG 1500  
GGACCCCTCC GCAGATCCC ACTAGCCAG GGCCTCAGC AGGGACGAAG GCCTCAAGC 1560  
TGAGAGGCC CTACCGTGG GTGATGGATA TCATCCCCG ACAGGTGAAG GGACAACCTGA 1620  
CTAGCAGCCC CAGAGCCCT ACCCTGCGA TCCAGCCTA AAAGACACA GAGACCTCAG 1680  
CTATGGAGC CTTGGAGCC ACTTCTACA GACTCTGSCA CTGGCCAGG CTGGAACCTG 1740  
GGACCCCTCC TCTGATGAC ACTACAGTG CTGAGGCATC AGCCCCGCG CAGGCCCTGT 1800  
AGGGACAGCA TTTGAAGAC ACATATTGA GTTGCTTGGT TGAAGTGCC TGTGCTGGA 1860  
CTGGCTGTA CTACTCATG GGAGCTGGCC CC

Seq ID NO: 404 Protein sequence  
Protein Accession #: NP\_003967.1

1 11 21 31 41 51  
5 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60  
PAGHLPGGRT ARWCSGRARR PPPQSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120  
RGCLRLSQLV FVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180  
RPVSPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGLG

10 Seq ID NO: 405 DNA sequence  
Nucleic Acid Accession #: NM\_057160.1  
Coding sequence: 1..714

1 11 21 31 41 51  
15 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCAAGGCC 60  
CACTGGGGTG CCCTCTTTCT CCCTGAGGCT CCCTTGCTC TCTCCGCGCA GCCTGCCCTG 120  
TGGCCACACC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCT CAGAGGCTCT CCTGGGCTCC 180  
GCGCCCCGCA GCCTGCCCTC CCGGAGAGGC CCCCGGCTG TCTTGGCTCT CCCCGGCTG 240  
20 CAGCTGCCGG GGGGACGAC GGGCGCTGG TGCAGTGGAA GAGCCGCGG GCGCGGCTG 300  
CAGCCTTCTC GGGCCGCGCC CCGCGGCTG GCACCCCAT CTGCTCTTCC CCGCGGCTG 360  
GCGCGGCTG GGGCTGGGG CCGCGGCTG CCGCTCGGG CAGCGGCTG GCGGGGCTG 420  
CGCTGCGCT CGCAGCTGGT GCGGCTGGC GCGCTCGGG TGGGCTGCG CTCCGACGAG 480  
CTGGTGGGT TCGCTCTCT CAGCGCTCC TCGCGCGGG CCGCTCTCC ACACGACCTC 540  
25 AGCTGGGCA GCCTACTGG GCGCGGCTG CTGCGACGG CCGCGGCTC CCGCGGCTC 600  
AGCCAGCCCT GCTGCGGAC CAGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660  
ACCTGGAGAA CCGTGGACCG CCTCTCGGC ACCGCTGCG GCTGCTGGG CTGAGGGCTC 720  
GCTCCAGGGC TTGTCAGACT GGACCTTAC CGGTGGCTCT TCTGCTGCG GACCTCCCG 780  
30 CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAG CCTCAAAGCT GAGAGGCCCC 840  
TACCGTGGG TGATGGATAT CATCCCGAA CAGGTGAAG GACAACTGAC TAGCAGCCCC 900  
AGAGCCCTCA CCTGCGGAT CCAGGCTAA AAGACACCAG AGACCTCAGC TATGAGCCCC 960  
TTGGAAGGCA CTCTCAGAG ACTCTGGAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020  
CTGATGAACA CTACAGTGGC TGAGGCATCA GCGCCCGGCC AGGCCCTGTA GGGACAGCAT 1080  
35 TTGAAGGACA CATATTGAG TTGCTTGGT GAAAGTGCT GTGCTGGAAC TGGCTGTATC 1140  
TCATCTATGG GAGCTGGCCC C

Seq ID NO: 406 Protein sequence  
Protein Accession #: NP\_476501.1

1 11 21 31 41 51  
40 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SVAEASLGS 60  
APRSPAPREG PPPVLASPA HLPGRRTARW CSGRRARRPP QPSRPAPPPP APPSALPRGG 120  
45 RAARAGGPGS RARAAGARGC RLRLSQLVPR ALGLGHRSD LVRFRFCSSG CRRARSPHDL 180  
SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TAGGCLG

Seq ID NO: 407 DNA sequence  
Nucleic Acid Accession #: NM\_057090.1  
Coding sequence: 29..715

1 11 21 31 41 51  
50 CTGATGGGGC CTCTCGGTGT TGATAGAGAT GGAAGTTGGA CTTGGAGGCC TCTCCAGCT 60  
GTCCCACTGC CCCTGGCCTA GCGGCGAGGC TCCACTTGGT CTCTCCGCGC AGCTTGCCT 120  
55 GTGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCTC CCTGGGCTC 180  
CGCGCCCGGC AGCCCTGCCC CCGCGAAGG CCCCGGCTG GTCTTGGCTC CCCCGGCTG 240  
CTACCTGCGC GGGGAGCGCA CCGCGCTG GTGAGTGGAA AGAGCCGCGC GCGCGGCTG 300  
GCAGCTTCTT CCGCCGCGGC CCGCGGCTG TGCACCCCA TCTGCTCTTC CCGCGGCTG 360  
60 CCGCGGCTG CCGGCTGGG GCGCGGCTG CCGCTCGG GCAGCGGCGC GCGCGGCTG 420  
COGCTCGGC TCGCAGTGG TCGCGTGGC CGCGCTGGC CTGGGCGACC GCTCCGACGA 480  
GCTGGTGGT TTCGCTTCT GCAGCGGCTC CTGCGCGGC GCGCGCTCT CACACGACCT 540  
CAGCCTGGCC AGCTACTGG GCGCGGCTC CTGCGGCTC CCGCGGCTC CCGCGGCTC 600  
CAGCCAGCCC TGCTGCGGAC CACGCGCTA CGAAGCGGTC TCTTCTATGG AGCTCAACAG 660  
65 CACCTGGAGA ACGTGGGACC GCCTCTCGC CACCGCTGCG GGTGCTGCG GCTGAGGGCT 720  
CGCTCCAGG CTTTGCAGAG TGGACCTTA CCGGTGGCTC TTCTGCTG GAGACCTCCC 780  
GCAGAGTCCC ACTAGCCAGC GCGCTCAGCC AGGACGAGG GCCTCAAAGC TGAGAGGCCC 840  
CTACCGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACACTGA CTAGAGCCCC 900  
CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGAGGCC 960  
70 CTGCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTGAACTCG GAGACCTCCC 1020  
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCGGCTC CAGGCGCTGT AGGACAGCA 1080  
TTTGAAGGAC ACATATTGCA GTTGTCTGGT TGAAGTGCC TGTGCTGGAA CTGGCTGTA 1140  
CTACTCATG GAGCTGGCCC C

75 Seq ID NO: 408 Protein sequence  
Protein Accession #: NP\_476431.1

1 11 21 31 41 51  
80 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60  
GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQSRPAPPPP PAPPALPRG GRAARAGGPG 120  
SRARAAGARG CLRLSQLVPR RALGLGHRSD ELVRFRFCSSG SCRRARSPHD LSLASLLGAG 180  
ALRPPPGSRP VSPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG



Seq ID NO: 409 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1746

5	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCTTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCAAC	120
10	GGGGCAGCA	TTGTGCGGT	GCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACAGCG	ACATCACTGA	ACTCAATGAG	TCCCGCTTCC	TCAATATCTC	AGCCCTCATC	240
	CCCTGAGGA	TTGAGAAGAA	TGAGCTGTGG	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
	GGCTGCTGC	GCTATCTCAG	CCTGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCACTG	GTTCGAGATC	420
15	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCAACCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCCGGC	TGTATGAGAA	CAGGCTCAGC	GATATCCCCA	TGGGCACCTT	TGATGGGCTT	660
	GTTAACTGCG	AGGAACCTGG	TCTACAGCAG	AACCAAGATTG	GACTGCTCTC	CCCTGGTCTC	720
20	TTCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACNACCACAT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTGGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGATTTC	TAGCGCGCAA	TCAGATCAGC	TTCACTCTCC	CGGGTGCCTT	CAACGGGCTA	1020
25	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGATGT	TGGCCAACT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAAAT	TCTTCGCCAA	CGTCAATGGC	CTCATGSCCA	TCCAGCTGCA	GAACAACCAG	1200
	CTGGAGAAAT	TGCCCTCGG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
30	AACCAGCCTA	GGTTAGGGAC	GGCACTGTA	CCTGTGTGTT	TCAGCCACGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTCTGTTT	CAAGCGTCCA	TGTCCTGAG	1440
	GTGCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCACTGA	GCTAACCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTGAGGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
35	ATTGCGGCCA	TTGTAATTGG	CATTGTGCCC	CTGGCTGCTC	CCCTGGCTGC	CTGCGTGGCC	1680
	TGTTGCTGCT	GCAAGAAGAG	GAGCCAAAGT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
40	CTAGATAAAG	GTGTGCTTAC	CTCTTCTGTA	CTTGCTGAT	TCTCCGCTAG	AGAAGCAGGT	1920
	CGTGCGGAC	CTTCTCAACA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCGGA	TTTCAATCCC	TGGGCTTCTT	TCCAGAGGGC	TCCTCTCTCA	AATCTCTCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTC	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCTCTCG	2160
45	CCTAAGTATT	ATGTAAGTTC	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
	ACCCAGCATG	TCCCTCAAA	TGAAGTTCT	CCCCCTGATT	TTCTGTCTCT	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAGAAA	GACTTCAAAC	CATTAAACTG	GTTTCTTAAG	AGCCGTCAAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAGAG	AGAAGGAAAA	TCATGCGGCT	CAGTTCTCTG	2400
	AGACAGAGA	CGCGTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAGAAACA	2460
50	CCCCAGCACA	CGAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAACTGCA	AACTTTCTT	2520
	TGAAAAGTTT	AGCCCTTTAA	GGAATGAAAT	CATGTAGAA	TTTGGACTTC	TAAAAACATT	2580
	AAAATCAGCT	TATTATATCG	GGATAGAGAA	AGAAATCTGG	TGCCCTGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TGAAAGCATG	TGAAGTGATC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCAACA	ACTGAACATA	CCTGTGTAAT	2760
55	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCAGA	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGA	GCCAGGACGG	2880
	TCCCCCACA	GTCAGCTGT	GCAAGGCCCC	CGTGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCCCTG	3000
	AGAGACCTCG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
60	GTCGCTGAG	CCACACCTCT	TTCCCTGCCA	GCAAGTGTGC	TGGGCTCAT	CGGAGGCCCC	3120
	TCCGCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTTAATT	TTCAATCTTC	3180
	ACTTAGGGGA	AGTGAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAAAG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTAGG	3360
65	GTCTGGGGCC	TCCCTGGAGC	TCCTCTGCG	TGTGTCTGG	TTAGGAGTTG	AGTTGTGTC	3420
	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACAGCAAT	ACCTGCCCTC	CTGTGCTTTC	3480
	CTGTATACAA	CATATTACAA	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGCTTTC	3540
	CTCTGGACAA	CTGGCCAGT	TTACAGTGAA	ATGGAGAAAT	TCAGGTCTCC	ACCTCTGCCC	3600
	AGGAAAGAAC	TTCACTGAC	TCCACGGGGA	TCTGGAAATC	CACGACCAAT	CCCGATCGGC	3660
70	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TGGCTCTTAA	TGAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTCC	CAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGG	TGCTGACCCAG	TTTTCCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CATAGTGCA	CTTTGTAGCT	TTTCAACCTC	TGTCACAGGG	AATCTAGGAG	3960
75	AGATGAGGCC	CGTCAAGTGC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAA	GCAATTCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAAAC	GGAAGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGCC	TGCTGTGCTC	GGTGCCAAAC	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGCCAC	AGACCTGTG	4200
	GGTGTCTCTG	TGAGTGGCTC	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
80	GAGGAGAGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAAACC	AGAACCCTTA	4320
	GGTATTCTTG	CGAGTAGCCA	TGACATTGGA	GCACCTTCTC	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCTAGAT	GACACCAACC	AGGAGCAACC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGGGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGA	GTCTCTTTC	CAACAGGATG	ATGCATTTCG	TCAATTCTCA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAAGTTT	4680

5  
10  
15  
20

CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA 4740  
GTGTTGGAGA AGAAACACAA AAAGCCAATT AGAACCACTA TTTTAAAAA GTGCTTACTG 4800  
TGCACAGATA CTCTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860  
GGTAGGAGTG CGSCCTCTAC CCACITGTGA TGGGGTACAG AGGCACCTGC TCTCTGTCAT 4920  
GGTGTTCAT AGGCTGGGAG TTTTATTTAT CTCTCAAAAC TTTGTACAAG AGCTCATGGC 4980  
TTGTCTTGGG CTCTGTGTCAT TAAACCAAG GAAATGGAAG CCATTCCTCTT GTTGCTCTCC 5040  
TTAGTCTTGG TCATCAGAAC CTCACCTGGT ACCATATAGA TCAAAAGCTT TGTAAACCACA 5100  
GGAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT 5160  
TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTAGA GATACAAGAG TTCTACTTAG 5220  
AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280  
GAACCTTCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG 5340  
AGTGTGTCGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400  
GCCCCAGAT CCCACAGTCA GAACTGAATC TGCCTTGTG GGAAGCCAGC AGTGGCCTTG 5460  
GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520  
CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTCTCACC AACCCGCTGC 5580  
CTTCATGCTG CCTTCAAAGC TAGATCATGT TTGCTTGTCT TAGAGAAATTA CTGCAATCA 5640  
GCCCCAGTGC TTGGCGATGC ATTACAGAT TTCTAGGCCC TCAGGGTTTT GTAGAGTGTG 5700  
AGCCCTGTGT GGCAGGGTGT GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATT 5760  
GGTGACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 410 Protein sequence  
Protein Accession #: BAB84587.1

25  
30  
35

1 11 21 31 41 51  
MPLKHYLLLL VGCQAWGAGL AYHGPCSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60  
LNTHITELNE SPFFINISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPGL 120  
FQGLDSLESL LLSSNQLLOI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVLTKLNL 180  
GKNSLTHISP RVFOHGLNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQO NQIGLLSPGL 240  
FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PPNRLRELWL 300  
YDNHISLDP NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLQDNV 360  
FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCLELRL 420  
YDNFWRCDSD ILPLRNLLLL NQPRLGTDTV PFCFSPANVR GQSLIIINVN VAVPSVHVPE 480  
VPSYPETPHY PDTPSYPDIT SVSSTIELTS FVEDYDILT IQVTDERSVW GMTQAGSGLA 540  
IAATVIGIVA LACSLAACVG CCCCCKRSQA VLMQMKAPNE C

Seq ID NO: 411 DNA sequence  
Nucleic Acid Accession #: XM\_098151  
Coding sequence: 1..447

40  
45  
50

1 11 21 31 41 51  
ATGATGCATT TGCTCAATTC TCAGGGCTGG AATGAGCCGG CTGGTCCCCC AGAAAGCTGG 60  
AGTGGGGTAC AGAGTTCAGT TTTCTCTCTT GTTACAGCT CCTTGACAGT CCCACGCCCA 120  
TCTGGAGTGG GAGCTGGGAG TCAGTGTGAG AGAAGAAACA ACAAAGCCCA ATTAGAACCA 180  
CTATTTTAA AAAGTGCCTA CTGTGCACAG ATACTCTTCA AGCACTGGAC GTGGATTCTC 240  
TCTTAGCCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCCT TACCCACTTG TGATGGGGTA 300  
CAGAGGCACT TGCTCTTCTG CATGGTGTTC AATAGGCTGG GAGTTTATT TATCTCTTCA 360  
AACTTTGTAC AAGAGCTCAT GCCTTGTCTT GGGCTTTCGT CATTAAACCA AAGGAAATGG 420  
AAGCATTCC CTGTTGCTC TCCTTAG

Seq ID NO: 412 Protein sequence  
Protein Accession #: XP\_098151

55  
60

1 11 21 31 41 51  
MMHLLNSQGW NEPAGPFESW SGVQSSVFLS VYSSLTVPRP SGVGAGSQCW RRNKNSQLEP 60  
LFLKSAICAQ ILFKHTWIL SLALSTPAVG VPPLFTCDGV QRHLLEFCMVF NRLGLVFISS 120  
NFVQELMACL GLSSLNQRKW KPFPCCSP

Seq ID NO: 413 DNA sequence  
Nucleic Acid Accession #: NM\_002658.1  
Coding sequence: 77..1372

65  
70  
75  
80

1 11 21 31 41 51  
GTCCCCGCGC CGCCGTGCGG CCTCCTGCCC GCAGGCCACC GAGGCCGCGG CCGTCTAGCG 60  
CCCCGACCTC GCCACCATGA GAGCCCTGCT GCGCGCCCTG CTCTCTGCG TCCTGGTCTG 120  
GAGCGACTCC AAAGCAGCA ATGAACCTCA TCAAGTTCCA TOGAAGTGTG ACTGTCTAAA 180  
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCAAA 240  
GAAATTCGGA GGGCAGCACT GTGAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300  
TCACITTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCTGGAA 360  
CTCTGCCACT GTCCCTCAGC AAACGTACCA TGCCACAGA TCTGATGCTC TTCAGCTGGG 420  
CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGCGACCTCT GGTGCTATGT 480  
GCAGGTGGGC CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540  
AAAGCCCTCC TCTCTCCAG AAGAATTAAA ATTTCAAGTG GSCCAAAA CTCTAGGCC 600  
CGCTTTAAG ATTATTGGGG GAGAATTAC CACCATCGAG AACAGCCCTT GTTTTGGGCG 660  
CATCTACAGG AGCACCAGG GGGCTCTGT CACTACGTG TGTGAGGCA GCCTCATCAG 720  
CCCTTGCTGG GTGATCAGCG CCACACTG CTTCATTGAT TACCCAAGA AGGAGGACTA 780  
CATCGTCTAC CTGGTCTGCT CAAGGCTTAA CTCCAACAG CAAGGGGAGA TGAAGTTGA 840  
GGTGGAAAAC CTCATCTAC ACAAGGACTA CAGCGCTGAC ACGCTGCTC ACCACAACGA 900  
CATTGCCCTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGACTAT 960  
ACAGACCTC TGCCCTGCCCT CGATGTATA CGATCCCCAG TTTGGCACA GCTGTGAGAT 1020  
CACTGGCTTT GGAAGAGAGA ATTCTACGA CTATCTCTAT CCGGAGCAGC TGAAGATGAC 1080

5 TGTGTGAAG CTGATTTCCT ACCGGGAGTG TCAGCAGCCC CACTACTAGG GCTCTGAAGT 1140  
 CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200  
 CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGATG ACTTTGACTG GAATTGTGAG 1260  
 CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACTATT 1320  
 CTTACCCCTG ATCCCGAGTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380  
 AGGGAGGAAA CGGGCACCAC CCGCTTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440  
 TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG 1500  
 CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC 1560  
 CAGACCCCTT GCCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620  
 10 TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAATAAGGG CAGGGCATCT CCTGTGCATG 1680  
 GGCTCGAAGG GAGAGCCAGC TCCCCGACC GGTGGGCATT TGTGAGGCC ATGTTTGAGA 1740  
 AATGAATAAT TTCCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800  
 AATGTGGGAG CAGCGGTTTG GGGAGCAGAG AACTAACGA CTTCAGGCA GGGCTCTGAT 1860  
 ATTCCATGAA TGTATCAGAA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTG 1920  
 15 GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT 1980  
 AAACGTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC 2040  
 CTGGGGCCTC TTGGGTCCCC CACGTGACAG TGCCTGGGAA TGTACTTATT CTGCAGCATG 2100  
 ACCGTGACAG AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGCCAGTT 2160  
 20 ATCCCTTCCT TTTAGCCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220  
 ACACGAATA TTTATATTTC ACTATTTTTA TTTATATTTT TGTAATTTTA AATAAAGTG 2280  
 ATCAATAAAA TGTGATTTT CTGA

Seq ID NO: 414 Protein sequence  
 Protein Accession #: NP\_002649.1

25 1 11 21 31 41 51  
 MRALLARLLL CVLVVSDSKG SNEHQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKKFGGQ 60  
 HCEIDKSKTC YEGNGHPYRG KASTDTMGRP CLPWN SATVL QQTTHAHRSD ALQLGLGKH 120  
 30 YCRNPDNRNR PWCVYVQGLK PLVQECMVHD CADGKKPSSP PEELKFQCGQ KTLRPRFKII 180  
 GGEFTTIENQ PWFPAIYRRH RGSVTVYCG GSLISPCWVI SATHCFIDYP KKEYDIVVILG 240  
 RSRINSNQFG ENKFEVENLI LHKDYSADTL AHNDIALLLK IRSKEGRCAQ PSRTIQTICL 300  
 PSMYNDPQFG TSCETITGFG ENSTDYLYPE QLKMTVVKLI SHRECCQPHY YGSEVTTKML 360  
 35 CAADPQWKTG SCQGDSSGGL VCSLQGRMTL TGIWSWGRGC ALKDKPGVYT RVSHFLPWIR 420  
 SHTKEENGLA L

Seq ID NO: 415 DNA sequence  
 Nucleic Acid Accession #: NM\_024422.1  
 Coding sequence: 202..2907

40 1 11 21 31 41 51  
 CGCCAAAGGA AAAGCCCTCT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60  
 CTCTCGCGCG GCCCACCCTC CTCGCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120  
 45 GCTCGCGCGCG CGGCCCTCGC CCCGCGGAGC CCTCCTACCC CGGCCGAGCG CTGCGCCGCG 180  
 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCC CGGCTCCTG GAACGAGGCC 240  
 CTCTGCGCGCG TGCTCCTGCT GACCTCGCG ATCTTAATAT TTGCCAGTGA TGCCGTGCAA 300  
 AATGTGACAT TACATGTTC CTCCAACTA GATGCGGAGA AACTGTGTGG TAGAGTTAAC 360  
 50 CTGAAAGAGT GCTTACAGC TGCAAACTA ATTCAATCAA GTGATCTGTA CTTCCAAATT 420  
 TTGGAGGATG GTTCAGTCTA TACACCAAT ACTATTCTAT TGTCTCTGGA GAAGAGAAGT 480  
 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAATATT TGTCTTTTGG 540  
 GAGCATCAAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAGTTCTT AAGGCGCGCC 600  
 AAGAGAGAT GGGCTCCAAT TCCTTGTTGG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660  
 55 CTTTCTCTTC AACAGGTTCA ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720  
 AGAGGTCCTG GAGTTGACCA AGAACCTCGG AATTATTTT ATGTGGAGAG AGACACTGGA 780  
 AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840  
 TTTGCAACAA CTCAGATGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900  
 GAGGATGAAA ATGATACTA CCAATTTT ACAGAAAGAA CTTTACTTTT TACAATTTT 960  
 60 GAAAAITGCA GAGTGGGCAC TACTGTGGGA CAGTGTGTG CTACTGACAA AGATGAGCCT 1020  
 GACAGGATGC ACACACGCTT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCAACCACC 1080  
 CTATTTTCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140  
 GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAG ACATGGATGG TCAGTATTTT 1200  
 GGTCTACAGA CACTTCAAC TTGTATCATT AACATTGATG ATGTAATGA CCACCTGCCA 1260  
 65 ACATTTACTC GTACTTCTTA TGTGACATCA GTGAAGAAA ATACAGTTGA TGTGGAAATC 1320  
 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATCTG CTAAGTGGAG AGCTAATTAT 1380  
 ACCATTTTAA AGGCAATGA AATGSCAAT TTTAAATTTG TAACAGATGC CAAACCAAT 1440  
 GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500  
 CAAATTTGGT TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560  
 70 AGCACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCTT 1620  
 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1680  
 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGCCATAA GGTATAAGAA ATTAACGTAT 1740  
 CCAACAGGGT GGGTCACCAT TGATGAAAT ACAGGATCAA TCAAGTTTTT CAGAAGCCTG 1800  
 GATAGAGAGG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCTT TGCATCAGAC 1860  
 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGAGCT GAATGATAAC 1920  
 75 AGCCCATTTA TACCTAAAAA GACAGTGATC ATCTGCAAC CCACCATGTC ATCTGCGGAG 1980  
 ATTGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCAC CCTTTGACTT TAGTCTGGAG 2040  
 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAAATGA TACAGCAGCA 2100  
 CGTCTTTCTT ATCAGATGA TCCTCAATT GGTCTATATG TAGTACCTAT AACAGTGAGA 2160  
 80 GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220  
 GAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGAGGAGT ACAACTTGGG 2280  
 AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCACT CCGTTTACG 2340  
 CTGCTCTGTT GGGCTCTCG GACCTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC 2400  
 CAGCAGAAC TAATTGTATG AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460  
 AATGCTTCA CAACCAAAAC TGTGGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520

5 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGGAGG ACACCAGACC 2580  
TCGGAATCCT GCGGGGGGGC TGGCCACCAT CACACCTCGG ACTCCTGCAG GGGAGGACAC 2640  
ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCGGT 2700  
CTTGGTGAAG AAGTGTATCT GTGTAATCAA GATGAAATC ACAAGCATGC CCAAGACTAT 2760  
GTCTTGACAT ATAACATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT 2820  
GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 2880  
CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTCTTAATA AGTCTCTGAA AGCCAGTGGC 2940  
TTTATGACTT TTAACAAAAA TTACAAACCA AGAATTTTTT AAAGCAGAAG ATGCTATTTG 3000  
TGGGGGTTTT TCTCTCATT TTTGGATGGA ATCTCTTTGG TCAATGCAC ATTTACAGAG 3060  
10 AGACACTATA AACAAATGAC CAAATTTTTC AATTTTTTACA TATTTTTTAA TTACTTATCT 3120  
TCTATCCAAG GAGGTCTACA GAGAAATTAA AGTCTGCTT ATTTGTTACA TTTGGGTATA 3180  
ATGACACAG CCAATTATA GTGCAATAAA ATGTAATTAA TTCAAGTCTT TATTATAGAC 3240  
TATTGAAGC ACAACCTAAT GGAAAATTGT AGAGACCTTG CTTTAACATT ATCTCCAGTT 3300  
15 AATTAAGTGT TCATGTGSGT CTTGGAAACT GTTGTITTC TGAACATCTA AAGTGTGTAG 3360  
ACTGCATTCT TGCTATTATT TTATCTTGT AATGTGACCT TTTACGTGT CAAAGGAGGA 3420  
TTTCTAGCCA GGCATTGACT ATTACAATTT CATT

Seq ID NO: 416 Protein sequence  
Protein Accession #: NP\_077740.1

20 1 11 21 31 41 51  
MEARPSPGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECF 60  
25 ANLIHSSDDP FOILEDGSVY TINTILLSSE KRSFTILLSN TENQKKKIF VFLEHOTKVL 120  
KRRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQVQV SDTAQNYTIY YSIRGPGVDQ 180  
EPRNLPTVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240  
PIFTEETYTF TIFENCVRGT TVGQVCATDK DEPDIMHTRL KYSIIGQVPP SPTLFSMHPT 300  
TGVITTTSSQ LDRELIDKYQ LKIKVQDMQG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360  
30 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTNQGVLCVV 420  
KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGE CNPPIQTVRM 480  
KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWTI DENTGSIKVF RSLDREAETI 540  
KNGIYNIIVL ASDQGRRTCT GTLGIIILQDV NDNSPFIKK TVIICKPTMS SAEIVAVDPD 600  
EPIHGPPDF SLESSTSEVO RMWRKKAIND TAARLSYQND PPFSGYVPEI TVRDLGMSS 660  
35 VTSLDVLTCD CITENDCTHR VDPRIQGGGV QLGKWAIIAI LLGIALLFCI LFTLVCGASG 720  
TSKQPKVIPD DLAAQNLIVS NTEAPGDDKV YSANGPTTQT VGASAGQVCG TVGSGIKNGG 780  
QETIEMVKGQ HQTSESCRGA GHHTILDSCR GHTEVDNCR YTYSEHNSPT QPRLGEKVYL 840  
CNQDENHKA QDVLTLYNYE GRGSVAGSVG CCSERQBEDG LEFLDNLEPK FRTLAECMK 900  
R

40 Seq ID NO: 417 DNA sequence  
Nucleic Acid Accession #: NM\_004949.1  
Coding sequence: 202..2745

45 1 11 21 31 41 51  
CGCCAAAGGA AAAGCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60  
CTCTCGCGCG GCCCCACCTC CTCGCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120  
GCTCGCGCGG CGGCCCTCGG CCGCGCGGAGC CCTCCTACCC CGGCCCGAGC CTCGCGCGCG 180  
50 GACCTGCCCG GAGCCCTCTC CATGGAGGCA GCGCCGCCCT CCGGCTCCTG GAACGGAGCC 240  
CTCTCGCGCG TGCTCCTGCT GACCCCTCGG ATCTTAATAT TTGCCAGTGA TGCCCTGCAA 300  
AATGTGACAT TACATGTTC CTCCAAACTA GATGCGGAGA AACTTGTTGG TAGAGTTAAC 360  
CTGAAAGAGT GCTTTACAGC TGCAAACTCA ATTCATTCAA GTGATCTCGA CTTCCAAATT 420  
TTGGAGGATG GTTCACTCTA TACAACAAAT ACTATTCTAT TGCTCTCGGA GAAGAGAAGT 480  
55 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540  
GAGCATCAA CAAAGGTCTT AAAGAAAAGA CATACIAAAG AAAAAGTTCT AAGGCGCGCC 600  
AAGAGAAGAT GGGCTCCAAT TCCTTGTTGG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660  
CTTTCTCCTT AACAGGTTC ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720  
AGAGGTCTTG GAGTTGACCA AGAACCTCGG AATTTAATTT ATGTGGAGAG AGACACTGGA 780  
60 AACTTGTAAT GTACTCGTCC TGTAGATGTT GAGCAGTATG AATCTTTTGA GATAATTGCC 840  
TTTGCAACAA CTCCAGATGG GTATACTCCA GAACITCCAC TGCCCTAAT AATCAAAATA 900  
GAGGATGAAA ATGATAACTA CCCAATTTT ACAGAAGAAA CTTATACTTT TACAATTTT 960  
GAAATATGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020  
GACACGATCG ACACACGCTT GAAGTACTCC ATCATTTGGC AGGTGCCACC ATCACCCACC 1080  
65 CTATTTTCTA TGATCCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140  
GAGTTAATTG ACAAGTACCA GTTGAAAATA AAGTACAAAG ACATGGATGG TCAGTATTTT 1200  
GGTCTACAGA CAACCTCAAC TTGTATCATT AACATTGATG ATGTAATGA CCACTTGCCA 1260  
ACATTACTC GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATTC 1320  
TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAAGTGGAG AGCTAATTAT 1380  
70 ACCATTTTAA AGGGCAATGA AATGGCAAT TTTAAATTTG TAACAGATGC CAAAACCAAT 1440  
GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500  
CAAAATTGTTG TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560  
AGCAGACGAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCTT 1620  
CCAATACGTA CTGTTGCGAT GAAAGAAAAT GCAGAGTGG GAACAACAAG CAATGGATAT 1680  
75 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAACGTAT 1740  
CCAACAGGGT GGTCCACCAT TGATGAAAAT ACAGGATCAA TCAAGTTTT CAGAAGCCTG 1800  
GATAGAGAGG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCTT TGCATCAGAC 1860  
CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGAGCT GAATGATAAC 1920  
AGCCCATTTA TCTTAAAAA GACAGTGATC ATCTGCAAA CCAACATGTC ATCTGCGGAG 1980  
80 ATTGTTGCGG TTGATCTCTA TGAGCCTATC CATGGCCAC CTTTGACTT TAGTCTGGAG 2040  
AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100  
GCTCTTCTCT ATCAGAAATGA TCCTCCATT GGCATCATAT TAGTACCTAT AACAGTGAGA 2160  
GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220  
GAAATGACTG GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGG 2280  
AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCAATGC TCTTTTGCAT CTTGTTTACG 2340

5  
10  
15  
20

```
CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC 2400
CAGCAGAACCC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460
AATGGCTTCA CAACCCAAAC TGTGGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520
TCAGGAATCA AAAACGGAGG TCAGSAGACC ATCGAAATGG TGAAAGGAGG ACACCAGACC 2580
TCGGAATCCT GCGGGGGGGG TGGCCACCAT CACACCTGG ACTCCTGCAG GGGAGGACAC 2640
ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCCGT 2700
CTTGGTGAAG AATCCATTAG AGGACACACT CTGATTAATA ATTAACAAT GAAAGAAAGT 2760
GTATCTGTGT AATCAAGATG AAAATCACAA GCATGCCCAA GACTATGTCC TGACATATAA 2820
CTATGAAGGA AGAGGATCGG TGGCTGGGTC TGTAGTTGT TGCAGTGAAC GACAAGAAGA 2880
AGATGGGCTT GAATTTTGTG ATAATTGGA GCCCAATTT AGGACACTAG CAGAAGCATG 2940
CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000
AAAAAATTAC AAACCAAGAA TTTTAAAG CAGAAGATGC TATTGTGGG GGTTTTCTC 3060
TCATTATTG GATGGAATCT CTTTGGTCAA ATGCACATT ACAGAGAGAC ACTATAAACA 3120
AGTACACAAA TTTTCAATT TTTACATATT TTTAAATTAC TTATCTTCTA TCCAAGGAGG 3180
TCTACAGAAA AATTAAAGTC TGCCTTATT GTTACATTG GGTATAATGA CAACAGCCAA 3240
TTTATAGTGC AATAAATCT AATTAAATCA AGTCCTTATT ATAGACTATT TGAAGCACAA 3300
CCTAATGAAA AATTGTAGAG ACCITGCTTT AACATTATCT CCAGTTAATT AAGTGTTCAT 3360
GTGGTGTCTG GAAACTGTTG TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
ATTATTTTAT TCTGTAATG TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480
TTGACTATTA CAATTCATT
```

Seq ID NO: 418 Protein sequence  
Protein Accession #: NP\_004940.1

25  
30  
35  
40

```
1 11 21 31 41 51
MEARPSGSW NGALCRLLLL TLAILFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFDA 60
ANLIHSSDPD FQILEDGQSVY TTNILLSE KRSFTILLSN TENQEKKIF VFLEHQTKVL 120
KIKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQVQV SDTAQNYTII YSIRGPGVDQ 180
EPRNLFFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240
PIFTEETTF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIQVPP SPTLFSMHFT 300
TGVIIITSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
VTSVEENTVD VEILRVTVDE KDLVNTANWR ANYTILKNE NGNFKIVTDA KINEGVLCVV 420
KPLNYEEKQQ MILQGVVNE APFSREASPR SAMSTATVIV NVEDQDEGPE CNPPIQTVRM 480
KENAEVGTTS NGKAYDPET RSSSGIRYK LIDPTGWVTI DENTGSIKVF RSLDREAETI 540
KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIKK TVIICKPTMS SAEIVAVDPD 600
EPIHGPFFDF SLESSTSEVQ RMWRLLKAIND TAARLSYQND PPFSGYVVP I TVRDLRGMSS 660
VTSLDVTLCD CITENDCTHR VDRIGGGGV QLKGWAILAI LLGIALLFPI LFTLVCGASG 720
TSKQPKVIED DLAQQLNLVS NTEAPGDDKV YSANGPTTQT VGASAQVCG TVSGGIKNGS 780
QETIEMVKGK HQTSESCRA GHHTLDSR GGHTEVDNCR YTYSEWHSFT QPRIGGESIR 840
GHTLIKN
```

Seq ID NO: 419 DNA sequence  
Nucleic Acid Accession #: NM\_002722.1  
Coding sequence: 14..301

45  
50  
55

```
1 11 21 31 41 51
ACTCTGGACT CGGATGGCT GCGGCAGGCC TCTGCCTCTC CTTGCTGCTC CTGTCCACCT 60
GCGTGGCTCT GTTACTACAG CCAGTGTCTG GTGCCAGGG AGCCCCACTG GAGCCAGTGT 120
ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCAGTA TGCAGCTGAT CTCCTAGAT 180
ACATCAACAT GCTGACCAGG CTTAGGTATG GGAAGAAGCA CAAAGAGGAC ACGCTGGCCT 240
TCTCGSAGTG GGGTCCCGG CATGCTGCTG TCCCAGGGA GCTCAGCCCG CTGGACTTAT 300
AATGCCACCT TCTGTCTCT ACGACTCCAT GAGCAGCGCC AGCCAGCTC TCCCCTCTGC 360
ACCCCTGGCT CTGGCCAAAG CTGTCTCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420
AAGCC
```

Seq ID NO: 420 Protein sequence  
Protein Accession #: NP\_002713.1

60  
65

```
1 11 21 31 41 51
MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPQMAQYA ADLRRYINML 60
TRPRYGRKHK EDTLAFSEWG SPHAAVPREL SPLDL
```

Seq ID NO: 421 DNA sequence  
Nucleic Acid Accession #: NM\_032545.1  
Coding sequence: 46..718

70  
75  
80

```
1 11 21 31 41 51
AAACTGATCT TCAATGCATC AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA 60
CCATGTCAGG CTCTCTGTTA CGGTCACTTT GGCATTACAG ATCATCAATT TGGGAAACAG 120
CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTG CCACTCAGAA 180
GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240
CGAGGGCTGG GGGCGGAGG AGCGCTCCC CTACTCCCGG GCTTCGAG AGGGTGCCTC 300
CGGCGGCGG CTCTGTGCA GGAACGGCGG TACCTGCTG CTGGGACGCT TCTGCTGTG 360
CCCGGCCAC TTAACGGGCC GCTACTGCGA GCATGACCA AGGCGCAGTG AATGCGGCGC 420
CCTGGAGCAC GGAGCCTGGA CCTCCGCGC CTGCCACCTC TGCAAGTGA TCTTCGGGGC 480
CCTGCATGCT CTCCCCCTCC AGAGCGCTGA CCGCTGTGAC CCGAAGACT TCTGGGCTC 540
CCAGCTCAC GGGCGAGCG CGGGGGCGC GCCAGCTG CTACTCTGCG TGCCCTGCGC 600
ACTCCTCAC GGCCTCTGCG GCCCGATGC GCCCGCGAC CCTCGGTCCT TGGTCCCTTC 660
CGTCTCGAG GGGAGCGGC GCCCTGCGG AAGGCCGGGA CTGGGCATC GCCTTTAATT 720
TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780
```

TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840  
AAAAAA

Seq ID NO: 422 Protein sequence  
Protein Accession #: NP\_115934.1

1 11 21 31 41 51  
MTWRHHVRL L FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSHFGE 60  
VTGSAEGWGP EEPLPYSRAP GEGASARPRC CRNGGTCVLG SFCVCPAHTF GRYCEHDQRR 120  
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTFDRCDPK DFLASHANGP SAGGAPSLLL 180  
LLPCALLHRL LRPDAPAPHR SLVPSVLQRE RRPCGRFGLG HRL

Seq ID NO: 423 DNA sequence  
Nucleic Acid Accession #: NM\_006533.1  
Coding sequence: 72..467

1 11 21 31 41 51  
AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60  
CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120  
TCTCCGAGAC TGGTGTGTCG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180  
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGCGTGTGGC CCTTCAGGAC TACATGGCCC 240  
CCGACTGCCG ATTCTGACCC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300  
AGGCGCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360  
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG 420  
GCAAGTCTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480  
CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAAAATC AATCAGCCCA GTGCAAAAC

Seq ID NO: 424 Protein sequence  
Protein Accession #: NP\_006524.1

1 11 21 31 41 51  
MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LDYMAPDCR 60  
FLTIIHQGVV YVFSKLKGRG RLFWGGSVQG DRYGDLAARL GYFPSSIVRE DQTLKPGKVD 120  
VKTDKWFYFC Q

Seq ID NO: 425 DNA sequence  
Nucleic Acid Accession #: NM\_080870.1  
Coding sequence: 3..710

1 11 21 31 41 51  
AGATGACACA AGTCACAGAA AAGTCCACAG AACACCCAGA AAAGACCAGG TCAACCCACG 60  
AGAAACACAC AAGAACCCTA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCACCA 120  
AAGGGAAAAA CACACCACTC CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCCACTCTA 180  
CCACTGAGAC CATAAAGCC CCACTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240  
TCACAAAGAC TATAAACCCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300  
CTTCTCATCT AAATAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCACCTCTC 360  
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAAGC CACAGGAAAC GAGAGCCATC 420  
CATACCTCAA TAAAGATGCG TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAAATG 480  
ATTCAATCCC TGCAATGGCC ATAGTTATTG TGGTCTCTGT GGCTGTGATT CTCCTCTCTG 540  
TGTTCCTTGG CCTGATCTTC TTGGTCTCTC ATATGATGCG GACACGCCGC ACCTAACCAC 600  
AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAACTCTCTC CCGGTCTACT 660  
TGATGAGACA CAGGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGAGTA 720  
GGCGCCACGC CCTGGCTCTT CCATGCTCTG CCCCTTCTCT GGATGAGGAA CCGGACTCAC 780  
AATTTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAAAC 840  
CTTCATCTGT TCTTGAAACT GGTGGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT 900  
AGGGGACAAA GAAGGAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGTT 960  
CTGAGATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020  
TGAGTCTCAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080  
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140  
TTATTTCAT TCACATTATC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTTCTC 1200  
AGGACCCCTG CCCCCACCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AAACGGATCC 1260  
AAGAAGAAAA GAGAATTAT TCCCTTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320  
CCAGAAGAAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTTCTC CCCAAATCCC 1380  
TTAGTTTTCC TAAATGTCTA CAGTGGACGC CCTGTTGGTT TGGCTTGCTG GGTGTGGGTT 1440  
GGACACGCAA GGAGGGGATT TTTATTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500  
GACCTTCCCT GATTGGTCTC TCAGCATTTA TTTTCTGTCT TCTTCCACCA AAAGCCAGCT 1560  
GTAGCTTTAT CTCGTAAGAG TTACCATCT TCTCTACTGT CCCCATTCTC TCTCTCCCA 1620  
CCTTCAACCC AGATCAAGT TTTCTCTCT GTAGGCATT CATCTGTGTG TGTTTTCTGG 1680  
ATTTTCTCTC TCTCTCTCTA TGGCCATTTC ACCTTATTAC TGATTGGGTA GAGGGGGAAA 1740  
AGGAGAATGA TGATGATAGT TTCCTTCTGT CTATTGACCT TTTTATAAT AAGTATAAC 1800  
ATGTT

Seq ID NO: 426 Protein sequence  
Protein Accession #: NP\_543146.1

1 11 21 31 41 51  
MTQVTEKSTE HPEKTTSTTE KTTTPEKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60  
TETIKAPVKS TENPEKTAIV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSFTLI 120  
TSRTKLSSIT SEATGNESHPI YLNKDGSSQKG IHAGQMGEND SPPAWAIVIV VLVAVILLLV 180

FLGLIFLVSY MMRTTRTLTQ NTQYNDAEDE GGPNSYPVYL MEQNLGMGQ IPSPR

Seq ID NO: 427 DNA sequence

Nucleic Acid Accession #: XM\_069480.1

Coding sequence: 1..4383

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51

ATGGACACTG TGCTGGTGCT GTCCTGGGGC CTGCAGGCCCT TGGCCGGACC CAGTCCGAAG 60  
 CCCAGAAAGG ACTCTGTCTC AGACTGGGGC ATTGTGTTGA TCACTCTCAC TTTGGTGGCA 120  
 GCAATTGTCA GCCTAATGTA CGGTATCAAG AAGGCCTGCC AGTTCGGAG GGAGATGAGT 180  
 CTGGGGTGTG GCTGTGGCTC TGTGACCCCT TACAGCAGCC ACCATGAGGG GGAGGCTGCC 240  
 AGCCAGCGCT ACTCTGTGCA AATGAAAGCT TCTTGGGGGG CAGGTGCTAC TACATTCCAA 300  
 GAAATATCAGA AAATCGGGGA ACTCTCAACA TCCGATCACA TATTTCCCT CACTCCAGGC 360  
 CTTGTTTATA GTATCCCTTT TGATCAGATT GTTCTGCATT CAGGACAAAG ACCTCCAGAG 420  
 CTCCTTAAAT CTACAGAAAT CCAATGAGCA AAAACGCCACT GCAACACCAK ACGCCATTCT 480  
 AAGCCAACTG ACAAGCCTAC AGGCACTCC AAAACTATAG ACCACAAAG CTCTACAGAT 540  
 AATCATGAGG CTCTCCAC TTCTGAAGAA AACTCCAGCA ACCAAGGAA AGACCCAATG 600  
 ATCCGGAAC AGCGCTCTGT TGATCCTGCT GACTCCACTA CCACACATAA AGAATCCGCT 660  
 GGAAAAAAG ATATAAGCC AGCACCAGAG AGCAAAATAA ACTGTCTGTA GTCCACRACA 720  
 GGCAATACAA CGTAAACAG AAAATCAGAT AAACTGGAA GACCTTTGGA AAAGTCCATG 780  
 AGTACTTTGG ATAAGACAAG TACCAGCTCA CATAAGACTA CACTTCTT CCACAACTCA 840  
 GGCAATTCAC AGACAGAGCA AAAAAGCACA TCTTTTCCAG AAAAATCAC AGCAGCCTCA 900  
 AAAACAACAT ACAAGACCA AGGAACCCCA GAAGAGTCAG AAAAACTGA AGATTCCAGA 960  
 ACAACAGTTG CCTCAGACAA GCTCCTGACA AAAACTACAA AAAACATACA AGAGACCATA 1020  
 TCAGCCAAATG AGCTCACACA ATCTCTAGCA GAGCCTACAG AACTGGAGG AAGGACAGCC 1080  
 AATGAGAACA ACACACCATC CCCAGCAGAG CCTACAGAAA ATAGAGAAAG GACGCCAAT 1140  
 GAGAACACCA CACTATCCCC AGCAGAGCCT ACAGAAAATA GAGAAAGGAC AGCCATGAG 1200  
 AACACCGCAC CATTCCAGC AGGGCCTACA GAAATAGAG AAATGACAGC CAATGAGAAT 1260  
 ACCACACTAT TCCCAGCAGA GCCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAACACC 1320  
 ACACCATCCC CAGCAGAGCC TACAGAACAT GGAGAAAGGA CAGCCAATGA GAACACTACA 1380  
 CCATCCCCAG CAGAGCCTAC AGAACATGGA GAAAGGACCC CATTGCCAA TGACAAAACC 1440  
 ACATCATCCT CAGCAGAGTC TACAGAACAT GGAGAAAGGA CCCACTGGC CAACGAGAAC 1500  
 ACCACACCAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA GGACAGCCAA TGAGAACACC 1560  
 ACACACTCCC CAGCAGGCCC TACAGAAAC AGAGAAACGA CAGCCAAAGA GAAGACCACA 1620  
 CTATCCCCAG TAGAGCCTAC AGAAATAGA GAAACAACAG CCAATGAGAA GACCAACCA 1680  
 TCCCCAGCAG AGCCTACAGA AAATGGACAA AGGACCCCAT TTGCCAATGA GAAACCCACA 1740  
 TCATCCTCAG CAGAGCCTAC AGAACACGA GAAAGGACCC CACTGGCCAA TGAGAACACC 1800  
 ACACCATCCC CAGCAGAGCC TACAGAAAT AGAGAAAGGA CAGCCAATGA GAAGACCACA 1860  
 CCATCCCCAG CAGAGCCTAC AGAAATGGA GACAGGACTC CTTGGCCAA TGAGAGAGCC 1920  
 AGCCATCTC TAGCAGAGCC TACAGAAAT GGACAAAGGA CCCCATTGCG CAATGAGAAG 1980  
 ACCACATCAT CCTCAGCAGA GCCTACAGAA CACGAAGAAA GGACTCCACT GGCCAATGAG 2040  
 AACACCACAT CATCCCCAGC AGAGCCTACA GAAATAGAG AAAGGACAGC CAATGAGAAG 2100  
 ACCACACCAT CCCCAGCAGG GCCTACAGAA AATAGAGAAA TGACAGCCAA CGAGAAGACC 2160  
 ACATATTTCC CAGCAGAGCC TACAGAAAT AGAGAAAGGA CAGCCAATGA GAAGACCACA 2220  
 TCATCCCCAG CAGAGCCTAC AGAAATGGA CAAGGACCC CATTGGCCAA TGAGAAACC 2280  
 ACATCATCCC CAGCAGAGCC TACAGAACAC GGAGAAAGGA CCCACTGGC CAATGAGAAG 2340  
 ACCACATAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA GGACAGCCAA TGAGAAGACC 2400  
 ACACCATTCC CAGCAGAGCC TACAGAAAT AGAGAAAGGA CAGCCAATGA GAACACCACA 2460  
 CCATCCCCAG CAGAGCCTAC AGAAATGGA GACAGGACTC CATTGGCCAA TGAGAAGACC 2520  
 ACACCATCTC TAGCAGAGCC TACAGAAAT GGAAAGGGA CCCCATTGCG CAATGAGAAG 2580  
 ACCACATCAT CCTCAGCAGA GCCTACAGAA CACGAGAAA GGACTCCACT GGCCAATGAG 2640  
 AACACCACAT CATCCCCAGC AGAGCCTACA GAAATAGAG AAAGGACAGC CAATGAGAAG 2700  
 ACCACACAT TCCCAGCAGA GCCTACAGAA AATAGAGAAA GCACAGCCAA TGAGAAGACC 2760  
 ACACCATTCC CAGCAGAGCC TACAGAAAT AGAGAAATGGA CAGCCAATGA GAACACCACA 2820  
 CTATCCCCAG CAGAGCCTAC AGAACATGAA GAAATGACCC CATTGGCCAA TGAGAAGACC 2880  
 ACATATTTCC CAGCAGAGCC TACAGAAAT GGAGAAAGGA CCCCATTGCG CAATGAGAAG 2940  
 ACCACACCAT CCTCAGCAGA GCCTACAGAA CATGGAGAAA GGACCCCACT GGCCAATGAG 3000  
 ATCACCACAT CATCCCCAGC AGAGCCTACA GAACATGGAG AAAGGATAGC CAATGAGAAG 3060  
 GCCACACCAT CCCCAGCAA GCCTACAGAA CATGGAGAAA CGACAGTCAA TGAGGACACC 3120  
 ACACCATCTC CAGCAGAGCC TACAGAAAT GGAGAAAGGA CCCCATTGCG CAATGAGAAG 3180  
 ACCACACAT CCCCAGCAGA GTCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAAGACC 3240  
 ACACCATCCC CAGCAGAGCC TACAGAACAT GGAGAAAGGA CACCATCAGC CAATGAGAAG 3300  
 ACCATACCAT CTCCAGCAA GCCTACAGAA CACGAAGAAA TGACCCCATC GGCCAATGAG 3360  
 AACACCACAT CATCCCCAGT AAAGCCTACA GAACATGGAG AAAGACTAC ATTGGCCAA 3420  
 GAGAGATCA CACTATCCCC AGAAGGGCCT ACAGAACATG GAGCAAAAAC TAGTCCGCC 3480  
 AATGAGAAGA TCACACCATC CTTAGCAAAG CCTACAGAAC ATGGAGAAAG GACCATCA 3540  
 CCCAATGACA AGATCACTC ATCTGCAGCA GAGTCTACAG AACATAGAGA TAGGGCTACA 3600  
 TCAGCCAATG TGATCACACC AGCCCCAGCA GAGCCTATAA AACATGCAA AAGGACCACA 3660  
 TTGGCCCATG AGAAGATGAC ACAAGTACA GAAAGTCCA CAGAACACCC AGAAAGACC 3720  
 AGCTCAACCA CAGAGAAAC CACAGAAACC CAGAGAAAGC CTACGTATA CTGAGAGAG 3780  
 ACCATATGCA CCAAGGGGAA AACACACCA GTCCAGAAA AGCCTACAGA AAACCTGGGG 3840  
 AACACCACAT TGACCACTGA GACCATAAAA GCCCAGTAA AGTCCACAGA AAACCCAGAA 3900  
 AAAACAGCAG CAGTCACAAA GACTATAAAA CCTTCAGTCA AGGTACAGG AGACAAATCT 3960  
 CTCACATCA CTTCTTCTCA TCTAATAAAA ACTGAAGTTA CTCATCAGT GCCACTGGT 4020  
 TCTTCAACC TCAATACATC TAGAACGAAG CTGAGTTCTA TCACATCAGA AGCCACAGGA 4080  
 AACGAGAGCC ATCCATACCT CAATAAGAT GGCTACAGA AAGGTATCCA CGCTGGACAG 4140  
 ATGGGAGAGA ATGATTCATT CCTTGCATG GCCATAGTTA TTGTGCTCT GGTGGCTGTG 4200  
 ATTCTCTCC TGTGTCTCT TGGCCTGATC TTCTTGGTCT CCTATATGAT GGGGACAGC 4260  
 CGCACACTAA CCCAGAACAC CAGTACAAAT GATGCAGAGG ATGAGGGTGG CCCCATTTC 4320  
 TACCGGTCT ACCTGATGGA GCAGCAGAA CTGGGATGAG GCCAGATCCC TTCCCAACGG 4380  
 TGA

Seq ID NO: 428 Protein sequence  
Protein Accession #: XP\_069480.1

```

5      1      11      21      31      41      51
MDTVLVLLLG LQALAGPSPK PQKDSVSDWA IVLITLTLVA AIVSLMYGIK KACQFRREMS 60
LGCGGGSVTP YSSHHEGEAA SQRYSCQKKA SWGAGATTFO EYQKTGELST SDHIFPLTPG 120
LVYSIPFDHI VLHSGQRPEE LPKSTIEHEQ KRHCNTRHS KPTDKPTGNS KTIDHKSSTD 180
NHEAPPTSEE NSSNQKDFM IRNQRSVDPD DSTTTHKESA GKXKITPAPK SKINCRKST 240
10    GKSTVTRKSD KTRPLEKSM STLDKTSSTSS HKTTTSFPHNS GNSQTKQKST SFPEKITAAS 300
KITTKITGTP EESEKTEDSR TTVASDKLLT KTKNIQETI SANELTQSLA EPTHEGGRTA 360
NEMNTPSPAE PTENRERTAN ENTTLSPAEP TENRERTANE NTAPFPAGPT ENREMTANEN 420
TTLFPAEPTE HGERTANENT TPSPAEPTEH GERTANENT TPSPAEPTEH ERTPFANDKT 480
TSSSAESTER GERTPLANEN TPSPAEPTE NRERTANENT TPSPAGPTEN RETTANENKT 540
15    LSPVEPTENR ETTANENKTP SPAEPTENGQ RTPFANEKTT SSSAEPTEHG ERTPLANEN 600
TPSPAEPTEH NREKTANEKT TPSPAEPTEH DRTPLANEKT TPSPAEPTEH GQRTPFANEK 660
TTSSSAEPTE HEERTPLANE NTTPSPAEPTE ENRERTANEN TPSPAEPTEH NREMTANEKT 720
TLFPAEPTEH RERTANEKTT SSPAEPTEH QRTPFANEKT TPSPAEPTEH GERTPLANEN 780
20    TTLSPAEPTE NRERTANEKT TPSPAEPTEH RERTANENT TPSPAEPTEH DRTPLANEKT 840
TPSLAEPTEH GKRTPFANEK TTSSSAEPTE HAERTPLANE NTTPSPAEPTE ENRERTANEK 900
TTQFPAEPTE NREKTANEKT TPSPAEPTEH RERTANENT TPSPAEPTEH EMTPLANENKT 960
TLSPAEPTEH GERTPFINEK TPSPAEPTEH HGERTPLANE ITTPSPAEPTE EHGERIANEK 1020
ATPSPAEPTE HGETTVNEDT TPSPAEPTEH GERTPLANEN TTPSPAEPTEH HGERTANEKT 1080
25    TPSPAEPTEH GERTPSANEK TPSPAEPTEH HEEMTPSANE NTTPSPVKPT EHGEKTTLAN 1140
EKITLSPPEP TEHGAKTISA NEKITPSLAK PTEHGERTTS PNDKITSSAA ESTEHRDRAT 1200
SANVITPAPA EPIKHAIRTT LAHEKMTQVT EKSTHEPEKT TSTTEKTRT PEKPTLYSEK 1260
TICTKGNTPT VPEKPTENLG NTTLITETIK APVKSTENPE KTAAVTKTIK PSVKVTGDKS 1320
LTTTSSHLNK TEVTHQVFTG SFTLITSRTK LSSITSEATG NESHPLYLND GSQKGIHAGQ 1380
30    MGENDSPFAW AIVIVLVAV ILLVLVGLI FLVSYMMRTR RLTQNTQYN DADEEGGPN 1440
YFVYLMEQQN LGMGQIPSPR

```

Seq ID NO: 429 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..10674

```

35      1      11      21      31      41      51
ATGTGGCCTC GCCTGGCCTT TTGTTGCTGG GGTCTGGCGC TCGTTTCGGG CTGGGCGACC 60
TTTCAGCAGA TGTCCCGGTC GCGCAATTC AGCTTCCGCC TCCTCCCGGA GACCGCGCCC 120
40    GGGGCCCCCG GGAGTATCCC CGCGCCGCC GCTCCTGGCG ACGAAGCGGC GGGGAGCAGA 180
GTGGAGCGGC TGGGCCAGCG GTTCCGCGCA CGCGTGCAGC TGCTGCGGGA GCTCAGCGAG 240
CGCCTGGASC TTGTCCTCCT GGTGGATGAT TCGTCCAGCG TGGGCGAAGT CAACTTCCGC 300
AGCGAGCTCA TGTTCGTCGG CAAGCTGCTG TCCGACTTCC CCGTGGTGCC CACGGCCAGC 360
45    CGCGTGGCCA TCGTGACCTT CTGTTCCAAG AACTAGTGG TGCCGCGCCT CGATTACATC 420
TCCACCCGCC GCGCGCGCCA GCACAAGTGC GCGCTGCTCC TCCAAGAGAT CCCTGCCATC 480
TCCTACCGAG GTGGCGGCAC CTACACCAAG GCGCCCTTCC AGCAAGCCGC GCAAAATCTT 540
CTTCATGCTA GAGAAAATCT AACAAAAGT GTATTCTCA TCACTGATGG ATATTCCAAT 600
GGGGGAGACC CTAGACCAAT TGCAGCGTCA CTGCGAGATT CAGGAGTGA GATCTTCACT 660
50    TTTGGCATAT GGCAGGGGAA CATTGAGAG CTGAATGACA TGGCTTCCAC CCCAAGGAG 720
GAGCACTGTT ACCTGCTACA CAGTTTGAAG GAATTTGAGG CTTTAGCTCG CCGGGCATTG 780
CATGAAGATG TACCTTCTGG GAGTTTATT CAAGATGATA TGGTCCAAGT CTCATATCTT 840
TGTGATGAAG GCAAGGACTG CTGTGACCGA ATGGGAAGCT GCAAAATGAG GACACACACA 900
GGCCATTTTG AGTGATCTGT TGAAGAGGGG TATTACGGGA AAGGTCTGCA GTATGAATGC 960
55    ACAGCTTGCC CATCGGGGAC ATACAAACCT GAAGGCTCAC CAGGAGGAAT CAGCAGTTGC 1020
ATTCCATGTC CTGATGAAAA TCACACCTCT CCACCTGGAA GCACATCCCC TGAAGACTGT 1080
GTCTGCGAG AGGTACATGC GGCATCTGGC CAGACCTGTG AACTTGTCCA CTGCCCTGCT 1140
CTGAAGCCTC CCGAAAATGG TTACTTTATC CAAACACTT GCAACAACCA CTTCATGCA 1200
GCCTGTGGGG TCCGATGTCA CCTGGAATT GATCTTGTGG GAAGCAGCAT CATCTTATGT 1260
60    CTACCCCAAT GTTTGTGGTC CGTTTCAGAG AGCTACTGCA GAGTAAGAAC ATGTCTCAT 1320
CTCGCCAGC CGAAACATGG CCACATCAGC TGTCTACAA GGGAAATGTT ATATAAGACA 1380
ACATGTTTGG TGCCCTGTGA TGAAGGGTAC AGACTAGAAG GCAGTGATA GCTTACTTGT 1440
CAAGGAAACA GCCAGTGGGA TGGGCCAGAA CCGCGGTGTG TGGAGCGCCA CTGTTCCACC 1500
TTTCAGATGC CCAAGATGT CATCATATCC CCCCACACT GTGGCAAGCA GCCAGCCAAA 1560
65    TTTGGGACGA TCTGCTATGT AAGTTGCGCG CAAGGGTTCA TTTTATCTGG AGTCAAAGAA 1620
ATGCTGAGAT GTACCACTTC TGGAAAATGG AATGTCGGAG TTCAGGCAGC TGTGTGTAAA 1680
GACGTGGAGG CTCCTCAAAT CAACTGTCT AAGGACATAG AGCTAAGAC TCTGGAACAG 1740
CAAGATCTCG CCAATGTTAC CTGCGAGATT CCAACAGCTA AAGACAACCT TGGTGAAGAG 1800
GTGTGAGTCC AGCTTTCACC CCACCTTACC TTTTCCCAAT TGGAGATGTT 1860
GCTATGCTAT ACACGGCAAC TGACCTATCC GGCACCCAGG CCAGCTGCAT TTTCCATATC 1920
70    AAGGTTATTT ATGCGAAGCC ACCTGTCTAT GACTGTGTGA GATCTCCACC TCCCGTCCAG 1980
GTCTCGGAGA AGGTACATGC CGCAAGCTGG GATGAGCCTC AGTTCTGAGA CAACTCAGGG 2040
GCTGAATTTG TCATTACAGC AAGTCATACA CAAGGAGACC TTTTCCCTCA AGGGGAGACT 2100
ATAGTACAGT ATACAGCCAC TGACCCCTCA GGCATAAACA GGACATGTA TATCCATATT 2160
GTCATAAAG GTTCTCCCTG TGAATTTCCA TTCACACCTG TAAATGGGGA TTTTATATGC 2220
75    ACTCCAGATA ATACTGGAGT CAACTGTACA TTAAGTTGCT TGGAGGGCTA TGATTTCACA 2280
GAAGGGTCTA GGCACAAGTA TTATTGTGCT TATGAAGATG GCGTCTGGAA ACCAATATAT 2340
ACCACTGAAT GGCCAGACTG TGCCAAAAAA CGTTTGTCAA ACCACGGGTT CAACTCCCTT 2400
GAGATGTTCT ACAAGCAGC TGTGTTGTAT GACACAGATC TGATGAAGAA GTTTTCTGAA 2460
80    GCATTTGAGA CGACCTGGG AAAAAATGGT CCATCATTTT GTAGTGATGC AGAGGACATT 2520
GACTGCAGAC TGGAGGAGAA CCTGACCAA AAATATTGCC TAGAATATTA TTATGACTAT 2580
GAAATGGGCT TTGCAATTGG ACCAGGTGGC TGGGGTGCAG CTAATAGGCT GATTACTCT 2640
TACGATGACT TCCTGGACAC TGTGCAAGAA ACAGCCACAA GCATCGGCAA TGCCAACTCC 2700
TCACGGATTA AAGCAAGTGC CCATTATCT GACTATAAAA TTAAGTTAAT TTTTAACATC 2760
ACAGCTAGTG TGCCATTACC CGATGAAAGA AATGATACCC TTGAATGGGA AAATCAGCAA 2820

```



	CGACTCCTTC	AGACATTGGA	AACATATCACA	AATAAACTGA	AAAGGACTCT	CAACAAAGAC	2880
	CCCATGTATT	CCTTTAGCT	TGCATCAGAA	ATACCTTAG	COGACAGCAA	TTTATTAGAA	2940
	ACAAAAAAGG	CTTCCCCCTT	CTGCAGACCA	GGCTCAGTGC	TGAGAGGGCG	TATGTGTGTC	3000
5	AATTGCCCTT	TGGGAACCTA	TTATAATCTG	GAACATTTC	CCTGTGAAAG	CTGCCGGATC	3060
	GGATCCCTATC	AAGATGAAGA	AGGGCAACTT	GAGTGCAAGC	TTTGCCCTTC	TGGGATGTAC	3120
	ACGGAATATA	TCCATTCAAG	AAACATCTCT	GATTGTAAAG	CTCAGTGTAA	ACAAGGCACC	3180
	TACTCATACA	GTGGACTTGA	GACTTGTGAA	TCGTGTCCAC	TGGGCACCTA	TCAGCCAAAA	3240
	TTTGGTTCCC	GGAGCTGCCT	CTCGTGTCCA	GAACACACT	CAACTGTGAA	AAGAGGAGCC	3300
	GTGAACATTT	CTGCATGTGG	AGTTCTTGT	CCAGAAGGAA	AATTCTCGCG	TTCTGGGTTA	3360
10	ATGCCCTGTC	ACCCATGTCC	TCGTGACTAT	TACCAACCTA	ATGCAGGGAA	GGCCTTCTGC	3420
	CTGGCCTGTC	CCTTTATGG	AACTACCCCA	TTCCGTGGTT	CCAGATCCAT	CACAGAATGT	3480
	TCAACTTCAG	TTCTGAATAT	TACTATTTC	GGTGGATTG	GGCATCTGGA	GTGTGTAAAT	3540
	TGTCCTCTG	AGGTTTCCA	TGAATGCTTC	TTTAAACCTT	GCCACAATAG	TGGAACCTGC	3600
15	CAGCAACTTG	GGCGTGGTTA	TGTTTGTCTC	TGTCCACTTG	GATATACAGG	CTTAAAGTGT	3660
	GAACACAGCA	TCGATGAGTG	CAGCCCACTG	CCTTGCTTCA	ACAATGGAGT	TTGTAAAGAC	3720
	CTAGTTGGGG	AATTCAATTG	TGAGTGCCCA	TCAGGTTTCA	CAGGTCAAGG	GTGTGAAGAA	3780
	AATATAAATG	AGTGTAGCTC	CAGTCTCTGT	TTAAATAAAG	GAATCTGTGT	TGATGTGTGT	3840
	GCTGGCTATC	GTTCGACATG	TGTGAAGGAA	TTTGTAGGCC	TGCATTGTGA	AACAGAAGTC	3900
20	AATGAATGCC	AGTCAAAACC	ATGCTTAAAT	AATGCAGTCT	GTGAAGACCA	GGTGTGGGGA	3960
	TTCTTGTGCA	AATGCCCAACC	TGGATTTTGT	GGTACCCGAT	GTGGAAGGAA	CGTCGATGAG	4020
	TGCTCTGTC	AGCCATGCAA	AAATGGAGCT	ACCTGTAAAG	ACGGTGCCAA	TAGCTTCAGA	4080
	TGCCCTGTG	CAGCTGGCTT	CACAGGATCA	CAGTGTGAAT	TGAACATCAA	TGAATGTCTG	4140
	TCTAATCCAT	GTAGAAATCA	GGCCACCTGT	GTGGATGAAT	TAAATTCATA	CAGTTGTAAA	4200
25	TGTCAGCCAG	GAATTTTCAGG	CAAAAGGTGT	GAACAGAAC	AGTCTACAGG	CTTAAACCTG	4260
	GAATTTGAAG	TTTCTGGCAT	CTATGGATAT	GTGATGCTAG	ATGGCATGCT	CCCATCTCTC	4320
	CATGCTCTAA	CCTGTACCTT	CTGGATGAAA	TCCTCTGAGC	ACATGAACCTA	TGGAACACCA	4380
	ATCTCCTATG	CAGTTGTATA	CGGCAGCGAC	AATACCTTGC	TCCTGACTGA	TTATAACCGG	4440
	TGGGTTCTTT	ATGTGAATGG	CAGGAAAGAG	ATAACAAACT	GTCCCTGGGT	GAATGATGGC	4500
30	AGATGGCATC	ATATTGCAAT	CACCTGGACA	AGTGCCAAATG	GCATCTGGAA	AGTCTATATC	4560
	GATGGGAAT	TATCTGACGG	TGGTGTCTGC	CTCTCTGTG	GTGTTGCCAT	ACCTGGTGGT	4620
	GGTGGCTTAG	TTCTGGGGCA	AGAGCAAGAC	AAAAAAGGAG	AGGGATTGAG	CCGAGCTGAG	4680
	TCCTTTGTGG	GCTCCATAAG	CCAGCTCAAC	CTCTGGGACT	ATGTCCTGTC	TCCACAGCAG	4740
	GTGAAGTCAC	TGGCTACCTC	CTGCCACAG	GAATCACTA	AAGGAAACGT	GTGATCATGG	4800
35	CCTGATTCT	TGTCAGGAAT	TGTGGGAAA	GTGAAGATCG	ATTCTAAGAG	CATATTTTGT	4860
	TCTGATTGCC	CAGCTTAGG	AGGGTCAAGT	CCTCATCTGA	GAATCTGATC	TGAAGATTTA	4920
	AAGCCAGGTT	CCAAAGTCAA	TCTGTTCTGT	GATCCAGGCT	TCCAGCTGGT	CGGGAACCTC	4980
	GTGCAGTACT	GTCTGAATCA	AGGACAGTGG	ACACAACCCAC	TTCTCTACTG	TGAACGCATT	5040
	AGCTGTGGGG	TGCCACCTCC	TTTGGAGAAT	GGCTTCCATT	CAGCCGATGA	CTTCTATGCT	5100
40	GGCAGCACAG	TAACTTACCA	GTGCAACAAT	GGCTACTATC	TATTGGGTGA	CTCAAGGATG	5160
	TTCTGTACAG	ATAATGGGAG	CTGGAACGGC	GTTCACCAT	CCTGCGCTGA	TGTCGATGAG	5220
	TGTGCAGTTG	GATCAGATTG	TAGTGAGCAT	GCTTCTTGCC	TGAACGTAGA	TGGATCTTAC	5280
	ATATGTTTAT	GTGTCACACC	GTACACAGGA	GATGGGAAAA	ACTGTGCAGA	ACCTATAAAA	5340
	TGTAAGGCTC	CAGGAATACC	GGAAATGGC	CACCTCTCAG	GTGAGATTTA	TACAGTAGGT	5400
45	GCCCGAGTCA	CATTTTCTGT	TCAGGAAGGA	TACCAGTTGA	TGGGAGTAAC	CAAAATCACA	5460
	TGTTTGGAGT	CTGGAGAATG	GAATCATCTA	ATACCATATT	GTAAAGCTGT	TTCATGTGGT	5520
	AAACCGGTTT	TCACAGAAAA	TGGTTGCATT	GAGGAGTTAG	CATTTACTTT	TGGCAGCAAA	5580
	GTGACATATA	GGTGTAAATA	AGGATATACT	CTGGCCGGTG	ATAAAGAAATC	ATCCTGTCTT	5640
	GCTAACAGTT	CTTGAGTCA	TTCCCTCTCT	GTGTGTGAAC	CAGTGAAGTG	TTCTAGTCCG	5700
50	GAATAATATA	ATAATGGAAA	ATATATTTTG	AGTGGGCTTA	CCTACCTTTC	TACTGCATCA	5760
	TATTTCATGG	ATACAGGATA	CAGCTTACAG	GGCCCTTCCA	TTATTGAATG	CAGGCTTCTT	5820
	GGCATCTGGG	GACAGCGGCC	ACCTGCCTGT	CACCTCGTCT	TCTGTGGAGA	ACCACTGGCC	5880
	ATCAAGATG	CTGTCAATTAC	GGGAATAAAC	TTCACTTTCA	GGAAACCCGT	CACCTACACT	5940
	TGCAAGAGAG	GCTATATCT	TGCTGGTCTT	GACACCAATT	AATGCCTGGC	CGACGGCAAG	6000
55	TGGAGTAGAA	GTGACCAGCA	GTGCTGGCT	GTCTCTGTG	ATGAGCCACC	CATTGTGGAC	6060
	CAGCGCTCTC	CAGAGACTGC	CCATCGGCTC	TTTGGAGACA	TTGCATTCTA	CTACTGCTCT	6120
	GATGGTTACA	GGCTAGCAGA	CAATTCCAG	CTTCTCTGCA	ATGCCAGGG	CAAGTGGGTA	6180
	CCCCAGAAAG	GTCAAGACAT	GGCCGGTGT	ATAGCTCATT	TCTGTGAAAA	ACCTCCATCG	6240
	GTTCCTATA	GCATCTTGA	ATCTGTGAGC	AAAGCAAAAT	TTGCAGCTGG	CTCAGTTGTG	6300
60	AGCTTTAAAT	GCATGGAAGG	CTTTGTACTG	AACACCTCAG	CAAGATTGTA	ATGTATGAGA	6360
	GGTGGGCACT	GGAAACCTTC	CCCCATGTCC	ATCCAGTGCA	TCCCTGTGCG	GTGTGGAGAG	6420
	CCACCAAGCA	TCATGAATGG	CTATGCAAGT	GGATCAAACT	ACAGTTTGG	AGCCATGGTG	6480
	GCTTACAGCT	GCAACAGGG	GTCTACATC	AAAGGGGAAA	AGAAGAGCAC	CTGCGAAGCC	6540
	ACAGGGCAGT	GGAGTAGTCC	TATACCGAGC	TGCCACCCGG	TATCTTGTGG	TGAACCACTT	6600
65	AAGGTTGAGA	ATGGCTTTCT	GGAGCATACA	ACTGGCAGGA	TCTTTGAGAG	TGAAGTGAGG	6660
	TATCAGTGTA	ACCCGGGCTA	TAAATCAGTC	GGAAAGTCTG	TATTTGTCTG	CCAAGCCAAAT	6720
	CGCCACTGGC	ACAGTGAATC	CCCTCTGATG	TGTGTTCTCT	TCGACTGTGG	AAAACCTCCC	6780
	CGATCCAGA	ATGCTTTCAT	GAAGAGGAAA	AACTTTGAAG	TAGGGTCCAA	GGTTTCAGTTT	6840
	TTCTGTAATG	AGGGTTATGA	GCTTGTGGT	GACAGTTCTT	GGACATGTCA	GAATCTGGC	6900
70	AAATGGAATA	AGAAGTCAAA	TCCAAAGTGC	ATGCCTGCCA	AGTGCCAGA	GCCGCCCTC	6960
	TTGGAAGAAC	AGCTAGTATT	AAAGGAGTTG	ACCACCGAGG	TAGGAGTTGT	GACATTTTCT	7020
	TGTAAGAGAG	GGCATGTCTT	GCAAGGCCCT	TCTGTCTGTA	AATGCTTGCC	ATCCAGCAAA	7080
	TGGAATGACT	CTTCCCTCTG	TTGTAAGATT	GTCTTTGTA	CCCCACCTCC	CCTAATTTCC	7140
	TTTGGTGTCC	CAATCTCTTC	TTCTGCTCTT	CATTTTGGAA	GTACTGTCAA	GTATTTCTGT	7200
75	GTAGGTGGGT	TTTCTTAAG	AGGAAATCTT	ACCACCTCTT	GCCAACTGTA	TGGCACTGG	7260
	AGCTCTCCAC	TGCCAGAAAT	TGTTCCAGTA	GAATGTCCCC	AACCTGAGGA	AATCCCCAAT	7320
	GGAAATCAAT	ATGTGCAAGG	CCTTGCCTAT	CTCAGCACAG	CTCTCTATAC	CTGCAAGCCA	7380
	GGCTTTGAAT	TGGTGGGAAA	TACTACCACC	CTTGTGGAG	AAAATGGTCA	CTGGCTTGG	7440
80	GGAAACCA	CATGTAAGC	CATTGAGTGC	CTGAACCCA	AGGAGATTTT	GAATGGCAAA	7500
	TTCTCTTACA	CGGACCTTACA	CTATGGACAG	ACCSITACCT	ACTCTTGCAA	CCGAGGCTTT	7560
	CGGCTCGAAG	GTCCAGTGC	CTTGACCTGT	TTAGAGACAG	GTGATTGGGA	TGTAGATGCC	7620
	CCATCTTGCA	ATGCCATCCA	CTGTGATTCC	CCACAACCCA	TTGAAAATGG	TTTTGTAGAA	7680
	GGTGAGATT	ACAGCTATGG	TGCCATAATC	ATCTACAGTT	GCTTCCCTGG	GTTCAGGTTG	7740
	GCTGGTCAAT	CCATGCGAGC	CTGTGAAGAG	TCAGGATGGT	CAAGTTCCAT	CCCAACATGT	7800
	ATGCCAATAG	ACTGTGGCCT	CCCTCTCTAT	ATAGATTTTG	GAGACTGTAC	TAAACTCAAA	7860

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

GATGACCAGG GATATTTTGA GCAAGAAGAC GACATGATGG AAGTTCATA TGTGACTCCT 7920  
 CACCCTCCTT ATCATTITGGG AGCAGTGGCT AAAACCTGGG AAAATACAAA GGAGTCTCCT 7980  
 GCTACACATT CATCAAACTT TCTGTATGGT ACCATGGTTT CATACACCTG TAATCCAGGA 8040  
 TATGAACCTC TGGGGAACCC TGTGCTGATC TGCCAGGAAG ATGGAACCTG GAATGGCAGT 8100  
 GCACCATCCT GCATTTCAAT TGAATGTGAC TTGCCTACTG CTCCTGAAAA TGGCTTTTGT 8160  
 CGTTTTACAG AGACTAGCAT GGGAAAGTGCT GTGCAGTATA GCTGTAAACC TGGACACATT 8220  
 CTAGCAGGCT CTGACTTAAG GCTTTGTCTA GAGAATAGAA AGTGGAGTGG TGCCTCCCCA 8280  
 OGTGTGAAG CCATTTTCATG CAAAAAGCCA AATCCAGTCA TGAATGGATC CATCAAAGGA 8340  
 AGCAACTACA CATACCTGAG CACGTTGTAC TATGAGTGTG ACCCCGGATA TGTGCTGAAT 8400  
 GGCACTGAGA GGAGAACATG CCAGGATGAC AAAAAGCTGG ATGAGGATGA GCCCATTGCG 8460  
 ATTCCGTGGG ACTGCAGTTC ACCCCAGTTC TCAGCCAAATG GCCAGGTGAG AGGAGACGAG 8520  
 TACACATTCC AAAAGAGAT TGAATACACT TGCAATGAAG GGTTCCTGCT TGAGGGAGCC 8580  
 AGGAGTCCGG TTGTCTTTCG CAATGGAAAT TGGAGTGGAG CCACTCCCGA CTGTGTGCCT 8640  
 GTCAGATGTG CCACCCCGCC ACAACTGGCC AATGGGGTGA CGGAAGGCCT GGACTATGGC 8700  
 TTCATGAAGG AAGTAACATT CCACGTGTAC GAGGGCTACA TCTTGACCGG TGCTCCAAAA 8760  
 CTACCTGTG AGTCAAGTGG CAACTGGGAT GCAGAGATTC CTCTCTGTAA ACCAGTCAAC 8820  
 TGTGGACCTC CTGAAGATCT TGCCCATGGT TTCCCTAATG GTTTTTCTCT TATTCTATGG 8880  
 GGCCATATAC AGTATCACTG CTTTCTGGT TATAAGCTCC ATGGAATTC ATCAAGAAGG 8940  
 TGCCCTCTCA ATGGCTCCTG GAGTGGCAGC TCACCTTCCT GCCTGCCTTG CAGATGTTCC 9000  
 ACACCACTAA TTGAATATGG AACTGTCAAT GGGACAGATT TTGACTGTGG AAAGGCAGCC 9060  
 CGGATTCAGT GCTTCAAGG CTTCAAGCTC CTAGGACTTT CTGAATTCAC CTGTGAAGCC 9120  
 GATGGCCAGT GGAGCTCTGG GTTCCCCAC TGTGAACACA CTCTCTGTGG TTCTCTTCCA 9180  
 ATGATACCAA AACTAGAGT CAGTGAGACC AGCTCTTGGG AGGAAAATGT GATAACTTAC 9240  
 AGCTGCAGGT CTGGATATGT CATACAAGGC AGTTGATGATC TGATTGTATC AGAGAAAGGG 9300  
 GTATGGAGCC AGCCTTATCC AGTCTGTGAG CCCTTGTCTT GTGGGTCCCC ACCGTCTGTC 9360  
 GCCAATGAGT TGGCAACTGG AGAGGCACAC ACCTATGAAA GTGAAGTGAA ACTCAGATGT 9420  
 CTGGAAGGTT ATACAGATGA TACAGATACA GATACATTCA CCTGTGAGAA AGATGGTGGC 9480  
 TGGTCCCTG AGAGAATCTC CTGCAGTCTT AAAAAATGTC CTCTCCCGGA AAACATAACA 9540  
 CATATACCTG TACATGGGGA CGATTTCAGT GTGAATAGGC AAGTTTCTGT GTCATGTGCA 9600  
 GAAGGGTATA CCTTTGAGGG AGTTAACATA TCAGTATGTC AGCTTGATGG AACCTGGGAG 9660  
 CCACCACTCT GCGATGAATC TTGCAGTCCA GTTCTTGTG GGAACCTGA AAGTCCAGAA 9720  
 CATGGATTGT TGGTTGGCAG TAAATACACC TTTGAAAGCA CAATTATTGA TCAGTGTGAG 9780  
 CTTGGCTATG AACTAGAGGG GAACAGGGAA CGTGTCTGCC AGGAGAACAG ACAGTGGAGT 9840  
 GGAGGGGTGG CAATATGCAA AGAGACCAGG TGTGAAACTC CACTTGAATT TCTCAATGGG 9900  
 AAAGCTGACA TTGAAAACAG GAGGACTGGA CCCAAGCTGG TATATTCCTG CAACAGAGGC 9960  
 TACAGTCTTG AAGGGCCATC TGAGGCACAC TGACACAGAA ATGGAACCTG GAGGCCACCA 10020  
 GTCCCTCTCT GCAAAACCAA TCCATGCCCT GTTCCCTTTG TGATTCCTGA GAATGTCTCTG 10080  
 CTGTCTGAAA AGGAGTTTGA TGTGATCAG AATGTGTCCA TCAATGTAG GGAAGGTTTT 10140  
 CTGCTGCAGG GCCACGGCAT CATTACCTGC AACCCCGACG AGAGCTGGAC ACAGACAAGC 10200  
 GCCAATGTG AAAAATCTCT ATGTGGTCCA CCAGCTCAGG TAGAAAATGC AATTGCTCGA 10260  
 GGCGTACATT ATCAATATGG AGACATGATC ACCTACTCAT GTTACAGTGG ATACATGTTG 10320  
 GAGGGTTTCC TGAGGAGTGT TTGTTTAGAA AATGGAACAT GGACATCACC TCCTATTTCG 10380  
 AGAGCTGTCT TGCATTTTCC ATGTGAGAA GGGGGCATCT GCCAACGCC AAATGCTTGT 10440  
 TCCTGTCCAG AGGGCTGGAT GGGGCGCCTC TGTGAAGAAC CAATCTGCAT TCTTCCCTGT 10500  
 CTGAACGAGG TGCCTGTGTG GGCCCTTAC CAGTGTGACT GCCCGCTTGG CTGGAAGGGG 10560  
 TCTGCTGTCT ATACAGCTGT TTGCCAGTCT CCCTGCTTAA ATGGTGGAAA ATGTGTAAGA 10620  
 CCAAACCGAT GTCACGTCTT TTCTTCTTGG ACGGGACATA ACTGTTCCAG GTAA

Seq ID NO: 430 Protein sequence  
 Protein Accession #: FGENESH predicted

55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
 MWPLAFPCW GLALVSGWAT FQOMSPSRNF SFLFEPETAP GAPGSIPAPP APGDEAAGSR 60  
 VERLGAQFRR RVRLLRELSE RLELVFLVDD SSSVGEVNF SELMFVRKLL SDFFVVPAT 120  
 RVAIVTFSK NYVVRVDYI STRRARQHKC ALLLQEIPI SYRGGGTYK GAFQQAQIL 180  
 LHARENSTK VFLITDGYN GGDPRPIAAS LRDSGVEIPT FGIWQGNIRE LNDMASTPKE 240  
 EHCYLESTF EFELARRAL HEDLPSGSFI QDDMVHCSYL CDEGDKCCDR MGSCCKGHT 300  
 GHFECICBK YYGKGLQYEC TACPSGTYPK EGSPPGISSC IPCPDENETS PPGSTSPEDC 360  
 VCREGYRASG QTCBLVCPA LKPPENGYFI QNTCRNHFNA ACGVRCHPGF DLVGSIIILC 420  
 LFNGLWSSGE SYCRVRTCPH LRQPKGHIS CSTREMLYKT TCLVACDEGY RLEGSDKLT 480  
 QGNSQWDWV PRCVERHCST FQMPKDVII PHNCGKQPAK FGTCYVSCR QGFILSGVKE 540  
 MLRCTTSGKW NVGVQAAVCK DVEAPQINCP KDIEAKTLEQ QDSANVTWQI PTKADNSGEK 600  
 VSVHVHFAFT PPYLPPIGDV AIVYTATDLS GNQASCFIHI KVDAEPPVI DWCRSPPPVQ 660  
 VSEKVAASH DEPQFSDNSG AELVITRSH QDGLFPQGET IVQYTATDPS GNNRTCDIHI 720  
 VIKGPSCEIP FTFVNGDFIC TPDNTGVNCT LTCLEGYDFT EGSTDKYYCA YEDGVWKPTY 780  
 TWEFDCAKK RFANHGPKSF EMFYKAARCD DTDLMKPFSE AFETTLGKRV PSPCSDAEDI 840  
 CDRLLENLTK KYCLEYNYDV ENGFAIGPGG WGAANRLDYS YDDFLDTVQE TATSIGNAKS 900  
 SRIKRSAPLS DYKIKLIENI TASVLPDER NDTLEWENQQ RLLQLETIT NKLEKRTLNKD 960  
 PMYSFQLASE ILIADSNLE TKKASPPCRP GSVLRGRMCV NCPLGTYYNL EHTCESCRI 1020  
 GSYQDEBGL ECKLCPSGMY TEYIHSRNI DCKAQCKQGT YSYSGLETCE SCPLGTGYQPK 1080  
 FGSRCLSCP ENTSTVKRGA VNISACGVPC PEGKPSRSLG MPCHPCPRDY YQPNAGKAPC 1140  
 LACPTFYGTP FAGSRITTEC STSVLNTIF GGFHLELLN CPSEVFHECF FNPCHNSGTC 1200  
 QQLGRGYVCL CPLGYTGLKC ETDIDECSP CLNNGVCKD LVGEFICECP SGYTGORCEE 1260  
 NINECSSSPC LNKGICVDGV AGYRCTCVKG FVGLHCETE NEQSNPCLN NAVCEDQVGG 1320  
 FLCKCPGFL GTRCGKNVDE CLSQPCNGA TCKDGANSFR CLCAAGFTGS HCELNINEQ 1380  
 SNPCRNQATC VDELNSYSCK QQPFGSGKRC ETEQSTGFNL DFEVSGIYGY VMDGLMPLSL 1440  
 HALTCTFMK SSDDMNYGTP ISYAVDNGSD NTLILLTDYNG WLYVNGREK ITNCPSVNDG 1500  
 RWEHIAITWT SANGIKWYVI DGKLSGGAG LSVGLPIPGG GALVLGQEQD KKGEGFSPA 1560  
 SFVGSISQLN LWDYVLPQK VKSLATSCPE ELKSGNVLAW FDLSGIVGK VKIDSKSIFC 1620  
 SDCPRLGGSV PHLRTASEDL KPGSKVNLFC DPGFQLVGNP VQYCLNQGW TQPLPHCERI 1680  
 SCGVPPPLEN GFHSADDPYA GSTVTVQCN GYLLGDSRM FCTDNGSWNG VSPSCLDVDE 1740  
 CAVGSDCEH ASCLNVDGSI ICSCVPPYTG DGKNCAEPIK CKAPGNFENG HSSGEITYVG 1800  
 AGVTFPSQEG YQLMGVTKIT CLESGEWNHL IPYCKAVSCG KPAIPENGCI BELAFTFGSK 1860

5 VTYRCNKGYT LAGDKESSCL ANSSWSHSP VCEPVKCSSP ENINNGKYIL SGLTYLSTAS 1920  
 YSCDTGVSILQ GPSIIETAS GIWDRAPPAC HLVPFCGEPPA IKDAVITGWN FTFRNTVTYT 1980  
 CKEGYTLAQL DTIECLADGK WSRSDQQLA VSCDEPPIVD HASPETAHRL FGDIAPFYCS 2040  
 DGYSLADNSQ LLCNAQKQWV PPEGQDMPRC IAHFCEKPPS VSYSILESVS KAKFAAGSVV 2100  
 SFKCMGFFVL NTSAKIECMR GGQWNPSPMS IQCIPVRCGE PPSIMNGYAS GSNYSFGAMV 2160  
 AYSCKGFFYI KGEKKSTCEA TGQWSSPIPT CHPVSCGEPP KVENGPLEHT TGRIFESEVR 2220  
 YQCNPGYKVS GSPVFVQAN RHWSSESPLM CVPLDCGKPP PIQNGFMKGE NFEVGSKVQP 2280  
 FCNEGVELVG DSSWTCQKSG KWNKSNPKC MPAKCEPPL LENQLVLKEL TTEVGVTTF 2340  
 10 CKEGHVLQGP SVLKCLPSQW WNDSPFVCKI VLCTPPPLIS FGVPISAL HFGSTVKYSC 2400  
 VGGFFLRGNS TTLQCPDGTW SSPLPECVPV ECPQPEEIPN GIIDVQGLAY LSTALYTKCP 2460  
 GFELVNTTT LCGENGHWLG GKPTCKAIEC LKPKIILNGK FSYTDLHYGQ TVTYSNCRGP 2520  
 RLEGPSALTC LETGDWDVDA PSCNAIHCDS PQPIENGFEV GADYSYGAI IYSCFPFGQV 2580  
 AGHAMQTCEE SGWSSSIPTC MPIDCGLPPH IDFGDCTRLK DDQGYFEQED DMMEVPYVTP 2640  
 15 HPPYHLGAVA KTWENTKESP ATHSSNPLYG TMVSYTCNPG YELIGNPVLI CQEDGTWNGS 2700  
 APSCISIECD LPTAPENGFL RFTETSMGSA VQYSCPKGHI LAGSDLRCL ENRKWSGASP 2760  
 RCEALSKFTT NPFVNGSIKG SNYTYLSTLY YEDCPGYVLN GTERRTQDD KNWDEDEPIC 2820  
 IPVDCSSPPV SANGQVRGDE YTFQKEIET CNEGFLLEGA RSRVCLANGS WSGATPDCVP 2880  
 VRCATPPQLA NGVTEGLDYC FMKEVTFHCH EGYILHGAPK LTCQSDGNWD AEIPLCKPVN 2940  
 CGPPEDLAHG FPNQFSFIHG GHIQYQCFPG YKLHGNSSRR CLSNGSWSGS SPSCLPKCRS 3000  
 20 TPVIEYGTVN GTDFDCGKAA RIQCFKGFKL LGLSEITCEA DGQWSSGFPF CEHTSCGSLP 3060  
 MIPNAFISET SSKENVITY SCRSQYVIQ SSDLICTEKV VWSQYPVCE PLSCGSPSPV 3120  
 ANAVATGEAH TYESEVKLRC LEGYTMDDT DTFTQKDGRR WFERISCSF KKCPLPENIT 3180  
 HILVHGDDFS VNRQVSVSCA EGYTFEGVNI SVQQLDGTWE PPFSDSCSP VSCGKPEPSE 3240  
 HGFVVGSKYT FESTIYQCE PGYELEGNRE RVQENRQWS GGAICKETR CETPLEFLNG 3300  
 25 KADIENTTGT PNVYSCNRG YSLEGPSEAH CTENGWNSHP VPLCKPNPCP VPVPIPENAL 3360  
 LSEKEFYVDQ NVSIKCREGF LLQGHGIITC NPDETWTQTS AKCEKISCGP PAHVENAIAR 3420  
 GVHYQYGDMI TYSYSGGYML EGFLRSVCLB NGTWTSPPIC RAVCRFPQCN GGICQRFNAC 3480  
 SCPEGWMRL CEEPICILPC LMGRCVAPY QCDPCPGWTG SRCHTAVCQS PCLNGGKCVR 3540  
 30 PNRCHLSSW TGHNCNR

Seq ID NO: 431 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..390

35 1 11 21 31 41 51  
 | | | | | |  
 ATGAGGTTCA GTGTCTCAGG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT 60  
 TATGTGTGAG TCTGTCTCCT CCTCTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA 120  
 40 GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTTGGAG 180  
 CAGTGTCTGT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCGGCAATG TGGTCCCCC 240  
 TGCACCTTCT GGCCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300  
 TTTGTGTGTA AGCTGAAGGT TCAGGGTGTG AATTCACAGT GCCACTCATC TCCCATCTCC 360  
 AGTAAATGTG AAAGAGGCCG GATATGTTAG

45 Seq ID NO: 432 Protein sequence  
 Protein Accession #: FGENESH predicted

50 1 11 21 31 41 51  
 | | | | | |  
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLC PREVIAPAGS EPWLCQAPAPR CGDKIYNPLE 60  
 QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLKVQGV NSQCHSSPIS 120  
 SKCERGRIC

55 Seq ID NO: 433 DNA sequence  
 Nucleic Acid Accession #: NM\_007231.1  
 Coding sequence: 89..2017

60 1 11 21 31 41 51  
 | | | | | |  
 TAGGAACAGG GGAGAGTGCA CCTGCTACCA GTCAAGCTCA GCCAGACTGC AAGAGGAGGC 60  
 GAGGCGGAGC CAGCCGAGGG AGTGAAACAT GGACAAGTTG AAATGCCCGA GTTCTTCAA 120  
 GTGCAGGGAG AAGGAGAAAG TGTGCGCTTC ATCAGAGAAT TTCCATGTTG GTGAAAATGA 180  
 TGAGAATCAG GACCGTGSTA ACTGGTCCAA AAAATGSGAT TATCTTCTAT CTATGATTGG 240  
 65 ATACGCAAGT GGATTAGGAA ATGTGTGGAG ATTTCATAT CTGACCTACA GCAATGGTGG 300  
 AGGCGCCTTC TTGATACCTT ATGCAATTAT GTTAGCATTG GCTGGTTTAC CTTTGTCTCT 360  
 TCTGGAGTGT TCACTGGGAC AATTGTCTAG CTAGGTCCA GTTTCAGITT GSAGGATTCT 420  
 TCCATTGTTT CAAGGTGTGG GAATTACAAT GGTCTGTATC TCCATTTTGT TGACAATCTA 480  
 TTACAATGTC ATAATTGCCT ATAGTCTTTA CTACATGTTT GCTTCTTTTC AAAGTGAAC 540  
 70 ACCATGGAAA AATTGTTCTT CGTGGTCAGA TAAAACTGT AGCAGATCAC CAATAGTAAC 600  
 TCACTGTAAT GTGAGTACAG TGAATAAAGG AATACAAGAG ATCATCCAAA TGAATAAAG 660  
 CTGGGTAGAC ATCAACAATT TTACCTGCAT CAACGGCAGT GAAATTTATC AGCCAGGGCA 720  
 GCTTCCCACT GAACAATATT GGAATAAAGT GGCCTCCAA CGGTCAAGTG GAATGAATGA 780  
 75 GACTGGAGTA ATTGTTGGT ATTAGCACT TTGTCTTCT CTGGCTTGGC TCATAGTTGG 840  
 AGCAGCACTA TTTAAAGGAA TCAATCTCT TGCAAGGTG GTATATTITA CAGCTCTTTT 900  
 CCCCTATTGT GTCCTACTCA TCCTGTTAGT ACGAGGTGCA ACTCTGGAGG GTGCTTCAA 960  
 AGGCATTTC TACTATATTG GAGCCCACTC AAATTTTACA AACTTAAAG AAGCTGAGGT 1020  
 ATGGAAGAT GCTGCCACTC AGATATTTTA CTCCCTTTC GTGGCTTGGG GTGGCTTAGT 1080  
 80 TGCTCTATCA TCTTACAATA AGTTCAAAA CACTGCTTC TCTGATGCCA TTGTGGTTTG 1140  
 TTTGACAAAC TGCTCACTA CGGTGTTTGC TGGATTGCT ATTTTCTTA TATTGGGACA 1200  
 CATGGCCCAT ATATCTGGAA AGGAAGTTTC TCAAGTTGTA AAATCAGGTT TTGATTGGC 1260  
 ATTCAATTGCC TATCCAGAGG CTCTAGCCCA ACTCCAGGT GGTCCATTTT GGTCCATATT 1320  
 ATTTTCTTTC ATGCTTTTAA CTTTGGGTCT CGATTCTCAG TTTGCTTCCA TTGAACGAT 1380  
 CACACACCA ATTCAAGATT TATTTCCCAA AGTGATGAAG AAAATGAGGG TTCCCATAAC 1440  
 TTTGGGCTGC TGCTTGGTTT TGTTTCTCTT TGTCTGTGTC TGTGTGACTC AGGCTGGAAT 1500

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50

TTACTGGGTT CATCTGATTG ACCACTTCTG TGCTGGATGG GGCATTTTAA TTGCAGCTAT 1560  
 ACTGGAGCTA GTTGGAAATCA TCTGGATTGA TGGAGGGAAC AGATTCATTG AGGATACAGA 1620  
 AATGATGATT GGAGCAAAAGA GGTGGATATT CTGGCTATGG TGGAGAGCTT GCTGGTTTGT 1680  
 AATTACGCCT ATCCTTTTGA TTGCAATATT TATCTGGTCA TTGGTGCAAT TTCATAGACC 1740  
 TAATTATGGC GCAATTCCAT ACCCTGACTG GGGAGTTGCT TTAGGCTGGT GTATGATTGT 1800  
 TTTCTGCATT ATTTGGATAC CAATTATGGC TATCATAAAA ATAATTCAGG CTAAGGAAAA 1860  
 CATCTTTCAA CGCCTTATAA GTTCTGCAG ACCAGCTTCT AACTGGGGTC CATACCTGGA 1920  
 ACAACATCGT GGGGAAAGAT ATAAAGACAT GGTAGATCCT AAAAAAGAGG CTGACCATGA 1980  
 AATACCTACT GTTAGTGGCA GCAGAAAACC GGAATGAGAT CTCATTGAAA AAAATATATG 2040  
 ATTGTATAAT GTGATTTTTT TTAGAATAGG GGGAACTTTA TTTATTGTGT TGTTAACTGA 2100  
 ATAGGAAAAA GTACATACTA TGTTTATGAT AGTGTGATTT TTTTCACATT TAAGCAGGAA 2160  
 TGCAATATAA AAATGTGAAT CTCTTAATTC TCAGCCATGT GCTTATTATA TTTCTTTTAA 2220  
 GATTGTCTAT CTGTATAACA CACACACACA CACCTAAGAG TCTCTATTTC ACAATTATAT 2280  
 TTTTGTAAAT AGTATATGCA TTTTAAATAC ATTGGAGGCT TTATTTTGAA CTAATTTCTT 2340  
 AGAGATAGT TATATTTTCT ATTACACAAG TTTAAAAATA TTATTAACCT GTATTTTCTT 2400  
 AATATACAAT CTATCTTTTC CACAAATATG AGTGGGAAAT AAATCAGCAC ATTTGAAAGA 2460  
 AAGTGTAAAT ACTGAAGGCC TCACCTAATT AGAAACGTGA TAAATATATG GACAAATGGA 2520  
 CTATACATAC TATAAGAGGA CTGTAGTTTA ATACTTTTTA CCCAAATATG TTTAAATACA 2580  
 TCGTGCAATT GTTACAGCTC ATGTTTTCTA TATGAACCTA GTCATTAAATG TTCCTTATAA 2640  
 AAGTGAAAT AAGATGGAAA AATTAGGATC CTACAGCCAG TACGTGATAA ATCTAGAAAA 2700  
 TTGAGTTTTG CCATCTTCTT TCCCATATA CAATCTTCTT TCCTTAGGTA ATTTGGAAGA 2760  
 AAACATAGAC CCATTYAAAT TCTATTGTGT TTCACCAAAT TCAGTGTGTG TCATTATACC 2820  
 TCTCTGAAT ATAGGTTTAA TTTCAAATAG AATATGGACT TAAATGTATA TGAGAACTG 2880  
 GCTTTAATCA ATTTCTAGCAT TTTATTACTG TAATACAGGG CTGATAGAGT GATTTTGTCT 2940  
 TATATGAGTC AGTTACTACT TACAGGTGAT AACTTGCATA CTATTGGAAG ATAAAGTTGT 3000  
 CAACTTGTC AAGAATGAGA AAAGCCAAAT TAGAAAAATCC TATGTCTTAG TTTCTTACC 3060  
 AAGGATAAAT AAATATATCA CTAAGAGCTT TATATATTGA TTATATATTG TTGACAACTG 3120  
 GTTTAAGCAT CATAGCCTAT GATGATAAAC ACTGCCTATA TATGTAAATA GCTTTTCATC 3180  
 AATTCTTAAA TTTCTTAAAC TAGGCTTCAG GGAGCATATG AAACCAAAAT TATATGGAAC 3240  
 ATTTCTGTGT TGATCATGTA CATGCAATTT TCTAGGGAGA GAGTCCGTAG GTTTATCAGA 3300  
 ATATCAAGSA AAACCTGTGAC CCAAGAAGT TTAAGAATCA CATACAGTGC TGCTGGCTTT 3360  
 TTGTGCTTGG CAAATGAGTG ACAATAGAAG AAATAATTTT TCTTACACAT TTTAAACGCT 3420  
 TTTCTCTTCC TTGTGATTGA AGATGAAAGG AGTAAGAAT TAAGGCAATT GTTTAATTAA 3480  
 TACTGGTAAC TTATTTAGGG GGGAGGGGAC ATGAAGGTAG GTAAATAGTT AGGCCTCTAA 3540  
 TTGAACCAAC TCTCTAAGTT ATGTACGTAT ATATAAGCTG AAATGTGTGT TGACATTCTG 3600  
 AGGCTTTTCT TTTTCTTTT CTTTCTTTT TTTTCTTGGT GGGGGGCTGG GGGTCAGAGT 3660  
 CTGTCTCTGT TGCTGGGCTT GGAGTGCAGT GGCATGATCT CAGCTCACTG CAACCTCTGC 3720  
 CTCTGGGATT CAAGTGATTC TCCTGCCTCA GCCTCTTGAG TAGCTGGGAC TACAGGTGCC 3780  
 CGCCACACA CCAAGCTAAT TTTGTATTTT TAGTAGAGGC GAAGTTTCCC CATGTGGGCC 3840  
 AGGCTGGTCT TGAACCTCCG ACCTCAAGTG ATCTGTCTAC CTCGGCCTCC TAAAGTGCTG 3900  
 AGATTACAGG TGTGAGGCCAC CGTGCCCGGC CCATTCTAAG GGTTTTCTTT GAAGACAGGT 3960  
 CAAATGCTGT TAGTAAGTTT CAGGAGATTG TTAATTCCTC AGTTATACCA GATTTTATAA 4020  
 AATATTGAG AATAGATGGC TAACAAGAGG TTAGAAATAC TTTTCTTAA TTTAATCCA 4080  
 CAGTATGTTA CATGCAATCT ACCACTACAT TTTGGTGCTA TTTAAGGTGT GCAATTTTCT 4140  
 ATAGGTGACT TTTGCAATTC AGGGAAAGAT TGGGCATATT AAATGAAAGA ATATCTAATT 4200  
 GGGGAGGTG TGAAGGGAAG GAAATCTTT TCAAAAGCTG ACCACAAAGA GTAGTTAAAA 4260  
 GTTTTGTCA CTAATCTTAC AAGTGTGTA AGCAGAGATT TCAACAGAGT GCTTGGCATA 4320  
 TTGTAGGGTG CTCATGGTG GTTTTTATTA TTATTACTCA GATTCCACAG TGGCAAGAAA 4380  
 CATCATCTA CATAATGGAA AACATTTACA TCAATCCCA CTIACCTTAA TCGCAACTTG 4440  
 GAGATAATTT ATGGTATTGT ATTGTAAACC ATTAATGAAA ACTTTTTCAC AGTTGAGTGA 4500  
 AATTAAATC ACTATATCTC

Seq ID NO: 434 Protein sequence  
Protein Accession #: NP\_009162.1

55  
 60  
 65

1 11 21 31 41 51  
 MDKLCPSFF KCREKEKUSA SSENPHVGEN DENQDRGNWS KKS DYLLSMI GYAVGLGNVW 60  
 RFPYLYSNG GGAFILIPYAI MLALAGLPLF FLECSLQQA SLGFSVWRI LPLFQGVGIT 120  
 MVLISIFVTI YYNVILAYS L YMFASFQSE LPWKNCSSWS DKNCRSRPIV THCNVSTVNK 180  
 GIQELIQMNK SWVDINNFTC INGSEIYQPG QLPSEYWNK VALQRSSGMN ETGVIVWYLA 240  
 LCLLLAWLIV GAALFKGIKS SGKVVFYFAL FPYVLLILL VRGATLEGAS KGISYYIGAQ 300  
 SNPTKLKEAE VWKDAATQIF YSLSVANGGL VALSSYNKFK NNCFSDAIVV CLINCLTSVF 360  
 AGPAIFSLG HMAHISGKEV SQVVKSGFDL AFIAYPEALA QLPFGPFWSI LFPFMLLTIG 420  
 LDSQFASIEI ITTTIQDLFP KVMKQMRVPI TLGCCLVLEL LGLVCVTQAG IYVWHLIDHP 480  
 CAGWGILIAA ILELVGIIWI YGGRPIEDT EMMIGAKRWI FWLWRACWF VITPILLIAI 540  
 FIWSLVQFHR PNYGAIPYED WGVALGWHI VFCLIWIPIM AIKIIQAKG NIFQRLISCC 600  
 RPASNNGPYL EQHRGERYKD MVDPKKEADH EIPVSGSRK PE

Seq ID NO: 435 DNA sequence  
Nucleic Acid Accession #: M18728.1  
Coding sequence: 51..1085

75  
 80

1 11 21 31 41 51  
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CTGGAAGGA GGTCTCTGCT ACAGCCTCAC 120  
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TOGCCACAA CCGTCCCCAG AATCGTATTG 240  
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
 TAGGAAGCTA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360  
 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480  
 TSCCAAGCC CTCCTCTCTC AGCAACAACCT CCAACCCCGT GGAGGACAGG GATGCTGTGG 540

5 CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
 GGCTCCCGGT CAGTCCCGAG 'TGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660  
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACCGCACTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780  
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840  
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
 TATAGCAGCC CTGGGTGATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140  
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGCTCG 1200  
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACCT AATGAAAATT TAAAGGGAAA 1260  
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320  
 GCAAAACATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
 AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
 TGCTCTTTCT GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560  
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
 AATGTACAG TGGTCTTTT CAGAGTTGGA CTCTAGACT CACCTGTTCT CACTCCCTGT 1680  
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
 GGAGGAGTCT GTGCAGTTTG TGACACTTGT TGTGGAACAT GGCTAAATAC AATGGGTATC 1800  
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATAGG CTACACTCAT 1860  
 CTGACTCATT CTTTATTTCT TTTTATTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
 CTCTTGGTAT TACCTCCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
 CTCTAAAGCC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
 GGCTGGAAAT ACAAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
 ATAAAAGCCC CAAATGTGTG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
 TCTCACTAG GTGAGCCCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTAAAAA AAAAAAAGA 2280  
 ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340  
 TTTACAAAAA GTGAACCTGA ACTAATCTGA TGTTAACCAA TGTATTATT TCTGTGGTTC 2400  
 TGTTCCTCTG TTCCAATTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460  
 CTATCACTGT ACTTGTAGAG TGGTGTCTCT TTAATTCATA AATCACAAAT AAAAGCCAA 2520  
 TAGCTCTATA ACT

Seq ID NO: 436 Protein sequence  
 Protein Accession #: AAA59907.1

40 1 11 21 31 41 51  
 | | | | |  
 MGPPSAPPCR LHPVPEKEVL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLAHNLPO 60  
 NRIGYSWKYG ERVDNSLIV GYVIGTQAT PGPAYSGRET IYPNASLLIQ NVTQNDTFY 120  
 TLQVTKSLDV NEBATGQFHV YPELPKPSIS SNNSNPVEDK DAVAFCEPE VQNTTYLWV 180  
 NGQSLFVSPR LQLSNGWMTL TLLSVKRNDA GSYECRIQNP ASANRSDPVT LNVLYGPDVP 240  
 TISPSKANYR PGENLNLSC AASNPPAQYS WFINGTQQQS TQELFIFPNIT VNNSGSMQ 300  
 AHNSATGLNR TTVTMITVSG SAPVLSAVAT VGITIGVLAR VALI

Seq ID NO: 437 DNA sequence  
 Nucleic Acid Accession #: M18728.1  
 Coding sequence: 1355..1657

50 1 11 21 31 41 51  
 | | | | |  
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTCTGTC ACAGCCTCAC 120  
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC AGCCCAITCA 180  
 ATGTGCAGGA GGGGAAGGAG GTTCTTCTAC TCGCCCAACA CCTGCCCCAG AATCGTATTG 240  
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
 TAGGAACCTA ACAAGCTACC CCAGGGCCCC CATACAGTGG TCGAGAGACA ATATACCCCA 360  
 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACGGGACA GTTCCATGTA TACCCGGAGC 480  
 TGCCCAAGCC CTCATCTCC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540  
 CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
 GCTTCCCGGT CAGTCCCGAG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660  
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACCGCACTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780  
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840  
 ACCCACTGCT ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
 TATAGCAGCC CTGGGTGATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140  
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGCTCG 1200  
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACCT AATGAAAATT TAAAGGGAAA 1260  
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320  
 GCAAAACATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
 AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
 TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560  
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
 AATGTACAG TGGTCTTTT CAGAGTTGGA CTCTAGACT CACCTGTTCT CACTCCCTGT 1680  
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGGAACAT GGCTAAATAC AATGGGTATC 1800  
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATAGG CTACACTCAT 1860

CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
5 ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTTAAAA AAAAAAAGA 2280  
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340  
10 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
TGTTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460  
CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520  
TAGCTCTATA ACT

Seq ID NO: 438 Protein sequence  
Protein Accession #: AAA59908.1

1 11 21 31 41 51  
| | | | |  
20 MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SFAWQDDAVI SISQVEASEG NLTECQIYLV 60  
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

Seq ID NO: 439 DNA sequence  
Nucleic Acid Accession #: M18728.1  
Coding sequence: 2370..2501

1 11 21 31 41 51  
| | | | |  
30 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
CCTCAGCCCC TCCTCTCAGA TTGCATGTCC CCTGGAAGGA GGTCCTGTCT ACAGCCCTCAC 120  
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG 240  
GTTACAGCTG GTACAAAGCG GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATAAGTGG TCGAGAGACA ATATACCCCA 360  
ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
35 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480  
TGCCCAAGCC CTCCTCTCC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540  
CCTTCACCTG TGAACCTGAG GTTCAGAA CAACCTACCT GTGGTGGSTA AATGGTCAGA 600  
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCT ACTCTACTCA 660  
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
40 ACGCAGTGA CCGAGTCAAC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780  
CCTCAAGGCG CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCTCTA 840  
ACCCACCTCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGTCTCTG 1020  
45 TCCTCTCAGC TGTGGCCACC GTGGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
TATAGCAGCC CTGGTGTATT TTGATATT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140  
GAATTCTTCT AGCTCTCTCA ATCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200  
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260  
ACCCCTCAGG CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320  
50 GCAAAACATG GTGAGAAATG GACGACTTCA CACTATGAC AGCTTTTCCC AAGATGTCAA 1380  
AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAAAAG 1560  
AGATCTCTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
55 AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTTCTAGACT CACCTGTCTT CACTCCCTGT 1680  
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800  
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860  
CTGACTCAIT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
60 CTCTTGATAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
65 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTTAAAA AAAAAAAGA 2280  
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340  
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
TGTTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460  
70 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520  
TAGCTCTATA ACT

Seq ID NO: 440 Protein sequence  
Protein Accession #: AAA59909.1

1 11 21 31 41 51  
| | | | |  
75 MLTNVPIVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 441 DNA sequence  
Nucleic Acid Accession #: NM\_002381.2  
Coding sequence: 64..1524

1 11 21 31 41 51

5  
10  
15  
20  
25  
30  
35  
40  
45

AAATCCGAGC	CTCGCGTGGG	CTCCTGGCCC	CCGACGGACA	CCACCAGGCC	CACGGAGCCC	60
ACCATGCGCG	GCCCCGCCCC	CGCGGCGCGC	CTCCGCGGAC	TCCTCCTGCT	GCTCTGGCCG	120
CTGCTGCTGC	TGCCCTTCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG	180
GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCGCCCTCT	CTCCTGCGGC	TCCCGACGGC	240
GCGCCGCTT	CCGGGACCGC	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
AGACCCCTGG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GGTACGGCC	CCTGGAATTC	360
ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
ACGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TCGAGTTCCA	ACTCCAGGCC	480
TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGAA	TCACACCTTT	GTCAACAGGC	540
ACCATGTGAG	GCCTAGCCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCGAGG	600
GCTGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC	660
CAGGACCAAG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
GTGGGCGTGG	ACCGGGCAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTAGAG	780
GAGCATGT	TCTACGTGGA	GACCTATGGG	GTCATTGAGA	AACTTTCCTC	TAGATTCCAG	840
GAAACCTTCT	GTGCGCTGGA	CCCCTGTGTG	CTTGGAAAC	ACCAGTGCCA	GCAGCTCTGC	900
ATCAGTGATG	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
GACAAGAAAA	CGTGTTCAGT	TCTGTATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
ATCTGTGTGA	ATGACAGAG	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
AATGAGACA	GGAAACTTTG	TTCACTCAAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
GGTGGCCAGC	ACATTTTGTG	GAGTGTAGGG	GCGCATCCTT	ACCAGTGTGA	TGCTATCTCT	1320
GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTACGCCA	CTGAGGAAGC	ACGAAGACTT	1380
GTTCCTCAGT	AGATGCTTGG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTCAGC	1440
TCGTATCTTC	AAAGACTGAA	CACATAAATT	GATGACATTT	TGGGAAGATT	GAAAAATAAT	1500
GAATATGGAC	AAATACATCG	TTAAATTGCT	CCAATTTCTC	ACCTGAAAAAT	GTGGACAGCT	1560
TGGTGTACTT	AAATCACTAG	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCCTGTCTAA	1620
TAAATTGGCA	TTATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTGTA	TGAAGATCTT	1680
CTGCAGAAAT	AGCATGATTT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
CITTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAT	GAAAAAGTTA	1800
GTGTTCTTTT	ATCTACTAAT	TGAGCCATTT	AAATTTTAAA	TGTTTATATT	AGATAACCAT	1860
ATTACAATG	GAAACTTTAG	GTCTAGTTTC	TTTTGATAGT	ATTATATAAT	TAAATCAATC	1920
TTATTAATGA	GAGTGCAAAAT	TGTACAAAGT	ATTACACAT	ACAACTTCAT	ATAACTGAGA	1980
TGAATGTAAT	TTTGAACCTG	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG	2100
TGAACATTAC	ATTGCCATTT	TTAATTCATT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
AGCACTAGTT	GTGAATTTAG	GGTGTAAAC	TTTTTACCAA	GTACAAAAAT	CCCAAAATTA	2220
CTTTATATAT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATAAA	ATTGCTATAA	2280
ATCGACAAAA	TCTAATGTTG	TCITTTTAAAT	GTTAGTGATC	CACCTGCTCT	AGCCTCCCAA	2340
AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
AAATCTTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AAATTTGCAC	2460
TGCTCAATTC	TGTTTTCTGT	TTGCAATGTC	TTAATATAAA	TAAAGATTAT	TACCTTTACA	2520
TATTATCATG	TCTATTTTGG	ATGACTCATC	AAATTTGTCT	ATTAAAGATA	TTTCTTTAAA	2580
TTAAAAA	AAAAA					

Seq ID NO: 442 Protein sequence  
Protein Accession #: NP\_002372.1

50  
55  
60

1	11	21	31	41	51	
MPRPAPARRL	PGLLLLLLWPL	LLLPSAAPDP	VARPGFRRLR	TRGPGGSPGR	RPSPAAPDGA	60
PASGTSEPER	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRRI	DTLDIGPADT	120
RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIGTAM	DEAFTVEAGA	180
REPSNIPKV	ALIIVTDGRPV	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
HVFYVETYG	TEKLSRRFQE	TFCALDPCVL	GTHQCHVCI	SDGBGKHICE	CSQGYTLNAD	300
KKTCALDR	ALNTHGCEHI	CVNDRSGSYH	CEBYEGYTLN	EDRKTCASQD	KCALGTHGCG	360
HICVNDRTG	HHCEYBGT	LNADKTCVS	RDKCALGSHG	QCHICVSDGA	ASYHCDCTPG	420
YTLNEDKKT	SATEEARRLV	STEDACGCEA	TLAFQDKVSS	YLQRLNKL	DILEKLKINE	480
YGQIHR						

Seq ID NO: 443 DNA sequence  
Nucleic Acid Accession #: NM\_016639.1  
Coding sequence: 40..429

65  
70  
75  
80

1	11	21	31	41	51	
GCGGCGGGCG	CAGACAGCGG	CGGGCGCAGG	ACGTGCACTA	TGGCTCGGGG	CTCGCTGCGC	60
CGGTGCTGCG	GGCTCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGGCTC	CGTGGCCGGG	120
GAGCAAGCGC	CAGGCACCGC	CCCCTGCTCC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
AAGTGATGCG	ACTGCGGCTC	TTGCAGGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
GCTGCAGCAC	CTCTGCCCCC	CTTCCGCGTG	CTTTGGCCCA	TCCTTGGGGG	CGCTCTGAGC	300
CTGACCTTCG	TGCTGGGGCT	GCTTTCTGGC	TTTTTGGTCT	GGAGACGATG	CGCGAGGAGA	360
GAGAAAGTCA	CAACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCGAGC	TGTGGCGCTG	420
ATCCAGTGAC	AATGTGCCCC	CTGCCAGCGG	GGGCTCGCCC	ACTCATCAIT	CATTATCCAA	480
TTCTAGAGCC	AGTCTCTGCC	TCOCAGACGC	GGCGGAGGCC	AAGCTCTCTC	AACCAACAGG	540
GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTGAGGG	GAACCTTCCA	600
AGGTGTCTGG	TGCTGGCTGC	CTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
ACAAAAAGC	TGACACTGAC	TAAGGAAGCT	CAGCATTTGC	ACAGGGGAGG	GGGGTGCCTT	720
CCTTCCTTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
TCACCTCAGAT	GTCTGAAAT	TCCACACCGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
TTAACAATAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCAACTC	900
CCCAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAAATTTATT	960

AATAAAGAA TCTTTAACTT TAAAAA AAAA

Seq ID NO: 444 Protein sequence  
Protein Accession #: NP\_057723.1

1 11 21 31 41 51  
MARGSLRRLL RLLVLGLNLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60  
SDFCLGCAAA PPAPFRLWLP ILGGALSLTF VLGLLSGFLV WRCRRREKF TTPIETTGGE 120  
GCPAVALIQ

Seq ID NO: 445 DNA sequence  
Nucleic Acid Accession #: AF322916.1  
Coding sequence: 50..4300

1 11 21 31 41 51  
GCACCTCCGA GCCTTTAAGG TTGCGCGGG GGCCAGGCAA GAGTTAGCCA TGAAGAGCCT 60  
CAAGTCCGCG CTGAGGAGGC AGGACGTGCC CGGCCCGCG TCGTCTGGCG CCGCCGCGCG 120  
CAGCGCGCAT GCAGCAGATT GGAATAAATA TGATGACCGA TTGATGAAAG CAGCAGAAAG 180  
GGGGGATGTA GAAAAAGTGA CCTCAATCCT TGCTAAAAAG GGGGTCAATC CAGGCAAACT 240  
AGATGTGGAA GGCAGATCTG TCTTCCATGT TGTGACCTCA AAGGGGAATC TTGAGTGTTC 300  
AATGCGCATC CTTATACATG GAGTTGATAT TACAACCAGT GACACTGCAG GGAGAAATGC 360  
TCTTCACTCG GCTGCTAAGT ATGGACATGC ATTGTGCTCA CAAAACTTC TACAGTACAA 420  
TTGTCCCACT GAGCATGCAG ACCTGCAGGG AAGAACTGCA CTTCAAAAAA AAGCAATGGC 480  
AGATTGTCTT TTAGCATATC AGCTGCTTTG TGACCATGGG GCCTCTGTGA ATGCCAAAGA 540  
TGTAAGAGGG CGGACACCACT TTGTTCTGGC TACTCAGATG AGTAGGCCAA CAATATGTCA 600  
ACTGTGATA GATAGAGGAG CGGATGTTAA TTCCAGAGAC AAACAAACCA GAACTGCCCT 660  
CATGCTAGGT TGCGAATATG GTTGACAGAGA TGCAGTAGAA GTCTTAATTA AAAATGGTGC 720  
TGATATAAGC TTGCTGGATG CGCTTGGCCA TGATAGTTCT TACTATGCAA GAATTGGTGA 780  
CAATCTGGAC ATTCTAACCT TGTGAAGAC TGCATCGGAA AATACCAACA AAGGAGAGA 840  
ACTTTGGAAG AAAGGACCAT CTTTGCAACA GCGAAATTTG ACACACATGC AAGATGAAGT 900  
AATGTGAAG TCAGATCAGA GGGAGCATCA AAATATTGAG GATTGGAGA TTGAAATGA 960  
AGATTGAAA GAGAGGTTGA GAAAAATCA GCAAGAACAA AGAATACTTT TGGATAAAGT 1020  
CAATGGTTTA CAGTTACAGC TGAATGAGGA AGTTATGGTT GCTGATGATC TGGAAAGCGA 1080  
GAGAGAAAAG CTGAAGTCCC TTTTGGCAGC TAAAGAAAAG CAACATGAAG AAAGCTTAAG 1140  
GACTATTGAG GCTCTGAAAA ATAGATTAA ATATTTTGAG AGTGATCATT TAGGATCAGG 1200  
AAGTCATTTC AGTAACCGAA AAGAGATAT GCTTCTTAAA CAAGGTGAGA TGTATATGGC 1260  
AGACTCACAG TGTACTTCCC CAGGTATACC AGCCCATATG CAAAGCAGAT CTATGTTAAG 1320  
ACCTCTGGA CTATCTTTAC CCAGTCAAC GCCTACTCTT GAAATGAAA TTTTAAAGAA 1380  
AGAGTTAGAA GCAATGCGAA CTTTCTGTGA GTCAGCAAAA CAAGACCGAC TGAAGCTCCA 1440  
AAATGAATCG GCACACAAAG TGGCAGAATG CAAAGCTTTA GCATTAGAAT GTGAAGGGGT 1500  
CAAGGAGATG TCAGATCAGA AGATAAAGCA ATTAGAAGAT GCATTAAAAG ATGTGCAGAA 1560  
GAGGATGATG GAGTCAGAAG GTAAAGTTAA ACAATGCGAG ACCATTTC TTGCCCTTAA 1620  
AGAACACTTA ACAAGTGAAG CAGCCTCAGG GAATCACAGA CTAACCGAGG AACTGAAGGA 1680  
TCAGTTGAAA GACTTGAAAG TAAAATATGA AGGTGCTTCA GCAGAAGTGG GGAATTAAG 1740  
AAACCAATC AAACAAATG AGATGATAGT AGAAGAGTTT AAGAGGGATG AAGGCAAGCT 1800  
GATAGAAGAA AATAAGCGAT TACAGAAGGA ACTTAGTATG TGTGAAATGG AGCGAGAGAA 1860  
GAAAGGAAGA AAGGTCACAG AGATGGAAGG CCAGGCAAAA GAATTGTGAG CGAAGTTGGC 1920  
CCTTTCCATT CCAGCTGAAA AATTTGAAA CATGAAGAGC TCATTATCAA ATGAAGTGA 1980  
TGAGAAAGCA AAAAAATTAG TAGAAATGGA AAGAGAACAT GAAAAATCAC TTAGTGAAT 2040  
TAGACAGTTA AAGAGAGAAC TTGAGAATGT TAAGGCCAAG CTTGCTCAGC ACCTCAAAAC 2100  
AGAGGAACAT GAACAGGTTA AGAGCAGATT AGAACAGAAA TCAGGAGAAC TTGGGAAGAA 2160  
GATCACTGAG TTAACATTGA AAAATCAGAC ACTACAAAAG GAAATTGAAA AAGTTTATTT 2220  
GGATAATAAG CTCCTCAGG AGCAAGCACA TAACTTAACT ATTGAATGA AAAATCATT 2280  
TGTCTCTTTA AAGTAAGTG AAGACATGAA AAGTCACTAT GATGCAATTA TTGATGATCT 2340  
TAATGAAAG CTTTTAGATG TAACACAAA ATATACAGAA AAGAAGTTGG AAATGGAGAA 2400  
ATTGCTACTG GAAATGACA GCTTAAGTAA GATGTGAAGC CGCTAGAAA CTGTGTTTGT 2460  
ACCTCTGAG AAACATGAAA AAGAGATAAT AGCTCTGAAA TCCAATATTG TTGAACCTTA 2520  
GAAACAGCTG TCTGAACCTA AGAAAAATG TGGTGAAGAC CAGGAGAAA TACAAGCTCT 2580  
CACATCTGAA AACACTAATC TGAAGAAGAT GATGAGTAAT CAGTATGTGC CAGTTAAAC 2640  
CCATGAAGAG GTTAAATGTA CACTGAATGA CAGTTAGCC AAAACTAACA GAGAATTATT 2700  
AGATGTGAAG AAAAAATTG AAGATATAAA TCAGGAATTT GTAAAAATAA AAGATAAGAA 2760  
TGAAATATTA AAAGAAACCC TGGAAAAAC TCAGAACCAA ATAAAGCTG AGTACATCAG 2820  
CCTGGCAGAG CAGGAGGCAA AGATGAGCTC GCTAAGTCAG AGCATGAGAA AGGTGACGGA 2880  
TAGTAATGCT GAAATCTTGG CCAACTACAG AAAAGGCCAA GAAGAGATTG TGACACTGCA 2940  
TGCCGAAATT AAAGCCGAGA AGAAGGAGCT CGACACAAATA CAAGAAATGCA TTAAGGTAAA 3000  
ATATGCCCTA ATTGTCAGCT TTGAGGAGTG CGAGAGAAAA TTTAAAGCAA CAGAGAAAAG 3060  
ACTAAAGAC CAGTTATCAG AGCAGACACA AAGTATAGT GTCAGTGAAG AAGAAGTCAA 3120  
GAAAAACAG CAAGAGAATG AAGATTAAA GAAGGAGATT TTTACCTTC AGAAAGATT 3180  
GAGAGATAAG ACAGTTCTCA TTGAGAGTGC TCATGAAATG GAAAGAGCAT TAAGCAGAAA 3240  
AACAGACGAG CTAAACAAAC AGTTAAAGAA CTGTCTCAG AAATACACGG AAGTAAAGAA 3300  
TGTGAAGAG AAGCTAGTAG AAGAAATGC CAAACAGACT TCTGAGATCT TTGCAAGTGA 3360  
AATCTTTTG CAAAAACAC ATGTTCCATT GGAACAGGTT GAGGCTCTGA AAAATCTCT 3420  
TAATGGCACA ATTGAAATC TAAAGGAAGA ACTGAAGAGT ATGCAAGGT GTTACGAGAA 3480  
AGAGCAGCAG ACAGTGACCA AACTGCATCA ATTGTTGGAG AATCAAAAGA ACTCTCTGT 3540  
ACCCCTGGCA GAGCATTTGC AGATTAAAGA AGCATTGAG AAAGAAGTTG GAATCATAAA 3600  
AGCCAGCTTG ATGAGAAAGG AAGAAAGAA CCAAAACAAA ATGGAAGAGG TCTCCAACT 3660  
TCAGTGGAG GTTCAGATA CTAAACAAAG ATTAAGAAAA TTAGAGACTA GAGAGGTAGT 3720  
TGACTTGTCT AAATATAAAG CAACAAAAG TGATTTGGAG ACACAGATT CTAGCTTAAA 3780  
TGAAAAATTG GCCAATCTGA ATAGAAAGTA TGAGGAAGTA TGTGAGGAG TTTTGCATGC 3840  
CAAAAGAGAG GAAATATCTG CAAAGATGA GAAGGAATTA CTGCATTCA GCATTGAGCA 3900  
AGAAATTAG GATCAGAGG AACGATGTGA TAAGTCCTTA ACAACATCA CAGAGTTACA 3960  
AAGAAGATA CAAGAATCTG CTAACAAAT AGAAGCAAAA GATAATAAGA TAACTGAAC 4020



5 GCTTAATGAT GTGGAAGAT TAAAAAGGC ACTCAATGGC CTTTCCAAC TCACCTACAC 4080  
 AAGTGGGAAC CCCACCAAGA GGCAGAGCCA GCTGATTGAC ACTCTGCAGC ACCAAGTGAA 4140  
 ATCTCTGGAG CAACAGCTGG CCGATGCTGA CAGACAGCAC CAAGAAGTAA TTGCAATTAA 4200  
 TCGACACAC CTTCTTAGTG CTGCACAGGG TCACATGGAT GAAGATGTTC AGGAGGCTCT 4260  
 GCTCCAGATC ATACAAATGC GGCAGGGGCT TGTGTGCTAG COGTAGCAC TGACTGCCAG 4320  
 TATCTGTTT ATCTTGCTGG TGCTGAACAT TCTTTGTGCA ACTCCATGGT CTTTCTGGGC 4380  
 CTTACTGTGC TGGTATAAT AAAATAAAT ATATTTTGT CTGGGTGT

10 Seq ID NO: 446 Protein sequence  
 Protein Accession #: AAG49577.1

1 11 21 31 41 51  
 15 MKSLKSLRR QDVPGPASSG AAAASAHAAD WNKYDDRLMK AAERGDVEKV TSILAKKGVN 60  
 PGKLDVEGRS VFHVVTSGKN LECLNAILIH GVDITTSDTA GRNALHLAAK YGHALCLQKL 120  
 LQYNCPTEHS DLQRTALQK KAMADCPSSI QLLCDHGASV NAKDVKGRTP LVLATQMSRP 180  
 TICQLLIDRG ADVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSSTYA 240  
 RIGDNLIDLT LKTASENTN KGRELWKKGP SLQQRNLTHM QDEVNVKSHQ REHQNIQDLE 300  
 20 IENEDLKERL RKIQEQEQRIL LDKVNGLQIQ LNEEVMVADD LESEREKLKS LLAKEKQHE 360  
 ESLRTIEALK NRPKYFESDH LGSGSHFSNR KEDMLLKQGG MYMADSQCTS PGIPAHMQSR 420  
 SMLRPLELSL PSQTSYSENE ILKKELEAMR TFCESAKQDR LKIQNELAHK VAECKALALE 480  
 CERVKESDE QIKQLEDALK DVQKRMYESE GKVKQMOTHF LALKEHLTSE AASGNHRLTE 540  
 ELKDQLKDLK VYEGASAEV GKLRNQIKQN EMIVEEPKRD EGKLIENKR LQKELSMCEM 600  
 25 EREKGRKRV EMEGQAKELS AKIALSIPAE KFENMKSSLS NEVNEKAKKL VEMEREHEKS 660  
 LSEIRQLKRE LENVAKALQ HVKPEEHEQV KSRLEQKSSE LGKKITELTL KNQTLQKEIE 720  
 KVVLDNKLK EQAHNLITIE KNIHVPLKVS EDMKSHDAI IDDLNRKLLD VTQKYTEKKL 780  
 EMEKLLEND SLKSDVSRLE TVFVPPKEHE KEIIALKSNI VELKKQLSEL KKKCGEDQEK 840  
 IHALTSENTN LKKMMSNQYV PVKTHEEVKM TLNDTLAKTN RELLDVKKKF EDINQEFVKI 900  
 30 KDKNEILKRN LENTQNIKA EYISLAHEA KMSLSQSMR KVQDSNAEIL ANYRKQEEI 960  
 VTLHAEIKAQ KRELDTIQEC IKVYAPIVS FECEKRFKA TEKELKQDLS EQTKYSVSE 1020  
 EEVKNKLEH DLKKEIFTL QKDLRDKTVL IEKSHEMERA LSRKTDELNK QLKDLQSKYT 1080  
 EVKNVKEKLV EENAKOTSEI LAVONLLQKQ HVPLEQVEAL KKSNGTIEI LKEELKSMQR 1140  
 35 CYEKQQTVT LKHQLENOK NSSVPLAEHL QIKEAFEKEV GIIKASLREK EESQNKMEE 1200  
 VSKLQSEVN TKQALKLET REVVDLSKYK ATKSDLETQI SSLAEKLANL NRKYEEVCEE 1260  
 VLHAKKEIS AKDEKELLHF SIEQEKDQK ERCDKSLTTI TELQRRIQES AKQIEAKDNK 1320  
 ITELNDVER LKQALNLSQ LTYTSGNPTK RQSLDITLQ HQVKSLEQL ADADRQHEV 1380  
 IAIYRTHLS AAQHMDDEDV QEALLQIIQM RQGLVC

40 Seq ID NO: 447 DNA sequence  
 Nucleic Acid Accession #: NM\_003020.1  
 Coding sequence: 29..664

1 11 21 31 41 51  
 45 CGCTCCTCGG GCTGCCCTTC GGTGACAAT GGTCTCCAGG ATGGTCTCTA CCATGCTATC 60  
 TGGCCTACTG TTTTGGCTGG CATCTGGATG GACTCCAGCA TTGCTTACA GCCCCCGGAC 120  
 CCCTGACCGG GTCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT 180  
 50 GGGCATTGGC AGGCCCGGAG TGAATATCC AGCTCACCAG GCCATGAATC TTGTGGGCCC 240  
 CCAGAGCATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGGTCTCT TTGGCAACAT 300  
 CCCCAACATC GTGGCAGAGT TGACTGGAGA CAACATTCTT AAGGACTTTA GTGAGGATCA 360  
 GGGGTACCCA GACCCCTCAA ATCCCTGTCC TGTGTGAAAA ACAGATGATG GATGTCTAGA 420  
 AAACACCCCT GACACTGCAG AGTTCAGTCG AGAGTTCAGG TTGCACCAGC ATCTCTTTGA 480  
 TCCGGAACAT GACTATCCAG GCTTGGGCAA GTGGAACAAG AAACCTCTTT ACGAGAAGAT 540  
 55 GAAGGGAGGA GAGAGACGAA AGCCGAGGAG TGTCAATCCA TATCTACAAG GACAGAGACT 600  
 GGATAATGTT GTTGCAAGA AGTCTGTCCC CCATTTTTC AATGAGGATCA AGGATCCAGA 660  
 GTAAAGAGAA CATCTAGAC GAAACCCAC ATTACCTGTT AGGCCTCAGC ATGGCTTATG 720  
 TGACGCTGTA AATGGAGTCC CTGTGAATGA CAGCATGTTT CTTACATAGA TAATTATGGA 780  
 TACAAAGCAG CTGTATGTAG ATAGTGTATT GTCTTCACAC CGATGATTCI GCTTTTGTCT 840  
 60 AAATTAGAAT AAGAGCTTTT TTGTTTCTTG GGTTTTAAAA ATGTGAATCT GCAATGATCA 900  
 TAAAAATTAA AATGTGAATG TCAACAATAA AAAGCAAGAC TATGAAAGGC TCAGATTCTCT 960  
 TGCAGTTTAA AATGGTGTCT GAGGTGTGAC TATTTTGGCC AAGTCTGTAG AAAGCTGTCA 1020  
 TTTGATTTTG ATTATGTAGT TCATCCAGCC CTGGGCGATT GTTATACACC AGTAAAGAAG 1080  
 GCTGTACTCA AGAGGAGGAG CTGACACATT TCACCTGGCT GCGTCTTAAT AAACATGAAT 1140  
 65 GCAAGCATTG GC

Seq ID NO: 448 Protein sequence  
 Protein Accession #: NP\_003011.1

70 1 11 21 31 41 51  
 MVSRMVSTML SGLLFWLASG WTPAFAYSFR TPDRVSEADI QRLHGVMEQ LGIARPRVEY 60  
 PAHQAMNLVG PQSIEGGAHE GLQHLGPFEN IPNIVAEITG DNIPKDFSED QGYPPDPNFC 120  
 FVGKTDGCL ENTPTDAEFS REFQLHQHLF DPEHDYPLG KWNKKLLYEK MKGGERRKR 180  
 75 SVNPLYQQOR LDNVVAKSKV PHFSDQD E

Seq ID NO: 449 DNA sequence  
 Nucleic Acid Accession #: NM\_003816.1  
 Coding sequence: 79..2538

80 1 11 21 31 41 51  
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60  
 CTTGCGGAA CTGCGGAGAT GGGGTCTGGC GCGCGCTTTC CTTGCGGAGC CTTTCTGTGC 120  
 CGGTGGTGGC TGTGCTTGG CCTGGTGGGC CAGTCTCTCG GTGCGGCGCG GCCAGGCTTT 180

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60

CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTTGGAGATT AACTAGAGAA 240  
 AGAAGAGAA CCCCAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTC A GCTGAAGGA 300  
 AAAGAGCATA TTATTCACCT GGAAGGAAC AAAGACCTTT TGCTGAAGA TTTTGTGGTT 360  
 TATACTTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420  
 CATTATCGGG GCTATGTGGA GGGAGTTTCA ATTCATCCCA TTGCTCTTAG CGACTGTTTT 480  
 GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCGCAGAAC 540  
 AGCTCTCATT TTGAGCAGAT CATTTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600  
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660  
 CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG 720  
 GAGCTGTGTA TTGTCTGAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780  
 GTGAGAGAA AGATGATTCT CCGGCAAAAC TACTGGGATA GTATGTATAT TATGTTAAAT 840  
 ATTGCAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900  
 GGGGGTGTCT GTGATGTGCT GGGGAACTTC GTGCAGTGGC GGGAAAAGTT TCTTATCACA 960  
 CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAAGAAAG GTTTTGGTGG AACTGCAGGA 1020  
 ATGGCATTGT TGGGAACAGT GTGTTCAAGG AGCCACGCGAG GCGGGATTAA TGTGTTTGA 1080  
 CAAATCACTG TGGAGCATTG TGCITCCATT GTTGCTCATG AATTGGGTCA TAATCTTGA 1140  
 ATGAATCAGC ATGATGGGAG AGATTGTTC TGTGGAGCAA AGAGCTGCAT CATGAATTC 1200  
 GGAGCATCGG GTTCCAGAAA CTTTAGCAGT TGCAGTGCAG AGGACTTTGA GAAGTTAACT 1260  
 TTAATAAAG GAGGAAACTG CCTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320  
 CCTCTCTGTG TGAATAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380  
 GAATGTAAT TGGACCTCTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440  
 TGTGCATATG GTGACTGTG TAAAGACTGT CGGTTCTCTC CAGGAGGTAC TTTATGCCGA 1500  
 GGAATAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTCTCA GTTCTGTGAG 1560  
 CCAGATGTTT TTATTAGAAA TGGATATCCT TGCCAGAAATA ACAAGCCTA TTGCTACAAC 1620  
 GGCATGTGCG AGTATTATGA TGCTCAATGT CAAGTCACTT TTGGCTCAAA AGCCAAAGCT 1680  
 GCGCCCAAG ATTGTTTCTC TGAAGTGAAT TCTAAAGGTG ACAGATTGG CAATTGTGGT 1740  
 TTCTCTGGCA ATGAATACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800  
 TGTGAGAAAT TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCT 1860  
 AGTCGAGGCA CAAATGTTG GGGGTGTGGT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920  
 GGGATGTTTA ACAGAGGAC AAAATGTGGT GCTGGAAGA TCTGTAGAAA CTTCAGTGT 1980  
 GTAGATGCTT GTTCTCTGAA TTATGACTGT GATGTTTCA AAAAGTGTCA TGGACATGGG 2040  
 GTATGTAATA GCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCCC AAATGTGAG 2100  
 ACTAAAGGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAAT GAATACTGCA 2160  
 TTAGGGGACG GACTCTGGT CTCTCTCTC CTAATTGTTC CCTTATTGT CTGCTATT 2220  
 TTTATCTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACA 2280  
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTTCCT 2340  
 CGACATGTTT CTCCAGTAC ACCTCCCAAG GAAGTTCTTA TATATGCAAA CAGATTGCA 2400  
 GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCTAT CAGGCCACC TCCACCACA 2460  
 CGAAGAGTAT CATCTCAGGG AAACCTAATT CCTGCCCTGC CTGCTCTGC ACCTCCTTTA 2520  
 TATAGTCCC TCACCTGATT TTTTAACTT TCTTTTGA CAATGCTTCA GGGAACTGAG 2580  
 TCAATCTTTT TTTTCTTCT TGTGTTTTT TTGAAAAGCC TTTCTGTTGC AACTATGAAT 2640  
 GAAAAACAAA CACCACAAA CAGACTTCAC TAACACAGAA AACAGAAAC TGAGTGTGAG 2700  
 AGTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC 2760  
 CATCATGAAA TAAAGCTTAT TCAGTCAATG GTGAGGTAAA TGCACTAATC ATGGATTTT 2820  
 TGAACATGTT ATTGCAAGTA TTCTCAAAAT AACTGTATTG GTGAAGATT TTTGTCTAT 2880  
 AGTGTGTTA TGTATTCTG AATTCTTAC CTTAGTTATC ATTAATGTAG TTCTCATG 2940  
 AACATGTGAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000  
 TTTTTCATCA TGCAGGAATT AATAATCATC ATACTCTAGA ATCTTGTCTG TCACTCACTA 3060  
 CATGAATAAG CAAATATTGT CTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA 3120  
 TATTTTGAAG AGTACAAAAT AATAAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT 3180  
 TCAATTTTAT TGACCTTTCA ACTATAGGTA ATAACCTTA GAGAAATTA TTTAATATTA 3240  
 GAATTTCTAT TATGAATCAT GTGAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA 3300  
 TAAATATATA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAATAT GTTGATTCAT 3360  
 GGCATATAA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420  
 CTTGAGAAAT TCATGAGCAC TTTAAATCT GAACTTCAA AGCTTGCTAT TAAATCATTT 3480  
 AGAATGTTT CATTTACTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540  
 CATAGAAAT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAAG 3600  
 TTAATGTGTT ATCTATGAGT TATCATCTTA GCTGTGTTAA AAATGAATTT TTACTATGGC 3660  
 AGATATGGTA TGGATCGTAA AATTTAAGC ACTAAAAAT TTTTATAAC CTTTATAAT 3720  
 AAGTTTAAAT AATAGTTTAA TTAAGTGAAT TTCATTAGTT TTTTAAAGT GTTTTGTGTT 3780  
 TGTGTATATA TACATATACA AATACACAT TTACAATAAA TAAATATCT GAAATCTCA 3840  
 AAAAAA AAAAAA AAAAA

Seq ID NO: 450 Protein sequence  
 Protein Accession #: NP\_003807.1

65  
70  
75  
80

1 11 21 31 41 51  
 MSGGARFPSS TLRVRWLLLL GLVGPVLGAA RFGPQQTSHL SSYEIITPWR LTRRRREAPR 60  
 PYSKQVSYVI QAEKGEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHYRGYV 120  
 EGVHNSIAL SDCEFLRGLL HLENASYGIE PLQNSHFEH ILYRMDVYK EPLKCGVSNK 180  
 DIEKETAKDE EEEPPSMTQL LRRRAVLPO TRYVELFIVV DKERYDMNGR NOTAVREEMI 240  
 LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300  
 AQLVLKKGFG GTAGMAPVGT VCSRHAGGI NVFGQITVET FASIVAHSL HNLGMHDDG 360  
 RDCSCGAGSC INNSGAGSSR NFSSCSAEDF EKLTLNKGGN CLINIPKPE AYSAPSCGNK 420  
 LVDAGEECDC GTPKECELD P CEGSTCGLK SFAECAYGDC CKDCRFLPGG TLRCRGTSEC 480  
 DVPEYCNSS QFCQPDVFIQ NGYPCQNNKA YCYNMGQYQ DAQCQVIFGS KAKAAPKDCF 540  
 IEVNSKGRDF GNCGFSNGEY KKCATGNALC GKLCQENVQE IPVFGIVPAI IQTPSRGKTC 600  
 WGVDPQLGSD VPDPMGVNEG TKCGAGKICR NFQCVDA SVL NYDCDVQKKC HGHGVCNSNK 660  
 NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFPIKIR 720  
 DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSFV TTPREVPIYA NRPVAPTYAA 780  
 KQPPQFPSPR PPPQPKVSSQ GNLIPARPA APPLYSSTLT

Seq ID NO: 451 DNA sequence  
Nucleic Acid Accession #: NM\_016650.1  
Coding sequence: 196..789

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
GGTTTCAATA TATGCAGATG TCTCGATATA GGAATGAAAT TACGTCTTTG GAACAACTTA 60
AATAAGTCAA ATATACTTGG AGCTTTTAAA ATTAAAAGGA GAGAGATTCG AGCACCTTTT 120
CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGTGTGT 180
10     CCCCAGCTGG GAAACATGGC TGTATACAT TCACATCTGT GGAAGAGATT GCAAGAGAAG 240
TTCTTGAAGG GAGAACCCTAA AGTCCTTGGG GTTGTGCAGA TTCTGACTGC CTTGATGAGC 300
CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCCCTATT 360
TCCGTGCATA TCGGGTACAC AATTGGGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG 420
TCAATTGCAG CAGGAATTAG AACTACARAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT 480
15     ATCACCAGCT CTGTACTGGC TGCATCAGGG ATCTTAATCA ACACATTTAG CTTGGCGTTT 540
TATTCATTCC ATCACCCTTA CTGTAACCTAC TATGGCAACT CAAATAATTG TCATGGGACT 600
ATGTCCATCT TAATGGGTCT GGAATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTCTGC 660
ATTGCTGTGT CCGCTCTCTG CTTTGGATGT AAAGTGCTCT GTTGTACCCC TGGTGGGGTT 720
GTGTTAAATC TGCCATCACA TTCTCACATG GCAGAAACAG CATCTCCAC ACCACTTAAT 780
20     GAGGTTTGAG GCCAACAAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
ACACAGAGAG CTCACATGAG AAATTACCAG TATCCAACTT CGATAGTGTG AGACGTGTGT 900
ATATTATTAT TATATGTAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC 960
AAAATTATGT TCTCATTTT TCCCTGGAA CTCAATACT CACTTCACTG GCTCTTTATC 1020
25     GAGAGTACTA GGAGTTAAAT TAATAAATAA TGCATTAAAT GAGGCCACAG GAAAAA

```

Seq ID NO: 452 Protein sequence  
Protein Accession #: NP\_057734.1

```

30     1      11      21      31      41      51
      |      |      |      |      |      |
MAVIHSHLWK GLQKFLKGE PKVLGVVQIL TALMSLSMGI TMMCMASNTY GSNPISVHIG 60
YTIWGSVMFI ISGSLSIAG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH 120
PYCNYVGNIN NCHGTMISLM GLDGMVLLLS VLEFCIAVSL SAFGCKVLCC TPGGVVLILP 180
35     SHSHMAETAS PTPLENEV

```

Seq ID NO: 453 DNA sequence  
Nucleic Acid Accession #: NM\_002091.1  
Coding sequence: 56..503

```

40     1      11      21      31      41      51
      |      |      |      |      |      |
AGTCTCTGCT CTTCACAGCC TCTCCGGGCG GCTCCAGGGG CTTCCCGTCC GGACCATGCG 60
CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGCTCCTC TGCTAGCGC CCGGGGGGCG 120
AGCGGTCCCG CTGCCTGGCG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
45     CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
GAATTGCTCG GGTCTCATAG AAGCAAGAGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
GGCCTTGGGC AATCAGCAGC CTTGCTGGGA TTCAGAGGAT AGCAGCAACT TCAAGATGT 420
AGGTTCAAAA GGCAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
50     CCCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAACCCCA 540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCTTGTGCA 600
AAATATTGTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
CTTCTGGTTT AAACCTGTTT GCTGTGAACA ATTGTGAAAA AGAGTCTTCC AATTAATGCT 720
55     TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAGGCCCC CGAGCTGTTA CCATTCAAA 780
TAAAGCTTA AACACAT

```

Seq ID NO: 454 Protein sequence  
Protein Accession #: NP\_002082.1

```

60     1      11      21      31      41      51
      |      |      |      |      |      |
MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTKMYPR GNHWAVGHLN GKSTGESS 60
VSEKSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPPS WDSEDSNFK 120
65     DVGSKGVKGR LSAPGSQREG RNPQLNQQ

```

Seq ID NO: 455 DNA sequence  
Nucleic Acid Accession #: NM\_016522.1  
Coding sequence: 265..1299

```

70     1      11      21      31      41      51
      |      |      |      |      |      |
GCGGAAGCAG CGAGGAGGGA GCCCCCTTTG GCGTCTCTCC GTGGAACCGG TTTTCCGAGG 60
CTGGCAAAAG CCGAGGCTGG ATTGGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGGCG 120
TTTCTCCTC CCGCGGCTCC CCGGTGCGCG CGGGTTCACC GCTCAGTCCC CGCGCTCGCT 180
75     CGCACCCCA CCCACTTCTT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG GTCTCGGAGT 240
TCGGGGAGGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
TGCCCTGCTG TCGTGTCTCT CAGGCTGCTG TTCCTGTGAC CCACAGGAGT GCCCGTGC 360
AGCGGAGATG CCACTTCCC CAAAGCTATG GACAACGTGA CGGTCCGCGA GGGGGAGAGC 420
GCCACCTCTA GGTGCACTAT TGACAACCGG GTCAACCGGG TGGCTCTGCT AAACCGCAGC 480
80     ACCATCTCTT ATGCTGGGAA TGACAAGTGG TGCTGTGATC CTCGCTGGT CTTCTGAGC 540
AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
TACACCTGCT CGGTGCAAGC AGACAACACC CCAAGACCT CTAGGCTCCA CCTCATTTG 660
CAAGTATCTC CAAAATGTG AGAGATTTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
ATTAGCTCTA CTGCATAGC AACTGGTAGA CCAGAGCTCA CGGTACTTTG GAGACACATC 780

```

5 TCTCCCAAAG CGGTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840  
 CGGGAAACAGT CAGGGGACTA CGAGTGCACT GCCTCCAATG ACCTGGCCGC GCCCGTGGTA 900  
 CGGAGAGTAA AGGTACCCGT GAACTATCCA CCATACATTT CAGAAGCCAA GGTACAGGT 960  
 GTCCCGGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020  
 TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080  
 AACAGACCTT TCCTCTCAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140  
 TACACTTGGC TGGCCTCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGTGT 1200  
 CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260  
 10 CTGCTCTTTC TGGTCTTGA CCTGCTTCTC AAATTTTGAT GTGAGTGCCA CTTCGCCACC 1320  
 CGGGAAAGGC TGCGCCACC ACCACCACCA ACACACAGC AATGGCAACA CCGACAGCAA 1380  
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTGTA 1440  
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAAATTG 1500  
 CCTTGACAGT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560  
 15 CCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGSCAAG 1620  
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CAGCTGGAAC ATTCTGGAGC TGGCCATCCC 1680  
 AAATTCAAAT AGTCTGAGC GACGAAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740  
 CCGGCCCAAG CGTGGCGCTG CCGGCACTTT GGTAGACTGT GCCACCAAGG CGTGTGTGT 1800  
 GAAACGTGAA ATAAAAAGAG CAAAAAAGAA AAAAAAAG

Seq ID NO: 456 Protein sequence

Protein Accession #: NP\_057606.1

25 1 11 21 31 41 51  
 MGVCGLFLP WKLVVLSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60  
 NRVTRVANLN RSTILYAGND KWCLDPRVVL LSNQTQYSI EIQNVDVYDE GPYTCVQTD 120  
 NHEKTSRVEL IVQVSKPIVE ISSDISINEG NNISLTCTAT GRPEPTVTWR HISPKAVGFV 180  
 SEDEYLEIQG ITRQSGDYE CSASNDVAAP VRRVKVTVN YPPYISEAKG TGVFVGQKGT 240  
 30 LQCEASAVPS AEFQWYKDDK RLIEGKKGK VNRPFPLSKL IFFNVSEHDY GNYTCVASNK 300  
 LGHTNASIML FPGAVSEVS NGTSRRAGCV WLLPLLVHLH LLKF

Seq ID NO: 457 DNA sequence

Nucleic Acid Accession #: NM\_012261.1

Coding sequence: 203..1045

35 1 11 21 31 41 51  
 GATTGTCTCT GCCAGCAGCT GTGGGTGCGG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60  
 ACAGAAATAG CGCTCCCTCC CTCCTCCCTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120  
 40 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCCGC CTCTGCAGCA GCACAGCCGG 180  
 CCTCATTCGG GGCCTGCGA GTATGGATCT CCAAGGAAGA GGGGTCCCA GCATCGACAG 240  
 ACTTCAGATT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAGAAGT 300  
 GGAATATCTC TCAGGCTTTT CCACTAACCC TGAAAAAGAT ATATTGTGG TGGGGGAAA 360  
 45 TGGGACGAGG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420  
 GGCCAGCAAC TACGTAGATC TGATCAGAGA ACAGGCCGAT ATCGCATTGA CCGGGGGAGC 480  
 TGAGGTGAGG GGCCGCTGTG GCCACAGCCA GTCCGAGCTG CAAGTGTCTT GGGTGGATCG 540  
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAGGCCAC AACATGTCCA AGGGACCTGA 600  
 GGCAGCTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660  
 50 CAAAGACGCA GTCAGTGTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCTTGGT 720  
 CACCCCGCT GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCTCTAG 780  
 TGATCCGAGG AAGACGGTCA CCATGATCCT GTCTGGGTTC CACATCCAAC CTTTGGACAT 840  
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900  
 GGAAGAAACC TTGCCCCCTG TTTTGGGGCT CATCTTGGGC CTGTCATCA TGGTAACACT 960  
 55 CGGATTTTAC CAGCTCCACC ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020  
 ATCCAGTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGTCTCC 1080  
 CCAACTGGAT CAGGTAGAAG AACAAAAGCA CTTTCCATC TTGTACAGCA GATACACCAA 1140  
 CATAGCTACA ATCAAACAGG CTTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200  
 AACCACGGA AGCGGGAGAG TCTTTGCGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260  
 60 ATGCTGGGGA GGAGGGGAGG AGGCTCTCAG ACAGCTTTCG TGCTCATGTT GCTTGGCTT 1320  
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCAA AGTTTAGGGA 1380  
 TTGAAAACAT GCTTCTTTGA GGAGGAAACC CTTTAGGTT CAGAAGAATA TGGGGTGTCT 1440  
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500  
 TCATGCTCCC TGCAGCAAGA CCCCAGAAAG TGATTATGTC TTCTGGCTGG CATTCTGCAT 1560  
 65 GTTTAGTGTAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620  
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGACTTCT TCCTGTGCCA GGTCCAAGTC 1680  
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AATGAAATA AAACACACTA 1740  
 TTCTCTGGC

Seq ID NO: 458 Protein sequence

Protein Accession #: NP\_036393.1

75 1 11 21 31 41 51  
 MDLQGRGVPS IDRLRVLLML PHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60  
 EPAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKRCRG HSQSELQVFW VDRAYALKML 120  
 FVKESHNSK GPBATWRLSK VQFVYDSEK THFKDAVSAG KHTANSHLS ALVTPACKSY 180  
 EQAQQTISL ASSDPQKTVT MILSAVHIQ FDIISDFVFS EEHKCPVDER EQLEETLPLI 240  
 LGLILGLVIM VTLAIYHVH KMTANQVQIP RDRSQYKMG

Seq ID NO: 459 DNA sequence

Nucleic Acid Accession #: NM\_001169.1

Coding sequence: 85..870

1 11 21 31 41 51

5  
10  
15  
20  
25

	TAGGAGATAA		GAGTATCTTG		CACAGCAGGT		GCAGGTTTCC		CAGCAGCTCA		GGCAAGAGTC	60
	CGATGTTTGT		GCCATCTGAT		CCTGATGTCT		GGAGAGATAG		CCATGTGTGA		GCCTGAATTT	120
	GGCAATGACA		AGGCCAGGGA		GCCGAGCGTG		GGTGGCAGGT		GGCGAGTGTC		CTGGTACGAA	180
	CGGTTTGTGC		AGCCATGTCT		GGTCGAACCTG		CTGGGCTCTG		CTCTCTTCAT		CTTCATCGGG	240
	TGCCTGTGCG		TCATTGAGAA		TGGGACGGAC		ACTGGGCTGC		TGCAGCCGCG		CCTGGCCAC	300
	GGGCTGGCTT		TGGGCTCGT		GATTGCCACG		CTGGGGAATA		TCAGTGGTGG		ACACTTCAAC	360
	CCTGCGGTGT		CCCTGGCAGC		CATGCTGATC		GGAGGCCTCA		ACCTGGTGAT		GCTCCTCCG	420
	TACTGGGTCT		CACAGCTGCT		CGGGGGGATG		CTCGGGGCTG		CCTTGGCCAA		GGTGGTGAGT	480
	CCTGAGGAGA		GGTTCTGGAA		TGCATCTGGG		CGCGCCTTTG		TGACAGTCCA		GGAGCAGGGG	540
	CAGGTGGCAG		GGGCGTGGT		GGCAGAGATC		ATCCTGACGA		CGCTGCTGGC		CCTGGCTGTA	600
	TGCATGGGTG		CCATCAATGA		GAAGACAAAG		GGCCCTCTGG		CCCGTTCCTC		CATCGGCTTT	660
	GCGTCACCG		TGGATATCCT		GGCTGGGGGG		CCTGTGTCTG		GAGGCTGCAT		GAATCCCGCC	720
	CGTGTCTTTG		GACCTGCGGT		GGTGGCCAA		CACCTGGAAC		TCCACTGGAT		CTACTGGCTG	780
	GGCCCACTCC		TGGCTGGCCT		GCTTGTGGGA		CTGCTCATTG		GGTGTTCAT		TGGAGATGGG	840
	AAGACCCGCG		TCATCTGAA		GGCTCGGTGA		GCAGAGCTCG		TGGGATTCCCT		GCTGTCCAG	900
	GTGTCTCAG		CTACCTCTGC		CCAGACTGAG		GACAGGGGAG		TTCCTGCATT		TCCTGCCAGG	960
	GCAGAGGCCC		AGAGGAGCGA		CCCCCTGCTT		CCACTGCTTG		GGCCTGCTTT		CTCAGATAGA	1020
	CTGACTGCTG		AGGAGGCTCT		AGGTTCTTGG		AATTCTTTTG		TGCTCATCAG		AGACCCACAG	1080
	CTGGGGAACA		CGCTGCCCGC		ACTGCCCAAG		GAGCAGTGCA		AACACCAACA		CACGAGCGTG	1140
	TTTCTTGAGA		GGAACTGTCC		CGAGTTGGAC		AAGGAGGCTG		TTTCTGCACA		TCAGCTCATT	1200
	TCCCGCACCC		CATTCTCTGC		TTGATTGCTT		TGTTGGGGGC		CTGGCCACTT		CCTTGTCTCT	1260
	CAAGCTGACA		ATTCTCACTT		TGCAATAAAT		AGTCCAGTGT		TTCCTTCAT			

Seq ID NO: 460 Protein sequence  
Protein Accession #: NP\_001160.1

30  
35

	1		11		21		31		41		51	
	MSGEIAMCEP		EFNGDKAREP		SVGGRWRVSW		YERFVQPCLV		ELLGSALFIF		IGCLSVIENG	60
	TDITGLIQLPAL		AHGLALGLVI		ATLGNISGGH		FNPVSLAAM		LIGGLNLVML		LPYVWSQLLG	120
	GMLGAALAKV		VSPEERFVNA		SGAAFTVQVE		OQVAGALVA		EIILTLTLLAL		AVCMGAINKEK	180
	TKGLPLAPFSI		GFATVTDILA		GGPVSGGCMN		PARAFGPAVV		ANHNWPHWIY		WLGPLLAGLL	240
	VGLLIRCFIG		DKGTRLILKA		R							

Seq ID NO: 461 DNA sequence  
Nucleic Acid Accession #: NM\_003226.1  
Coding sequence: 2..226

40  
45  
50

	1		11		21		31		41		51	
	GATGCTGGGG		CTGGTCTCGG		CCTTGTCTGC		CTCCAGCTCT		GCTGAGGAGT		ACGTGGGCCT	60
	GTCTGCAAAAC		CAGTGTGCCG		TGCCGGCCAA		GGACAGGGTG		GACTGCGGCT		ACCCCCATGT	120
	CACCCCCAAG		GAGTGCACAA		ACCGGGGCTG		CTGCTTTGAC		TCCAGGATCC		CTGGAGTGCC	180
	TTGGTGTTC		AAGCCCCCTGA		CTAGGAAGAC		AGAATGCACC		TTCTGAGGCA		CCTCCAGCTG	240
	CCCCCTGGGAT		GCAGGCTGAG		CACCCCTGCC		CGGCTGTGAT		TGCTGCCAGG		CACGTTCAT	300
	CTCAGTTTTT		CTGTCCCTTT		GCTCCCGGCA		AGCTTTCTGC		TGAAAGTTCA		TATCTGGAGC	360
	CTGATGCTT		AACGAATAAA		GGTCCCATGC		TCCACCCG					

Seq ID NO: 462 Protein sequence  
Protein Accession #: NP\_003217.1

55  
60

	1		11		21		31		41		51	
	MLGLVLALLS		SSSAEEYVGL		SANQCAVPAK		DRVDCGYPHV		TPKECNNRGC		CFDSRIPIGV	60
	WCFKPLTRKT		ECTFP									

Seq ID NO: 463 DNA sequence  
Nucleic Acid Accession #: NM\_002993.1  
Coding sequence: 64..408

65  
70  
75  
80

	1		11		21		31		41		51	
	GGCAGGAGCC		AGTCTCCGCG		CCTCCACCCA		GCTCAGGAAC		CCGGAACCC		TCTCTGACC	60
	ACTATGAGCC		TCCGTCGCG		CGCGCGGGCC		CGTGTCCCGG		GTCTTCCGGG		CTCCTTGTC	120
	GCGCTGCTCG		CGCTGCTGCT		CCTGCTGACG		CGCGCGGGG		CCCTCGCCAG		CGCTGGTCT	180
	GTCTCTGCTG		TGCTGACAGA		GCTGCGTTCG		ACTTGTTCAC		CGCTTACGCT		GAGAGTAAAC	240
	CCCAAAACGA		TTGTAAACT		GCAGGTGTTT		CCCGCAGGCC		CGCAGTGCTC		CAAGGTGSA	300
	TGGTAGCCT		CCCTGAAGAA		CGGGAAGCAA		GTTTGTCTGG		ACCCGGAAGC		CCCTTTTCTA	360
	AAGAAAGTCA		TCCAGAAAT		TTTGACAGT		GGAAACAAGA		AAACTGAGT		AACAAAAAAG	420
	ACCATGCATC		ATAAAATTGC		CCAGTCTTCA		CGGAGCAGT		TTTCTGGAGA		TCCTGGACC	480
	CAGTAAGAAT		AGAAGGAAG		GGTTGGTTTT		TTTCCATTTT		CTACATGGAT		TCCTACTTT	540
	GAAGAGTGTG		GGGGAAGCC		TACGCTTCTC		CCTGAAGTTT		ACAGCTCAGC		TAATGAAGTA	600
	CTAATATAGT		ATTTCCACTA		TTTACTGTTA		TTTACCTGA		TAAGTTATTG		AACCTTTGG	660
	CAATTGACCA		TATTGTGAGC		AAAGAAATC		TGTTTATTAG		TCTTTCAATG		AATATTGAAT	720
	TGAAGATAAC		TATTGTATTT		CTATCATACA		TTCTTAAAG		TCTTACCGAA		AAGGCTGTGG	780
	ATTTCTGATG		GAAATAATGT		TTTATTAGTG		TGCTGTTGAG		GGAGGTATCC		TGTTGTTCTT	840
	ACTCACTCTT		CTCATAAAT		AGGAAATATT		TTAGTTCTGT		TTTCTTGGGG		AATATGTTAC	900
	TCCTTACCTT		AGGATGCTAT		TTAAGTTGTA		CTGTATTAGA		ACACTGGGTG		TGTCATACCG	960
	TTATCTGTGC		AGAATATATT		TCCTTATTCA		GAATTTCTAA		AAATTTAAGT		TCTGTAAGGG	1020
	CTAATATATT		CTCTTCTCAT		GGTTTATGAT		GTTTATGTC		TCTTAGTAT		GGCATAATGT	1080
	CATGATTAC		TCATTAACT		TTGATTTTGT		ATGCTATTTT		TTCATATAG		GATGACTATA	1140

5  
ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCAAAAAACA GATAAATTCC 1200  
TGATTGCTAA TTTACATAGA AATGTATCT CTGGTTTTT TAAATAAAG CAAAATTAAAC 1260  
AATGATCTGT GCTCTGCAAA GTTTTGAAA TATATTGAA CATTGTGAAT ATAAATTCAT 1320  
CATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380  
TTTAAAGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440  
AAATTGCAT TTTATTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT 1500  
TGGAGAAACA ATAAAGATT TCTAAACCA AAAAAAAAAA AAAAAA

10  
Seq ID NO: 464 Protein sequence  
Protein Accession #: NP\_002984.1

15  
1 11 21 31 41 51  
MSLPSSRAAR VPGPSGSLCA LLALLLLTP PGPLASAGPV SAVLTELRCR CLRVTLRVNP 60  
KTIGLQVFP AGPQCSKVEV VASLKNKQV CLDPEAPFLK KVIQKILDSG NKKN

20  
Seq ID NO: 465 DNA sequence  
Nucleic Acid Accession #: NM\_002038.2  
Coding sequence: 108..500

25  
1 11 21 31 41 51  
GAACCGTTTA CTGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGGCTGAA GATTGCTTCT 60  
CTTCTCTCT CCAAGGTCTA GTGACGGAGC CCGCGCGCGG CGCCACCATG CGGCAGAGG 120  
CGGTATCGCT TTTCTTGTC TACCTGCTGC TCITCACTTG CAGTGGGGTG GAGGCAGGTA 180  
AGAAAAGTG CTGGAGAGC TCGGACAGCG GCTCCGGGTT CTGGAAGGCC CTGACCTTCA 240  
TGGCCGTCGG AGGAGGACTC GCAGTCGCGG GGCTGCCCGC GCTGGGCTTC ACCGGCGCCG 300  
GCATCGCGGC CACTCGGTG GCTGCTCGC TGATGAGCTG GTCTGCGATC CTGAATGGGG 360  
CGGGCGTGCC CGCGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA 420  
CGGTGTCAT AGGTAATATT GGTGCCCTGA TGGGCTACGC CACCCACAAG TATCTCGATA 480  
GTGAGAGGA TGAGAGTAG CACAGAGCTC CCAGAACCTC TTCTTCCTTC TTGGCTTAAC 540  
TCTTCCAGTT AGGATCTAGA ACTTTGCCCT TTTTCTTTT TTTTCTTTT TTGAGATGG 600  
GTTCTCACTA TATGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660  
ACTGCAGCT CCAACTCTTA GCCTCAAGTG ATCCTCTGT CTCAACCTCC CAGTAGGAT 720  
35 TACAAGCATG CGCGAGCAT GCCCAGAATC CAGAACTTG TCTATCACTC TCCCAACAA 780  
CCTAGATGTG AAAACAGAAT AAACCTCACC CAGAAAA

40  
Seq ID NO: 466 Protein sequence  
Protein Accession #: NP\_002029.3

45  
1 11 21 31 41 51  
MRQKAVSLFL CYLLFTCSG VEAGKKKCSE SSDSGSGFEWK ALTFMAVGGG LAVAGLPALG 60  
FTGAGIAANS VAASLMSWSA ILNNGGVPA GVLATLQSLG AGGSSVVIGN IGALMGYATH 120  
KYLDSEDEE

50  
Seq ID NO: 467 DNA sequence  
Nucleic Acid Accession #: NM\_003469.2  
Coding sequence: 92..1945

55  
1 11 21 31 41 51  
GAAACGGCCC GAGAAGCTCG CCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60  
CATATAAACA AAAAGAGGAA ATCTTTCAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG 120  
AGCAGCCCTG TCTCTATCC CTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180  
TCAGAGAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAAAAATG TCCAAAAGTT 240  
TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACCAAGCTCA 300  
TAAGGAAGAA AGCAGCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCTTCAGCA 360  
AAAAGAAAT GGCGATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420  
GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA 480  
AGAAAATAAG CCTATGCCT TGAATTGAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540  
TTATGAGACA CAGCAGTGGC CAGAAAGAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA 600  
TGAAGAGAAT TCCAGGGATA ACCCTTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660  
TACTCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG 720  
65 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTTATA CGGATGATGA 780  
AGATGATATC TACAAGGCTA ATAACTTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840  
GAACCCAGTA GAGGAGAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900  
GAATATAGGA AAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960  
CCAGGAGAA GATCTTCGGA AAGAGAGTAA AGACCACTC TCAGATGATG TCTCCAAAGT 1020  
70 AATTGCCTAT TTGAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080  
AAATGGGGA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTTATCA 1140  
GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGGAA GACTTAATTG AGATGCTCAA 1200  
AACTGGGGAG AAGCCGATG GATCAGTGA ACCGAGCGG GAGCTTGACC TTCTGTGTA 1260  
CCTAGATGAC ATCTCAGAG CTGACTTAGA CCATCCAGAC CTGTTCCAA ATAGGATGCT 1320  
75 CTCCAAGAGT GGCTACCTTA AAACACCTGG TGTGCTGGG ACTGAGGCC TACCAGACGG 1380  
GCTCAGTGT GAGAGATTT TAAATCTTT AGGGATGGAG AGTCAGCAA ATCAGAAAC 1440  
GTGTATTTT CCCATCCAT ATAACAGGA GAAAGTCTG CCAAGGCTCC CTATGCTGC 1500  
TGAAGATCT AGATCGAACC AGCTTCCCA AGCTGCTGG ATTCACATG TTGAAAACAG 1560  
ACAGATGGCA TATGAAACCC TGAACGACAA GGATCAAGAA TTAGTGAGT ACTTGGCCAG 1620  
80 GATGCTAGTT AAATACCTG AGATCATTA TTCAAACCAA GTGAAGCGAG TTCCTGGTCA 1680  
AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAAT GAGCAGGCCA TCAAGAGCA 1740  
TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC 1800  
TGTGGGGCCC CGAAGAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860  
AATGAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGAAGGG AGCATATTGC 1920

5  
10  
15  
20  
25  
TAAGAGAGCA ATGAAAAATA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCTCTC 1980  
CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTGA CTCTATCCT GTTAACACTG 2040  
TAATATCTTT AATGATGTA CAGGCAGATG AAACCAAGTC ACTGGGGAGT CTGCTTCATT 2100  
TCCTCTGAGC TGTATCTTG TGTATGGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160  
ATTTATTATG TCCATTATTG AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT 2220  
GGCTGTGGCA TTGTTGATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280  
TTTTTAATAT TTATTGAATT ATTTTGITAC TGTCTGTAGC GTTTTGTGGA GACTGAGACC 2340  
AAAAAATAA AGCATTATAA ATATA

Seq ID NO: 468 Protein sequence  
Protein Accession #: NP\_003460.1

1 11 21 31 41 51  
15  
20  
25  
MAEAKTHWLG AALSLIPLIF LISGAEAAAF QRNQLLQKEP DLRLENVQKF PSPEMIRALE 60  
YIENLRQQAH KEESSPDYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120  
AENEPSAPK ENKPYALNSE KNFPMDSDD YETQOWPERK LKHMQFPMPY EENSRLNPFK 180  
RTNEIVEBQY TPQSLATLES VPQELGKLTG PNNQKRERMD EEQKLYTDDE DDIYKANNIA 240  
YEDVVGGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQQLGI QEEDLRKESK 300  
DQLSDVSVK IAYLRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRLNLI 360  
PPEDLIEMLK TGEKNGSVSE PERELDLFVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420  
RAGTEALPDG LSVEDILNLL GMESAANQKT SYFFNPYNQE KVLPRLPYGA GRSRSNQLPK 480  
AAWIPHVENR QMAYENLMDK DQELGEYLAR MLVKYPEIIN SNQVKRVPQG GSSEDDLQEE 540  
EQIEQAIEKH LNQSSSQETD KLAPVSKRFP VGPPKNDDTP NRQYWEDELL MKVLEYLNQE 600  
KAEKGREHIA KRAMENM

Seq ID NO: 469 DNA sequence  
Nucleic Acid Accession #: NM\_006398.1  
Coding sequence: 19..516

1 11 21 31 41 51  
30  
35  
40  
45  
GGCCCCCTGT CTGCAGAGAT GGCTCCCAAT GCCTCCTGCC TCTGTGTGCA TGTCCGTTCC 60  
GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCATA 120  
GAACATGTCC GGTCTAAGAC CAAGGTTTCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180  
AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGCA TTGACAAAGA GAAGACCATC 240  
CACCTTACCC TGAAGTGGT GAAGCCCACT GATGAGGAGC TGCCCTTGT TCTTGTGGAG 300  
TCAGGTGATG AGGCAAGAG ACACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACA 360  
GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420  
AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480  
TTACTCTTCC TGGCATCTTA TTGTAATTGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540  
AGGGGTCAA AAGCTTATT CTTTAACTCT CTTACTCAAC GAACACATCT TCTGATGATT 600  
TCCCAAAAT AATGAGAATG AGATGAGTAG AGTAAGATT GGGTGGGATG GGTAGGATGA 660  
AGTATATTGC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAG TGACATGATT 720  
TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCATAATAG AGCATTTC

Seq ID NO: 470 Protein sequence  
Protein Accession #: NP\_006389.1

50  
55  
MAPNASCLCV HVRSEEWDLN TFDANPYDSV KIKIHEVRSK TKVPVQDQVL LLGSKILKPR 60  
RSLSSYGIDK ERTIHLTKV VKPSDEELPL FLVESGDEAK RHLQVRRSS SVAQVKAMIE 120  
TKTGIIPETQ IVCNGKRLE DGKMMADYGI RKNLLFLAS YCIGG

Seq ID NO: 471 DNA sequence  
Nucleic Acid Accession #: XM\_094741.1  
Coding sequence: 1..948

60  
65  
70  
75  
80  
1 11 21 31 41 51  
ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTCTCCTGCT TGGGTTTCTC GACTGGCCT 60  
TCCCTGCAGC CGGTCTCTTT CGCCTTGTC CTCTGTGCT ACCTCCTGAC CTTGACGGGC 120  
AACTCGGCGC TGGTGCTGCT GCGCGTGGC GACCGCGCC TGCAACGCC CATGTACTAC 180  
TTCTCTGCC ACCTGGCCTT GGTAGACGCG GCGTTCCTA CTAGCGTGTG GCGCGGCTG 240  
CTGGCCAACC TGCGCGGACC AGCGCTCTGG CTGCGCGCA GCACTGACG GCGCCAGCTG 300  
TGCGCATCGC TGGCTCTGGG TTGCGCGGAA TGCGTCTCTC TGGCGGTGAT GGCTCTGGAC 360  
CGCGCGCGCG CAGTGTGCGG CCGCTGCGC TATGCGGGGC TGGTCTCCCC GCGCCTATGT 420  
CGCACGCTGG CCGAGCGCTC CTGGCTAAGC GCGCTCACA ACTCGGTGCG GCAAAACGCG 480  
CTCTGGCTG AGCGGCGGCT GTGCGCGGCC CGCTGCTGG ACCACTTCAT CTGTGAGCTG 540  
CCGGCGTTGC TCAAGCTGGC CTGCGGAGGC GACGAGACA CTACCGAGAA CCAGATGTTT 600  
GCGCGCGCGC TGGTCACTCT GCTGCTGCGG TTGCGCGTCA TCCTGGCCTC CTACGGTGCC 660  
GTGCGCGGAG CTGCTGTTG CATGCGTTT AGCGGAGGCC GAGGAGGGC GGTGGGCAAG 720  
TGTTGGTCCC ACCTGACAGC CGTCTGCTGT TTCTACGGCT CCGCATCTA CACCTACCTG 780  
CAGCGCGCGC AGCGCTACAA CCGAGCAGCG GCGAAGTTCT TATCGCTCTT CTACACGCTG 840  
GTCAACCTG CTCTCAACCC GCTCATCTAC ACCCTCAGGA ATAAGAAAGT GAAGGGGGCA 900  
GCGAGGAGGC TGCTGCGGAG TCTGGGGAGA GCGCAGGCTG GCGAGTGA

Seq ID NO: 472 Protein sequence  
Protein Accession #: XP\_094741.1

1 11 21 31 41 51  
MKANYSABER FLLLGPSDWP SLQFVLFAV LLCYLLTLTG NSALVLLAVR DPLRLTPMY 60

FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSSE CVLLAVMALD 120  
 RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLDDHFICEL 180  
 PALLKLACGG DGDITENQMF AARVVILLFP FAVILASYGA VARAVCCMRP SGGRRRAVGT 240  
 CGSHLTAVCL FYGSAIYTYL QPAQRYNQAR GKFVSLFTYV VTPALNPLIY TLRNKKVKGA 300  
 ARRLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence  
 Nucleic Acid Accession #: NM\_001062.1  
 Coding sequence: 76..1380

1 11 21 31 41 51  
 GCTCTCATT CCTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60  
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT 120  
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180  
 CTAAAACCTC TGTGAAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240  
 AATGTTGTGT TGTCCCTCAA ACTTGTGTGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300  
 ATCCAACAAA TCAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCTT AATATATGAT 420  
 TACCACCTGA CTGACAAGCT AGAAAAATAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480  
 CACAATGGCA CTCCTCTGAC TAACTACTAC CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540  
 CTGTTCAATG GGAATCTCTC AACCCGCGAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600  
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CTTGGCTCTG 660  
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720  
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAT 780  
 GGTCTCATTT GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840  
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCACGGAA 900  
 ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960  
 GGAAAGACCT TCTTGGATAT TAACAAAGAC TCTTCTTGGC TCTCTGCTC AGGTAACCTC 1020  
 AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCTCG ACTCACAATC ATATATCTCC 1080  
 GTCAATTACT CTGTGAGAAAT CAATGAAACA TATTTCACCA ATGTCACTGT GCTAAATGGT 1140  
 TCTGTCTTCC TCAGTGTGAT GGAGAAAAGC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200  
 ACAATGGAGG AGCGCTCAG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260  
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320  
 GGTAGTTACG TTGTCCGCAA TGGAGAAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380  
 GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCATG TTTATTGTCC 1440  
 TTATGCTTCT TTCTTCATT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500  
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence  
 Protein Accession #: NP\_001053.1

1 11 21 31 41 51  
 MRQSHQLPLV GLLLFSPFIP QICEICEVSE ENYIRLKLPL NTMIQSNYNR GTSAVNVVLS 60  
 LKLVGIQIGT LMQKMIQKIK YNVKSLSDV SSGELALIL ALGVCRNAEE NLIYDYHLTD 120  
 KLENKQAEI ENMEAHNGTP LTNYQLSLD VLALCLFNNG YSTAEVVNHF TPENKYYFPG 180  
 SQPSVDTGAM AVIALTCTVKK SLINGQIKAD ESSLKINISY TKSLEVKILS EKKENGLIGN 240  
 TFSSTGEAMQ LFVSSDYNE MDWNCQQLN TVLTEISQGA FSNPNAAQV LPALMGKTFL 300  
 DINKDSSCVS ASGNFNISAD EPITVTPPDS QSYISVNVSV RINETYFTNV TVLNGSVFLS 360  
 VMEKAQMDND TIFGPTMEER SWGPYITCIQ GLCANNDRT YWELLSGSEP LSQGAGSYVV 420  
 RNGENLEVRW SKY

Seq ID NO: 475 DNA sequence  
 Nucleic Acid Accession #: NM\_004852.1  
 Coding sequence: 89..1546

1 11 21 31 41 51  
 GCCCCCGCCC GCCCCGGGCC CTGATGGACT GAATGAAGGC TGCCTACACC GCCTATCGAT 60  
 GCCTCACCAA AGACCTAGAA CGTGGCCAT GAACCCGGAG CTGACAATGG AAAGTCTGGG 120  
 CACTTTGACG GCGCGCGCGG GCGGCGGCGG TGGCGGGGGG GCGGCGGGGG GCGGCGGGGG 180  
 GCGGCGGGGG GCGGCGGGGG ATGAGCAGGA GCTGCTGGCC AGCCCCAGCC CCCACCAAGC 240  
 GCGGCGGGGG GCGGCTGGCT CGCTGCGGGG CCTCCGCGG CCTCCAACCG CGCACCAGGA 300  
 GCTGGGCAGG GCGGCGGCGG CGGCAGCGGC GCGGTGCGGC TCGGCATGG TCACCAGCAT 360  
 GGCCTCGATC CTGGAACGCG GCGACTACCG GCCCGAGCTC TCCATCCCGC TGCACCAAGC 420  
 CATGAGCATG TCTCGGACT CGTCTCGGCC TGGCATGGGC ATGAGCAACA CCTACACCA 480  
 GCTGACACCG CTCACCGCGG TGCCACCCAT CTCCACCGTG TCTGACAAGT TCCACCAACC 540  
 TCACCCGCGC CACCATCCCG ACCACCAACA CCACCAACAC CACAGCGCGG TGTCCGGCAA 600  
 CGTCAGCGGC AGCTTCACCC TCATGCGCGA CGAGCGCGGG CTCGCGGCCA TGAACAACCT 660  
 CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC CTGTCCCGCG TGGCGCCAC 720  
 GCGGCTGGGC AACCGGGTAG GCGGCTCCA CAACGCGCAG CAGAGTCTGC CCAACTACGG 780  
 TCGGCGGGGG CAGCAACAAA TGCTCAGCCC CAACTTCGAG GCGCACCACA CTGCCATGCT 840  
 GACCGCGGGT GAGCAACACC TGTCGCGCGG CCTGGGCACC CCACCTGCGG CCATGATGTC 900  
 GCACCTGAAC GGCCTGCACC ACCCGGGCCA CACTCAGTCT CAGCGGCGGG TGCTGGCACC 960  
 CAGTGGGAGG CGGCCACCTT CGTCTCATC GGGCTCGCAG GTGGCCACGT CGSGCCAGCT 1020  
 GGAAGAAATC AACACCAAG AGGTGGCCCA GCGCATCACA GCGGAGCTGA AGCGCTACAG 1080  
 TATCCCCCAG GCGACTTTTG CGCAGAGGGT GCTGTGCGGG TCTCAGGGGA CTCTCTCGA 1140  
 CTTGCTCGGG AATCCAAAAC CGTGGAGTAA ACTCAAATCT GGCAGGGAGA CTTCCGCGAG 1200  
 GATGTGGAAG TGGCTTCAGG AGCCCGAGTT CCAGCGCATG TCGGCTTAC GCTGGCAGC 1260  
 GTGAAACGCG AAGAGCAAG AACCAACAA AGACAGGAAC AATTCACAGA AGAAGTCCCG 1320  
 CCGTGTGTTT ACTGACCTCC AACCCGGAAC ACTCTTGGC ATCTTCAAGG AGAACAACCG 1380  
 CCGTCAAGG GAGATGAGA TCACCATTC CCAGCAGCTG GGCCTGGAGC TCAACACCGT 1440  
 CAGCAACTTC TTCATGAAG CCCGGCGCGG CAGCCTGGAG AAGTGGCAAG ACGATCTGAG 1500



CACAGGGGGC TCCTCGTCCA CCTCCAGCAC GTGTACAAA GCATGATGGA AGGACTCTCA 1560  
 CTTGGGCACA AGTCACCTCC AAATGAGGAC AACAGATACC AAAAGAAAC AAAGGAAAAA 1620  
 GACACCGGAT TCCTAGCTGG GCCCTTCAC TGGTG

5 Seq ID NO: 476 Protein sequence  
 Protein Accession #: NP\_004843.1

1 11 21 31 41 51  
 10 MNPELTMESL GTLHGARGGG SGGGGGGGGG GGGGGPGHEQ ELLASPSPHH ARRGRGSLR 60  
 GPPPPPTAHQ ELGTAAGAAA AASRSAMVTS MASILDGGDY RPELSIPLHH AMSMCDSSP 120  
 PGMGMSNTYT TLTPQLPLPP ISTVSDKFHH PHPHHHPHHH HHHHHQRLSG NVSGSFTLMR 180  
 DERGLPAMNN LYSYKEMPG MSQSLSPPLAA TPLNGLGLL HNAQQSLPNY GPPGHDKMLS 240  
 15 PNFDAAHTAM LTRGEQHLNR GLGTPPAAMM SHLNLGHPG HTQSHGPVLA PSRERPPSSS 300  
 SGSQVATSGQ LEEINTKEVA QRITAEKRY SIPOAIFAQR VLCSRQGLTS DLLRNPKPWS 360  
 KLKSGRETFR RMWKWLQEPF FORMSALRLA ACKRKEQEPN KDRNNSQKKS RLVTDLQRR 420  
 TLFALPKENK RPSKEMQITI SSQLGLELTT VSNFFMNARR RSLKRWQDDL STGSSSTSS 480  
 TCTKA

20 Seq ID NO: 477 DNA sequence  
 Nucleic Acid Accession #: NM\_013271.1  
 Coding sequence: 27..809

25 1 11 21 31 41 51  
 TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60  
 CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCCT GTTTCGGCCG CCCCOCGCGC 120  
 TCTGCGCGCG CGCGGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGCGTG 180  
 30 AGACTGGCGC TCTCGCCGCG TTCGCGCGGT CAGTGCCCCG AGGTGAGGCG GCGGGGGCGG 240  
 TGCAGGAGCT GCGCGGGGCG CTGGCGCATC TGCTGAGGCG CGAACGTCAG GAGCGGGCGC 300  
 GGGCGGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360  
 TCTGGGGCGC CCCCAGCAAC TCTGATCCGG CTCTGGGCTT GGACGACGAC CCGCAGCGCG 420  
 CTGAGCGGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCCCTGCC GCCCTAGCAG 480  
 35 CCCAGCTTGT CCCCAGCGCC GTCCCCGCGC CGCGCGTCCG ACCCCGGGCC CCGGTCTACG 540  
 ACGACGGGCT CCGCGGGGCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600  
 CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGCG AAGCGCGGAC TCCGAGGGGG 660  
 TGGAGCCCC CGCCCGCCTC CGCCGTGCGC CGACCAACGA TGTGGGCTCT GAGCTGCCCC 720  
 CTGAGGGGCT GCTGGGGGCG CTGCTGCGTG TGAAACCGCT AGAGACCCCG GCGCCCCAGG 780  
 40 TGCTCTGACG CGCCCTCTTG CCACCTGAGC CACTGCCCCG ATCCCGTGCA CCCTGGGACC 840  
 CAGAAGTCCC CGCCCATCCG CGCCACGAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900  
 TTACCCCGGC CAGCCAGCCC TCTACCCGGA GGATCCCTAC CCCCCTGGCC ACAAATACAT 960  
 GATCTGAGC

45 Seq ID NO: 478 Protein sequence  
 Protein Accession #: NP\_037403.1

1 11 21 31 41 51  
 50 MAGSPLLWGP RAGGVGLVLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60  
 RSVPRGEAAG AVQELARALA HLEAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD 120  
 PALGLDDDDP APAQLARAL LRARLDPAAL AAQLVPAPVP AAALRPRPVV YDDGPAGPDA 180  
 EEAGDETPIV DPPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSSEL PPEGVLGALL 240  
 RVKRLTPAP QVPARLLLP

55 Seq ID NO: 479 DNA sequence  
 Nucleic Acid Accession #: NM\_002214  
 Coding sequence: 681..2990

60 1 11 21 31 41 51  
 CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCTTGCC AGCCAGGACG 60  
 CTGCGGACTT GTCTTTGCCG GCTGCTCGCG AGACGGGGCT GCAAAGCTGC AACTAATGGT 120  
 GTTGGCTCCG CTGCCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180  
 65 TCCCCTGACG CTGCGCGGCG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240  
 TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300  
 CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT 360  
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCGGGGCCCT 420  
 TGGCCGTGGA AGGAGGTGCT TCTGCGGAG ACCGCGGAC CCGCGGTGCC GAGCCGGGAG 480  
 70 GGCCGTAGGG GCCCTGAGAT GCGGAGCGGT GCGCGGGGCC GCTTACCTGC ACCGCTTGT 540  
 CGAGCGCGCG GGGTCCGCT GCTAGGCGCT CGGAAAAGT CCTAGCGACA CTGCCCCGCG 600  
 GGCCCGGAGG TGSCCGGGA GGCCGAGCCC GCGTCCGAA GGCAGCCAGG CCGCGGGGCG 660  
 GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITACC GCTGCATTG 720  
 TCTGCTGCA AAACGACCG CGAGGTCCCG CCTCGTTCCT CTGGGCAGCC TGGGTGTTTT 780  
 75 CACTTGTCTT TGACTGGGCG CAGGCTGAAG ACAATAGATG TGATCTTCA AATGCAGCAT 840  
 CCTGTGCGAG GTGCTTGGCG CTGGGTCCAG AATGTGATG GTGTGTTCAA GAGGATTTC 900  
 TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTAATA AGCAAAGGCT 960  
 GCTCAGTTGA TTCAATAGAA TACCATCTG TGCTGTTAT AATACCCACT GAAATGAAA 1020  
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT CGCTCCAGGA GCGGAAGCTA 1080  
 80 ATTTTATGCT GAAAGTTTAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140  
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTGGA AACGATTAT 1200  
 CTAGAAAAT GGCATTTTTC TCCCGTGACT TTCGTCTGG ATTTGGCTCA TACGTTGATA 1260  
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCACTGACT 1320  
 ACAAATTAGA CTGATGCTCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAA 1380  
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440

5 AAGGAGGTTT TGACGCCATG CTTGAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACACGCTCT 1620  
 ACGTCAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680  
 ACACACAT TAATGTCATC TTGTCAGTTC AAGGAAAAACA ATTTTCATTG TATAAGGATC 1740  
 TTCTACCCCT CTGCGCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800  
 ATAATTGGT AGTGGAGGCC TATCAGAAGC TCATTTTCAGA AGTGAAGATT CAGGTGGAAA 1860  
 ACCAGGTACA AGGCATCTAT TTAAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920  
 10 CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTCTTTTC AATGTAACAG 1980  
 TTCAATGAA AAAATGTGAT GTCAACAGGAG GAAAAAATA TGCAATATC AAACCTATTG 2040  
 GTTTTAATG AACCGCTAAA ATTCATATAC ACAGAACTG CAGCTGTGAG TGTGAGGACA 2100  
 ACAGAGACC TAAAGGAAAG TGTGTAGATG AAATTTTCT AGATTCCAAG TGTTTCCAGT 2160  
 GTGATGAGAA TAAATGTCAAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220  
 15 ACAAGGATCA GCCTGTTTGC AGTGTGCGAG GAGTTTGTGT TTGTGGGAAA TGTTTATGTC 2280  
 ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACCTGTA AAAGGATGAC TTTTCTTGTC 2340  
 CATATACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGT TGGGAAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAA AGGCCAAGT TGCAGTGGAA GAGGCACGTG TGTGTGTTGA AGGTGTGAGT 2520  
 20 GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580  
 GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTGTGCT CAGGCTATAC 2640  
 TTGATCAGTG CAAACCTCAA TGTGCTCTCA TGGAAACACA CATTATGTC GACCAAACTT 2700  
 CAGAATGTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760  
 TCTTGTGAG GTTGTCTTAA GTCCCTGATCA TTAGACAGGT GATACTACAA TGGAAATGTA 2820  
 25 ATAAATTTAA GTCCCTATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATTC 2880  
 TGCAAAAGTG TTGCACAGA GCAGTCACCT ACOGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATACAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATT 3000  
 TTAACACTT AATGGGAAAC TGGAAATGTT AATAATGCT CCTAAGATT ATAATTTTAA 3060  
 AAGTCAAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTGT ACACCTGAAC 3120  
 30 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGCTGTGA GCATTCTACT GTAATATATA 3240  
 ACTTATTAG CTACAGATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAG 3300  
 TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTT AGCATTGTGT 3360  
 CACTACAGG GTACAGTAT CCCTGCACGT GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 35 TATATTCTAA GGTGTCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT GATTGCTGTT TCACTCTTTC AAGAGGTGAA CAGATACAA CTTAATCTTA 3540  
 AAAGATTATT GCTTTTAAAG GTGTGTAGTT TTATGATGTT GTGTTTATGG TTTGCTTATT 3600  
 TTTGCAAGT GGATACTAAT TCCAGCATTC TCTCCTCTT GCCTTTATGT TTTGTTTTCT 3660  
 TTTTACAGG ATTAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 40 TACTGCCATA AAAAATAAT AATACATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780  
 GAATGTTAA

Seq ID NO: 480 Protein sequence  
Protein Accession #: NP\_002205

45 1 11 21 31 41 51  
 | | | | |  
 MCGSALAFFT AAFVCLQNDR RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60  
 LGPECGWCVQ EDPISSGSR ECDIVENLI SKGCSVDSIE YPSVHVLIPT ENEINTQVPT 120  
 50 GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLSVSG NDLSRKMAFP 180  
 SRDFRLPGS YVDKTVSPYI SIHFERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240  
 VHRQKISGNI DTEPGGFDM LQAAVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300  
 VPNDGNCBLK NNYYVKSTTM EHPSLQGLSE KLIDNNINVI FAVQGGKQFW YKDLLPLLP 360  
 TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPMGEGR 420  
 55 NVTSNDEVLF NVVTMMKKCD VTGGKNYAI KPIGFNETAK IHIHRNCSQ CEDNRGPKGK 480  
 CVDETFLDSK CFQCDENKCH FDEQDFSES CKSHKDQPV C SGRGVCVCGK CSCHKIKLGK 540  
 VYKGYKISNI DTEPGGFDM LQAAVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300  
 CSRGTCVCG RCCECTDPSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660  
 CALMEQOHV DQTECEFSF SYLRIFFIIF IVTFILGLLK VLIIRVILV WNSNRIKSSS 720  
 60 DYRVASASKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETPRNF

Seq ID NO: 481 DNA sequence  
Nucleic Acid Accession #: NM\_003318.1  
Coding sequence: 1..2574

65 1 11 21 31 41 51  
 | | | | |  
 ATGGAATCCG AGGATTAAAG TGGCAGAGAA TTGCAATTG ATTCATAAT GAACAAAGTG 60  
 AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACTAAG CTTGAATAAA 120  
 70 ATTTCTGCTG ATACTACAGA TAACCTCGGA ACTGTTAACC AAATATGAT GATGGCAAC 180  
 AACCCAGAGG ACTGGTTGAG TTTGTTGCTC AAACCTAGAG AAAACAGTGT TCCGCTAAGT 240  
 GATGCTCTTT TAAATAAATT GATTGGTCTG TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300  
 GATAAATATG GCCAAAATGA GAGTTTGTCT AGAATTCAAG TGAGATTGCG TGAATTAATA 360  
 GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAACCTCAAG 420  
 75 AAATTGCTT TTGTTTATAT ATCTTTTGCA CAATTGGAAC TGTCACAAGG TAATGTCAAA 480  
 AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCACT AGAAATGCTG 540  
 GAAATTGCCC TCCGGAATTT AAACCTCCAA AAAAAGCAGC TGCTTTTACA GGAGGAAAG 600  
 AAGAATTTAT CAGCATCTAC GGTATTAACT GCCCAAGAAAT CATTTTCCGG TTCACTTGGG 660  
 CATTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT 720  
 80 TTATATGGAG AGAACATGCC ACCACAAGAT GCAGAAATAG GTTACCGGAA TTCAATTGAGA 780  
 CAACTAACA AACTAACAAC GTCAATGCCA TTTGGAAGAG TCCCAAGTAA CCTTCTAAT 840  
 AGCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTGTTTATG GAAAGACAA 900  
 ACCTCTAGAT CAGAAATGCC AGATTGTGTT GTGCCCTGAT CTAACCAAG TGAATATGAT 960  
 TCCGTGTAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGT 1020  
 TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCTGAA GAATAAAGC 1080

5  
10  
15  
20  
25

GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTCCA 1140  
GAGAGTAACC AGAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGATTATA CCAGAATCCT 1200  
GCTGCATCTT CAAATCACTG GCAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG 1260  
AAACATACCA CTTTGTAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA 1320  
ACATCTAAAT GGTGTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT 1380  
GATTACATGA GCTGTTTAG AACTCCAGTT GTAAAGAATG ACITTCACC TGCTGTGTCAG 1440  
TTGTCAACAC CTTATGGCCA ACCTGCCTGT TTCCAGCAGC AACAGCATCA AATACCTGCC 1500  
ACTCCACTTC AAAATTACA GGTTTTAGCA TCTTCTTCAG CAAATGAATG CATTTCGGTT 1560  
AAAGGAAGAA TTTATTCAT TTTAAAGCAG ATAGGAAGTG GAGGTTCAAG CAAGGTATTT 1620  
CAGGTGTATA ATGAAAGAA ACAGATATAT GCTATAAAAT ATGTGAACCT AGAAGAAGCA 1680  
GATAACCAAA CTCCTGTATG TTACCGGAAC GAAATAGCTT ATTTGAATAA ACTACAACAA 1740  
CACAGTGATA AGATCATCOG ACTTTATGAT TATGAAATCA CGGACCACTA CATCTACATG 1800  
GTAATGGAGT GTGGAATAT TGATCTTAAT AGTTGGCTTA AAAAGAAAAA ATCCATTGAT 1860  
CCATGGGAAC GCAAGAGTTA CTGGAATAAT ATGTTAGAGG CAGTTTCACAC AATCCATCAA 1920  
CATGGCATTG TTTACAGTGA TCTTAAACCA GCTAACTTTC TGATAGTTGA TGGAAATGCTA 1980  
AAGCTAATTG ATCTTGGGAT TGCAAAACCA ATGCAACCAAG ATACAACCAAG TGTGTTTAA 2040  
GATTCTCAGG TTGGCAGAGT TAATTATATG CCACAGAAAG CAATCAAGA TATGCTCTCC 2100  
TCCAGAGAGA ATGGSAATAT TAAGTCAAAG ATAAGCCCCA AAAGTATGT TTGTCCTTA 2160  
GGATGTATTT TGTAATATAT GACTTACGGG AAAACACCAT TTCAGCAGAT AATTAATCAG 2220  
ATTTCTAAAT TACATGCCAT AATTGATCCT AATCATGAAA TTGAATTTCC CGATATTCCA 2280  
GAGAAAGATC TTCAAGATGT GTTAAAGTGT TGTATAAAA GGGACCCAAA ACAGAGGATA 2340  
TCCATTCTCG AGCTCCTGCC TCATCCCTAT GTTCAAATTC AAACCTCATCC AGTTAACCAA 2400  
ATGGCCAAAG GAACCAATGA AGAAATGAAA TATGTTCTGG GCCAATCTGT TGGTCTGAAT 2460  
TCTCTAACT CCATTTTGAA AGCTGCTAAA ACCTTATATG AACACTATAG TGGTGGTGAA 2520  
AGTCATAATT CTTTATCCTC CAAGACTTTT GAAAAAATAA GGGGAAAAAA ATGA

Seq ID NO: 482 Protein sequence  
Protein Accession #: NP\_003309.1

30  
35  
40  
45

1 11 21 31 41 51  
MESDLSGRE LTIDSIMNKV RDIKNKFKNE DLTDELSLNK ISADTTDMSG TVNQIMMMAN 60  
NPEDWLSLLL KLEKNSVPLS DALLNKLIGR YSQAIKALPP DKYQNESFA RIQVRFAELK 120  
AIQEPDDARD YFQMARANCK KFAFVHISFA QFELSQGNVK KSKQLLQKAV ERGAVPLEML 180  
ETALRNLMQ KQQLLSEEEK KNLSASTVLT AQESFSGSLG HLQNRNNSCD SRGQTTKARF 240  
LYGENMPQD AEIGYRNSLR QTNKTKQSCP FGRVFNLLN SPDCDVKTDD SVVPCFMKRG 300  
TSRSECRDLV VPGSKPSGND SCLEARNLKSQ QNSHFKEPLV SDEKSSSELI TDSITLKNKT 360  
ESSLLAKLEE TKEYQPEVP ESNQKQWQSK RKSECIQNP AASNHWQIP ELARKVNTQ 420  
KHTTFEPVP TSKSQSPPI TSKWFDPKSI CKTPSSNTLD DYMSCFRTPV VKNDFPFACQ 480  
LSTPYGPAC FQQQHQHILA TPLQNLQVLA SSSANECISV KGRISYILKQ IGSOGSSKVF 540  
QVLNEKQIY AIKYVNLLEA DNQTLDSYRN EIAYLNLKQ HSDKIIRLYD YEITDQYIYM 600  
VMECCNDLNL SWLKKKKSID PWERKSYWKN MLEAVHTIHQ HGIVHSDLPK ANPLIVDGM 660  
KLIDFGIANQ MQPDTTSUVK DSQVGTVMY PPEAIKDMSS SRENGKSKSK ISPKSDVWML 720  
GCILYYMTYG KTFPQQIINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLKC CLKRDPKQRI 780  
SIPPELLAHFY VQIQTHPVNQ MAKGTTEEMK YVLGQLVGLN SPNSILKAAK TLYEHYSGGE 840  
SHNSSSSKTF EKIIRGK

Seq ID NO: 483 DNA sequence  
Nucleic Acid Accession #: NM\_003667.1  
Coding sequence: 1..2651

50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
ATGGACACCT CCGGGCTCGG TGTGCTCCTG TCCTTGCTCG TGCTGCTGCA GCTGGCGACC 60  
GGGGGACGCT CTCGCCAGGT TGGTGTGTTG CTGAGGGGCT GCCCCACACA CTGTCATTGC 120  
GAGGCCGACG CTCAGGATGT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTGGGAGCTG 180  
CCTTCAACCA TCAGCTCTCT CACCTCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240  
CTGCTCCGCA ATCCCTCGCC CAGTCTCCG TTCTGGAGG AGTTACGTCT TCGCGGAAAC 300  
GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG 360  
CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAATTT GCGAGGCCTT 420  
CAATCCCTTC CTCTGGATGC TAACCAATC AGCTATGTGC CCCCAGCTG TTTCACTGGC 480  
CTGCATTCCC TGAGGCCACCT GTGGCTGGAT GACATGCGT TAACAGAAAT CCCCCTCCAG 540  
GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC 600  
ATACCAACT ATGCTTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAA 660  
AGAATCCACT CCGTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT 720  
TTAAATTACA ATAACCTTGA TGAATTCCTT ACTGCAATTA GGACACTCTC CAACCTTAAA 780  
GAACCTACT TCTATGACAA TCCCATCCAA TTGTTGGGA GATCTGCTTT TCAACATTTA 840  
CCTGAACATA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA 900  
ACTGGAAGTG CAAACCTGGA GAGTCTGACT TTAACCTGAG CACAGATCTC ATCTCTTCT 960  
CAACCCGCTC GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA 1020  
GAGACTTTAC CAGATTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT 1080  
GAACTCTAGG AAATTAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT 1140  
TTGGCTTGGG ACAAAATTGC TATTATTCAC CCAATGCAT TTTCACATT GCCATCCCTA 1200  
ATAAGCTGG ACCTATCGTC CAACCTCTG TCGTCTTTTC CTATACTGG GTTACATGGT 1260  
TTAACTCACT TAAATTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC 1320  
TTCCAGAGT TCAAGGTTAT AGAAATGCCT TATGCTTACC AGTGCTGTGC ATTTGGAGTG 1380  
TGTGAGATG CCTATAAGAT TTCTAATCAA TGAATAAAG GTGACAAACAG CAGTATGGAC 1440  
GACCTTCTAG AGAAAGATGC TGGAAATGTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT 1500  
TTCTTGCTTG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCACTG TTCACCTTCC 1560  
CCAGGCCCTC TCAAACTCTG TGAACACCTG CTGTATGGCT GGCTGATCAG AATTGGAGTG 1620  
TGAACCATAG CAGTCTCTGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA 1680  
TCCCCTCTGT ACATTTCCCC CATTAACCTG TTAATGGGG TCATGCGAGC AGTGAACATG 1740  
CTCAGGGGAG TCTCCAGTGC CGTGCTGGCT GGTGTGGATG CGTTCACTTT TGGCAGCTTT 1800  
GCACGACATG GTGCCCTGGT GGAGAAATGG GTTGGTTGCC ATGTCACTGG TTTTGTGTC 1860

5  
 10  
 15

```

ATTTTGTGCT CAGAATCATC TGTTCCTCTG CTTACTCTGG CAGCCCTGGA GCGTGGGTTT 1920
TCTGTGAAAT ATTCGTGAAA ATTTGAAACG AAAGCTCCAT TTCTAGCCT GAAAGTAATC 1980
ATTTTGTGCT GTGCCCTGCT GGCCTTGACC ATGGCCGCGAG TTCCCTGCT GGGTGGCAGC 2040
AAGTATGGCG CCTCCCTCT CTGCCCTGCT TTGCCCTTTG GGGAGCCGAG CACCATGGGC 2100
TACATGGTCG CTCTCATCTT GCTCAATTC CTTTGCTTCC TCATGATGAC CATTGCCTAC 2160
ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTGGGA CTGCTCTATG 2220
GTAAACACA TTGCCCTGTT GCTCTTACC AACTGCATCC TAAACTGCC TTGTGGCTTC 2280
TGTCTCTCT CTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC 2340
CTTCTGGTGG TAGTCCCACT TCCTGCATGT CTCATCCCC TTCTCTACAT CTGTGTCAAT 2400
CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAA CCTACGCTG GACAAGATCA 2460
AAACACCCAA GCTTGATGTC AATTAACCTT GATGATGTCG AAAACAGTC CTGTGACTCA 2520
ACTCAAGCTT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCCAGTTCC 2580
GTGCCATCAC CAGCTTATCC AGTGACTGAG AGCTGCCATC TTTCTCTGT GGCATTGTTC 2640
CCATGTCTTA A
  
```

Seq ID NO: 484 Protein sequence  
 Protein Accession #: NP\_003658.1

20  
 25  
 30  
 35

```

1 11 21 31 41 51
MDTSRLGVLL SLFVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
PSNLSVFTSY LDLSMNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGF TGLVSLKVLN 120
LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVFPSCFSG LHSRLHLWLD DNALTEIPVQ 180
AFRSLSLAQA MTLALNKIHH IPDYAFGNLS SLVVHLHLNN RIHSLGKKCF DGLHSLLETD 240
LNNYMLDEFP TAJRTLSNLK ELHFYDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEPPDL 300
TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSFSVQC KLQKIDLRHN 360
EIYEIKVDTF QQLSLRSLSN LAWNKIAIIR PNAFSTLPSL IKLDLSSNLL SSFPITGLHG 420
LTHLKLTKNH ALQSLISSEN FPELKVIE MP YAYQCCAFV CENAYKISN WNKGDNSMD 480
DLHKDAGMF QAQDERDLED FLDFEEDLK ALHSVQCSPS PQPKPCEHL LDGWLIRIGV 540
WTIAVLALTC NALVTSVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDATFGSF 600
ARHGAWWENG VGCNVIGFLS IFASESSVFL LTLAALERGF SVKYSKAFET KAPFSSLRVI 660
ILLCALLALT MAAPVILGGS KYGASPLCLP LPFGEPSTMG YMVALLILNS LCFMLMTIAY 720
TKLYCNLDKG DLENIWDCSM VKHIALLLFT NCILNCPVAF LSFSSLINLT FISPEVIKFI 780
LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DVEKQSCDS 840
TQALVFTTSS SITYDLPPSS VSPAYPVTE SCHLSSVAFV PCL
  
```

Seq ID NO: 485 DNA sequence  
 Nucleic Acid Accession #: NM\_005756.1  
 Coding sequence: 73..3117

40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

1 11 21 31 41 51
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
CTCGCGGTCA GGATGGTTTT CTCTGTGAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTACTGTA CGTTCAAGAT ATTCCTGTGC ATCATTGTGC TTCATGTGCT TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATCCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
GTCACTTTTG CCCCCTCTCT CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
AGCTTACTCC CTTCAACGCA AACAGAAAA ACTAAATCA CTATAGTAAA AACCTTCAT 360
GCTTCAGGCG TCAAAACCCCA GAGAAATATC TGCAATTTGT CATCTATTG CAATGACTCA 420
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATARAAG AAAGCACTGT TCCCCAGAAT 480
CAACATATAA CGAATGGCAC CTTAAGTGA GTCTGTCTCT TAAGTAATT AAAACGCTCA 540
GAGCTCAACA AAACCTGCA AACCCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCCAAA GCACATTAAA TTGTACATT ACAATAAAC TGAATAATC AATGAATGCA 660
TGTGCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
TCTGTGAGGA TACCTTGCCC TTCTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGCTGTGCT TGCTGACCAT CCACTGGGCC CACCATTTTC TTCCAGCCAA 840
TCCATCCGAG TGGTGCCTCG GGCCACTGTG CTTTCCGAG TCCCCAAGC TACCTCTTTT 900
GCTGAGCCTC CAGATTATT ACCTGTGACC CACAATGTT CCTCTCCAAT AGGGAGATT 960
CAACCCCTTT CACCCAGGCC TTCAGTCCC ATAGCTTCCA GCCTGCCAT TGACATGCC 1020
CCACAGTCTG AAACGATCTC TTCCCTATG CCCCACACCC ATGCTCTCGG CACCCACCT 1080
CCTGTGAAAG CCTCATTTTC CTCTCCACC GTGTCTGCC CTGCGAATGT CAACACTACC 1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTCTGA TCTTGAGAAC 1200
CAAGTGTTCG AGATGGAGAA GGCTCTGTCC TTGGGAGGCC TGGAGCTAA CCTGCGAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCGCCGC CTGACATGCT GGCCCTCTG 1320
GCTCAAGAT TGCTGAAAGT AGTGGATGAC ATTTGGCTAC AGCTGAACCT TTCAAACAG 1380
ACTATAATTC TAACCTCCCC TTCTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCGTCAAATC TTCAGTTTC TCTGGAAC 1500
CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCTT CATGCTGAT GAATAATTTA 1560
CCAGCTCATG ACATGAGCT AGCTTCCAG GTTCAGTTCA ATTTTGTGA AACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680
GTGCAAAACC TGACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
AACCCGAGCC AGGATGAGT AACAGTGAGA TGTGATTTT GGGACTTGGG CAGAAATGGT 1800
GGCAGAGGAG CTTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAC 1860
ATCTGTACCT GTAGCCATCT AACAAAGCTC GGCGTTCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCTG CTCAATGAT GGCTCTGAGC TTCATTACAT ATATTGGTTG TGGCTTTTCA 1980
TCAATTTTTC TCTCAGTGC TCTGTAAACC TACATAGCTT TTGAAAGAT CGGAGGGGAT 2040
TACCTTCCA AATCTCTAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CTGTGCTTTC 2100
CTCCTGAGCT CAGTATTTG TCTGTATAAG ATGCAAGGCC TCTGATCTC AGTGGCTGTA 2160
TTTCTTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCCTAGAAGC ATTCCATATG 2220
TACCTGGCCC TTGTCAAAGT ATTTAACTACT TACATCCGAA AATACATCCT TAAATCTGTC 2280
ATTGTGCGTT GGGGGGTACC AGCTGTGTT GTGACCATCA TCTGACTACT ATCCCCAGAT 2340
AATCTGGGCG TTGATCCTA TGGGAAATTC CCAATGGTT CACCGAGTGA CTTCTGCTGG 2400
ATCAACACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTGT 2460
CTGAACGTCA GCATGTTTCA TTGTGCTCTG GTTCAGCTCT GTCGAATTAA AAAGAAGAAG 2520
  
```

5  
10  
15  
20  
25  
30  
35

CAACTGGGAG CCCAGCGAAA AACCACTATT CAAGACCTCA GGAGTATGCG TGGCCTTACA 2580  
TTTTACTTGG GAATAACTTG GGGCTTTGCC TTCTTTGCC TGGGACCACT TAACGTGACC 2640  
TTCACTGATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700  
TGTGTGGCCA AAGAAATGT CAGGAAGCAA TGGAGCGGCT ATCTTTGTGT TGGAAAGTTA 2760  
CGGCTGGCTG AAAATTTCTGA CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT 2820  
GTAAACCAAG GAGTGTCCAG CTCTTCAAAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC 2880  
TCCACCACAC TGCTAGTGAA TAATGATTGC TCAGTACACG CAAGCGGGAA TGGAAATGCT 2940  
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAAATG GAGATGTGTG CCTTCACGAT 3000  
TTCAGTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT 3060  
ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTG 3120  
CTTTCTTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180  
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240  
AAGCTAATTA AGGCGCATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300  
TTTAGACATT TCTGATTGGG TTTCTTATCT TTCAATTTAT AAGAAGGTGT GTTTTAAACA 3360  
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420  
TTTAAAGAGG CTAACTTATC TTTGATAACA TCATATAAAG CAACCTGTGA CTTCAGCCTG 3480  
TTGGTGAAGT TAGTGTGACA TGCCCTTTGT GTATATAAGC TAAATCTAG TGACCCATGT 3540  
GTCAAAATC TTACTTCTAC ATTTTITGT ATTTATTTTC TACTGTGTAA ATGTATTCTT 3600  
TTGTAGAATC ATGGTTGTTT TGTCTCACGT GATAATTCAG AAAATCCTTG CTCGTTCCGC 3660  
AAATCTCTAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720  
TCAAGAAATA ATGATCCAGC CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTTAGC 3780  
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840  
TGGGTCTATG TTTGCAAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900  
GTGCAGAGCC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCCGAT 3960  
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020  
AGAGGGATGA ACTGTCTATC AGACCATGTG TCAGGAAAAT TGTGAACGTA GATGAGGTAC 4080  
ATACACTGCC GCTTCTCAAC TCCCAGAGGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140  
CTTCTCTTAA AAGGCTACAT ATATATGAAA AAAAATCATA TTGCGTCTT TTAAGAGGCA 4200  
ACTGCATGGT ACATTGTGTA TTGTTATGAC TGTACACTC TGGCCAGCC AGAGCTATAA 4260  
TTGTTTITTA AATGTGTCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320  
GGGAACCTGC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCTAGTTA 4380  
TATACAGGGT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440  
TTATTAGGAA CATTTCAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGCATAT 4500  
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCAATAGTAAT AATACACATT TCTGTGAGTG 4560  
CTGACTGTCT TTTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT 4620  
AAAAACAAA ATGTTAAAT CAATGAATA AATTGCACT TAAGA

Seq ID NO: 486 Protein sequence  
Protein Accession #: NP\_005747.1

40  
45  
50  
55  
60

1 11 21 31 41 51  
MVFSVRQGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60  
PSSNEVETTS LNDVLSLLP SNETGVKQPR NICNLSSICN DSAFFRGEIM FQYDKESTVP 120  
QNQHITNGTL TGVLSLSELK RSELNKTLOT LSETYFIMCA TAEAQSTLNC TFTIKLNYTM 180  
NACAVIAALE RVKIRPMEHC CCSVRIPCPS SPEELEKLQC DLQDPVCLA DHPRGPPFSS 240  
SQSIEVVFRA TVLSQVPKAT SFAEPDYPSP VTHNVSPIG EIQPLSPQPS APIASSPAID 300  
MPFQSETISS PMPQTHVSGT PPFVKASFSS PTVSAPANVN TTSAPPVQTD IVNTSSISDL 360  
ENQVLQMEKA LSLGSLLEPNL AGEVINQVSR LLHSPDMLA PLAQRLLKVV DDIGLQINLS 420  
NTTISLTSPS LALAVIRVNA SSFNTTTFVA QDPANLQVSL ETQAPENSIG TITLPSLLMN 480  
NLPAHDMELA SRVQNFYET PALFQDPSLE NLSLSYVIS SSVANLTVRN LTRNVTVLK 540  
HNPSPQBLT VRCVFNLDGR NGGRGGWSDN GCSVKDRRLN ETICTCSHLT SFGVLLDLR 600  
TSVLPQAQMA LFTFIYIGCG LSSIPLSVTL VTYIAFEKIR RDYPSKILIQ LCAALLLNL 660  
VFLDSWIAL YKMQGLCISV AVFLHYFLLV SFTWMGLEAF HMYLALVKVF NTYIRKYILK 720  
FCIVGWGVPA VVVTIILITIS PDNYGLGSYG KFPNGSPDDF CWINNNVAFY ITVVGYFCVI 780  
FLNVMFPIV VLVQLCRIKK KQLGAQRKT SIQDLRSIAG LTFLLGITWG FAFWFANGPN 840  
VTFMYLFAIF NTLQGFYFI FYCAKENVR KQWRRYLCCG KLRLAENSDW SKTATNGLKK 900  
QTVNQGVSSS SNSLQSSSNS TNSTLLVNN DCSVHASGNG NASTERNGVS FSVQNGDVCL 960  
HDFPTGQHMF NEKEDSCNGK GRMALRRTSK RGSLLHFIEQM

Seq ID NO: 487 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2904

65  
70  
75  
80

1 11 21 31 41 51  
ATGGTITTTCT CTGTCAAGCA GTGTGGCCAT GTTGGCAGAA CTGAAGAAGT TTTACTGACG 60  
TTCAAGATAT TCCTTGTGCT CATTTGTCTT CATGTGCTTC TGGTAACATC CCTGGAAGAA 120  
GATACTGATA ATTCCAGTTT GTCACCACCA CCTGATGTTA CTTTAAAGCT ACTCCCTTCA 180  
AACGAAACAG AAAAACTTAA AATCACTATA GTAAAAACCT TCAATGCTTC AGGCGTCAAA 240  
CCCCAGAGAA ATATCTGCAA TTTGTCTATCT ATTTGCAATG ACTCAGCAIT TTTTAGAGGT 300  
GAGATCATGT TTCAATATGA TAAAGAAAGC ACTGTTCCCC AGAATCAACA TATAACGAAT 360  
GGCACCTTAA CTGGAGTCCT GTCTCTAAGT GAATTAACCA CATTAAATTG TACATTCA 420  
ATAAACTGA ATAATACAT GAATGCATGT GCTGTAATAG CTGCTTTGGA AAGAGTAAAG 480  
ATTGACCAA TGGAACTCTG CTGCTGTTCT GTCAGGATAC CCTGCCCTTC CTCCCCAGAA 540  
GAGTTGGAAA AGCTTCAGTG TGACCTGCAG GATCCCATG TCTGTCTTGC TGACCATCCA 600  
CGTGGCCACC CATTTCTTCT CAGCCAATCC ATCCCACTGG TGCCCTCGGG CACTGTGCTT 660  
TCCAGATGCC CCAAGCTAC CTCTTTTGTG GAGCCTCCAG ATTATTCACC TGTGACCCAC 720  
AATGTTCCCT CTCCAATAGG GGAGATTCAA CCCCTTTCAC CCCAGCCTTC AGCTCCCAT 780  
GCTTCCAGCC CTGCCATTGA CATGCCCCCA CAGTCTGAAA CGATCTCTTC CCTATGCC 840  
CAAAACCATG TCTCCGGCAC CCCACCTCCT GTGAAAGCCT CATTTTCTCT TCCCACCGTG 900  
TCTGCCCTGG CGAATGTCAA CACTACCAAG GCACCTCCTG TCCAGACAGA CATGCTCAAC 960  
ACCAAGCTAT TTTCTGATCT TGAGAACCAA GTGTTGCAGA TGGAGAAGGC TCTGCTCTG 1020  
GGCAGCCTGG AGCCTAACCT CGCAGGAGAA ATGATCAACC AAGTCAGCAG ACTCCTTCAT 1080

5  
 10  
 15  
 20  
 25  
 30

```

TCCCGCCTG ACATGCTGGC CCCTCTGGCT CAAAGATTGC TGAAAGTAGT GGATGACATT 1140
GGCCTACAGC TGAACCTTTC AAACACGACT ATAAGTCTAA CCTCCCTTC TTTGGCTCTG 1200
GCTGTGATCA GAGTGAATGC CAGTAGTTTC AACACAACTA CCTTTGTGGC CCAAGACCTC 1260
GCAAACTTCT AGGTTTCTCT GGAACCCAA GCTCCTGAGA ACAGTATTGG CACAATTACT 1320
CTTCCTTCAT CGCTGATGAA TAATTTACCA GCTCATGACA TGGAGCTAGC TTCCAGGGTT 1380
CAGTTCAATT TTTTGAAC ACCTGCTTTG TTTGAGGATC CTTCCTGGA GAACCTCTCT 1440
CTGATCAGCT ACCTCATATC ATCGAGTGT CCAAACCTGA CCGTCAGGAA CTTGACAAGA 1500
AACGTGACAG TCACATTAAA GCACATCAAC CCGAGCCAGG ATGAGTTAAT AGTGAGATGT 1560
GTATTTTGGG ACTTGGGCAG AAATGGTGGC AGAGGAGGCT GGTGAGACAA TGGCTGCTCT 1620
GTCAAAGACA GGAGATTGAA TGAAACCATC TGTACCTGTA GCCATCTAAC AAGCTTCGGC 1680
GTTCTGCTGG AACTTCTAG GACATCTGTG CTGCTGCTC AAATGATGGC TCTGACGTTT 1740
ATTACATATA TTGGTTGTGG GCTTTCATCA ATTTTCTGT CAGTACTCT TGTAACTTAC 1800
ATAGCTTTTG AAAAGATCCG GAGGGATTAC CCTTCCAAAA TCCTCATCCA GCTGTGTGCT 1860
GCTCTGCTTC TGCTGAACCT GGTCTTCTC CTGACTCGT GGATTGCTCT GTATAAGATG 1920
CAAGGCTCTC GCATCTCAGT GGCTGTATT CTTCATTATT TTCTCTGGT CTCATTCA 1980
TGGATGGGCC TAGAAGCAT CCATATGTAC CTGGCCCTTG TCAAAGTATT TAATACTTAC 2040
ATCCGAAATC ACATCTTAA ATTCTGCATT GTCGGTTGGG GGGTACCAGC TGTGGTTGTG 2100
ACCATCATCC TGACTATATC CCCAGATAAC TATGGGCTTG GATCCTATGG GAAATTCCCC 2160
AATGGTTCAC CGGATGACT CTGCTGGATC AACACAATG CAGTATTCTA CATTACGGTG 2220
GTGGGATATT TCTGTGTGAT ATTTTGTCTG AACGTCAGCA TGTTCATTGT GGTCTCGGTT 2280
CAGCTCTGTC GAATTAAGAA GAAGAAGCAA CTGGGAGCCC AGCGAAAAAC CAGTATTCAA 2340
GACCTCAGAA GTATCGCTGG CCTTACATT TTACTGGGAA TAACTGGGG CTTGCTCTC 2400
TTTGCCTGGG GACCATTTAA CGTGACCTTC ATGTATCTGT TTGCCATCTT TAATACCTTA 2460
CAAGGATTTT TCATATTTCAT CTTTACTGT GTGGCCAAAG AAAATGTCAG GAAGCAATGG 2520
AGCGGCTATC TTTGTGTGG AAAAGTACGG CTGGCTGAAA ATTCTGACTG GAGTAAAACT 2580
GCTACTAATG GTTTAAAGAA GCAGACTGTA AACCAAGGAG TGTCCAGCTC TTCAAATTC 2640
TTACAGTCAA GCATAACTC CACTAACTCC ACCACACTGC TAGTGAATAA TGATTGCTCA 2700
GTACACGCAA GCGGAATGG AAATGCTTCT ACAGAGAGGA ATGGGGTCTC TTTAGTGTT 2760
CAGAAATGGG ATGTGTGCTC TCACGATTTC ACTGGAAGAA AGCACATGTT TAACGAGAAG 2820
GAAGATTCTC GCAATGGGAA AGCGCGTATG GCTCTCAGAA GGACTTCAAA GCGGGGAAGC 2880
TTACACTTTA TTGAGCAATG GTGA
  
```

Seq ID NO: 488 Protein sequence  
 Protein Accession #: Eos sequence

35  
 40  
 45  
 50  
 55

```

1 11 21 31 41 51
MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPD PDVTLSSLPS 60
NETERTKITI VKTFNASGVK PQRNINLSS IONDSAPFRG EIMFQYDKES TVPQNQHITN 120
GLTGLVLSLS ELNLTNCTFT IKLNNTMNAC AVIALALERV IRPMEHCCCS VRIPCPSSPE 180
ELEKLQCDLQ DPLVCLADHP RGPFFSSSQS IPVVPRTATV SQVPKATSPA EPPDYSPTV 240
NVPSPIGHIQ PLSPQPSAPI ASSPAIDMPP QSETISSPMP QTHVSGTPPP VKASFSSPTV 300
SAPANVNTTS APFVQTDIVN TSSISDLENQ VLQMEKALSL GSLEPNLAGE MINQVSRLLH 360
SPPDMLAPLA QRLKVVDDI GLQLNFSNTT ISLTSPLAL AVIRVNASSP NTTTTFVAQDP 420
ANLQVLSLEQ APENSIGTIT LPSSLMNLP AHMELASRV QNFFFETPAL FQDPSLENLS 480
LISYVISSSV ANLTVRNLR NVTVLKHIN FSQDELTVRC VFDLGRNGG RGGWSDNGCS 540
VKDRRLNETI CTCSHLTSEF VLLDLRSTV LPAQMMALT ITIYICGLSS IFLSVTLVTY 600
IAFEKIRDIY PSKILIQCAA ALLLNLVFL LDSWIALYKM QGLCISVAVF LHYFLVSTF 660
WMGLEAFHMY LALVKVFNTY IRKYILKPCI VGVGVPAVVV TIILITSPDN YGLGSYKPP 720
NGSPDDFCWI MNNAVFIYTV VGYFCVIFLL NVSMFIVVLV QLCRIKKKKQ LGAQRKTSIQ 780
DLRSIAGLTF LIGITWGFAP FAWGPVNVTF MYLFAIFNTL QGFFIFIPYC VAKENVKQW 840
RRYLCCGKLR LAENSDWSKT ATNGLKKQTV NQGVSSSSNS LQSSSNSTNS TTLVNNDCS 900
VHASNGNAS TERNGVSFSV QNGDVCLHDF TGKQHMFEK EDCNGKGRM ALRRTSKRGS 960
LHFIEQM
  
```

Seq ID NO: 489 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2811

60  
 65  
 70  
 75  
 80

```

1 11 21 31 41 51
ATGGTTTCT CTGTCAGGCA GTGTGGCCAT GTTGGCAGAA CTGAAGAAGT TTTACTGACG 60
TTCAAGATAT TCCTTGTCAT CATTGTCTT CATGTGTTT TGGTAACATC CCTGGAAGAA 120
GATACTGATA ATTCCAGTTT GTCACCACCA CTGAGGTTG AAACAACAAG CCTCAATGAT 180
GTTACTTTAA GCCTACTCCC TTCAAACGAA ACAGGCGTCA AACCCAGAG AAATATCTGC 240
AATTGTGCTA CTATTGCAA TGACTCAGCA TTTTGTAGAG GTGAGATCAT GTTCAATAT 300
GATAAAGAAA GCCTGTGTC CCAGATCAA CATATAACGA ATGGACACTT AACTGGAGTG 360
CTGTCTTAA GTGAATTAAA ACGCTCAGAG CTCACAAAA CCTGCAAAAC CCTAAGTGAG 420
ACTTACTTTA TAATGTGTG TACAGCAGAG GCCCAAAGCA CATTAAATTG TACATTACA 480
ATAAACTGA ATAATACAAT GAATGCATGT GCTGTAATAG CTGCTTTGGA AAGAGTAAAG 540
ATTGACCAA TGGAACTAG CTGCTGTTCT CTGAGGATAC CTGCGCTTC CCCCCAGAA 600
GAGTGGGAAA AGCTTCAGTG TGACCTGCGA GATCCCATG TCTGTCTTGC TGACCATCCA 660
CGTGGCCCAT CATTTCTTC CAGCCAATCC ATCCCACTGG TGCCCTGGGC CACTGTGCTT 720
TCCCAGGTCC CCAAGCTAC CTCCTTTGCT GAGCCTCCAG ATTATTCACT TGTGACCCAC 780
AATGTTCCCT CTCCAATAGG GGAGATTCAA CCCCCTTCAC CCCAGCCTTC AGCTCCATA 840
GCTTCCAGCG CTGCAATTGA CATGCCCCCA CAGTCTGAAA CGATCTCTCT CCCTATGCC 900
CAAAACCATG TCTCCGCAC CCCACCTCCT GTGAAAGCCT CATTTCTCT TCCCACCGTG 960
TCTGCCCTG GAAATGTCAA CACTACCAGC GCACCTCCTG TCCAGACAGA CATGCTCAAC 1020
ACCAGCAGTA TTTCTGATCT TGAGAACCAA GTGTTGAGA TGGAGAAGGC TCTGCTCTG 1080
GGCAGCCTGG AGCCTAACCT CGCAGGAGAA ATGATCAACC AAGTCAGCAG ACTCCTTCAT 1140
TCCCGCCTG ACATGCTGGC CCTCTGSGT CAAAGATTGC TGAAAGTAGT GGATGACATT 1200
GGCTACAGC TGAACCTTTC AAACAAGACT ATAAGTCTAA CCTCCCTTC TTTGGCTCTG 1260
GCTGTGATCA GAGTGAATGC CAGTAGTTTC AACACAATA CCTTTGTGGC CCAAGACCTC 1320
GCAATCTTCT AGGTTTCTCT GGAACCCCAA GCTCCTGAGA ACAGTATTGG CACAATTACT 1380
  
```

5  
 10  
 15  
 20  
 25

CTTCCTTCAT CGCTGATGAA TAATTTACCA GCTCATGACA TGGAGCTAGC TTCCAGGGTT 1440  
 CAGTTCAATT TTTTGAAGAC ACCTGCTTTG TTTTCAGGATC CTTCCTCGGA GAACCTCTCT 1500  
 CTGATCAGCT ACGTCATATC ATOGAGTGTG GCAAACCTGA CCGTCAGGAA CTGACAAAGA 1560  
 AACGTGACAG TCACATTAAA GCACATCAAC CCGAGCCAGG ATGAGTTAAC AGTGAGATGT 1620  
 GTATTTTGGG ACTTGGCCAG AAATGGTGGC AGAGGAGGCT GGTACAGCAA TGGCTGCTCT 1680  
 GTCAAGACA GGAGATTGAA TGAACCATC TGTACCTGTA GCCATCTAAC AAGCTTCGGC 1740  
 GTTCTGCTGG ACCTATCTAG GACATCTGTG CTGCTGCTC AAATGATGGC TCTGACGTTT 1800  
 ATTACATATA TTGGTTGTGG GCTTTTCATCA ATTTTCTGT CAGTGACTCT TGTAACTAC 1860  
 ATAGCTTTTG AAAAGATCCG GAGGATTAC CCTTCCAAA CTCTCATCCA GCTGTGTGCT 1920  
 GCTCTGCTTC TGCTGAACCT GGTCTTCTC CTGGACTCGT GGATTGCTCT GTATAAGATG 1980  
 CAAGGCTCT GCATCTCAGT GGTGTATTT CTTCATTATT TTCTCTTGGT CTCATTACCA 2040  
 TGGATGGGCC TAGAAGCATT CCATATGTAC CTGCCCCCTG TCAAAGTATT TAATACTTAC 2100  
 ATCCGAAAT ACATCTTAA ATTCTGCATT GTGGTTGGG GGTACACAGC TGTGGTTGTG 2160  
 ACCATCATCC TGACTATATC CCCAGATAAC TATGGGCTTG GATCCTATGG GAAATTCCTC 2220  
 AATGGTTCAC CGGATGACTT CTGCTGGATC AACACAATG CAGTATTCTA CATTACGGTG 2280  
 TGGGGATATT TCTGTGTGAT ATTTTGTCTG AACGTACAGA TGTTCATTGT GGTCTCTGTT 2340  
 CAGCTCTGTC GAATTAATAA GAAGAAGCAA CTGGGAGCCC AGCGAAACAC CAGTATTCAA 2400  
 GACCTCAGAG GTATCTGCTG CCTTACATT TTAAGTGGGA TAACTTGGGG CTTTGCCTTC 2460  
 TTTGCTGGG GACCAGTTAA CGTGACCTTC ATGTATCTGT TTGCCATCTT TAATACCTTA 2520  
 CAAGGATTTT TCATATTCAT CTTTACTGT GTGGCCAAAG AAAATGTCAG GAAGCAATGG 2580  
 AGGCGGTATC TTTGTTGTGG AAAGTTAAGG CTGGCTGAAA ATTCGGGAAA TGCTTCTACA 2640  
 GAGAGGATG GGGTCTCTTT TAGTGTTCAG AATGGAGATG TGTGCTTCA CGATTTCATC 2700  
 GGAACACAGC ACATGTTTAA CGAGAAGGAA GATTCCTGCA ATGGGAAAGG CCGTATGGCT 2760  
 CTCAGAAGGA CTTCAAGCG GGAAGCTTA CACTTTATTG AGCAATGTG A

Seq ID NO: 490 Protein sequence  
 Protein Accession #: Eos sequence

30  
 35  
 40  
 45

1 11 21 31 41 51  
 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVIVTSLEE DTDNSSLSP P EVETTSLND 60  
 VTLSSLPSNE TGVKRPQNIC NLSSICNDSA FFRGEIMFQY DKESTVPQNG HITNGTLTGV 120  
 LSLSELKRSE LNKLTQLTSE TYFIMCATAE AQSTLNCTFT IKLNMNMAC AVIAALERVK 180  
 IRPMEHCCCS VRIPCPSPE ELEKLQCDLQ DPLVCLADHP RGPFPSSSQS IPVVPRTVL 240  
 SQVPKATSEA EPPDYSVPTH NVFSPIGEIQ PLSPQPSAPI ASSPAIDMPP QSETISSPMP 300  
 QTHVSGTPPP VKASFSSPTV SAPANVNTS APPVQTDIVN TSSISDLENQ VLQMEKALS 360  
 GSLEPNLAGE MINQVSRLLH SPFDMLAPLA QRLKLVDDI GLQLNFSNTT ISLTSPSLAL 420  
 AVIRVNASFP NMTTVAQDP ANLQVSLETO APENSIGTIT LPSSLMNLP AHDMELASRV 480  
 QFNFFETPAL PQDPSLENLS LISYVISSSV ANLTVRNLTR NVTVTLKHIN PSQDELTVRC 540  
 VFWDLGRNGG RGGWSDNGCS VKDRRLNETI CTCSHLTSFG VLLDLSTSV LPAQMMALTF 600  
 IYIISGCLSS IFLSVTLVTV IAFEKIRRDY PSKILQLCA ALLLNVLVFL LDSWIALYK 660  
 QGLCISVAVF LHYFLVLSFT WMGLEAFHMY LALVKVFNTY IRKYILKPCI VGMGPVAVV 720  
 TILLISPDN YGLGSYGKFP NGSPDDFCNI MNNAVFIITV VGYFCVIFLL NVSMFIVLV 780  
 QLCRIKKKKQ LGAQRKTSIQ DLRSIAGLTF LLGITWGFAP FAWGPNVTF MYLFAIFNL 840  
 QGFFIFIFYC VAKENVRKQW RRYLCCGKLR LAENSGNAST ERNGVSFSVQ NGDVCLDEFT 900  
 GKQHMENEKE DSCNGKGRMA LRRTSKRGLS HFIEQM

Seq ID NO: 491 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..3045

50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 ATGGTTTTCT CTGTCAGGCA GTGTGGCCAT GTTGCCAGAA CTGAAGAAGT TTTACTGACG 60  
 TTCAAGATAT TCCTTGTCAT CATTGTGCTT CATGTCGTTT TGGTAACATC CCTGGAAGAA 120  
 GATACTGATA ATTCCAGTTT GTACCCACCA CTGCTAAAT TATCTGTGT CAGTTTTGCC 180  
 CCTCTCTCCA ATGAGGTGGA AACACAAGC CTCAATGATG TACTTTAAG CTACTCTCT 240  
 TCAAAGGAAA CAGAAAGAAC TAAATCACT ATAGTAAAAA CCTTCAATGC TTCAGGCTC 300  
 AAACCCGAGA GAAATATCTG CAATTGTCA TCTATTGCA ATGACTCAGC ATTTTTAGA 360  
 GGTGAGATCA GTTTCAATA TGATAAGAA AGCACTGTTT CCCAGAATCA ACATATAACG 420  
 AATGGCACCT TAACGTGAGT CCTGTCTCTA AGTGAATTAA AACGCTCAGA GCTCAACAAA 480  
 ACCCTGCAAA CCCTAAGTGA GACTTACTTT ATAATGTGTG CTACAGCAGA GGCCCCAAGC 540  
 ACATTAAAT GTACATTCA CATAAACTG AATAATACAA TGAATGCATG TGCTGCAATA 600  
 GCCGCTTTGG AAAGAGTAAA GATTGACCA ATGGAACACT GCTGCTGTTT TGTGAGATA 660  
 CCTGCCCCCT CCTCCCCAGA AGAGTTGGGA AAGCTTCAGT GTGACCTGCA GGATCCCAT 720  
 GTCTGTCTTG CTGACCATCC ACGTGGCCCA CCATTTTCTT CCAGCCAATC CATCCCAGTG 780  
 GTGCTGCTGG CCACGTGTCT TTCCAGGCTC CCAAAAGCTA CTTCTTTTGC TGAGCCTCCA 840  
 GATTATTGSS CTGTGACCCA CAATGTTCCC TCTCCAATAG GGGAGATTCA ACCCTTTCA 900  
 CCCCAGCCTT CAGCTCCCAT AGCTTCCAGC CTGCCCATTG ACATGCCCCC ACAGTCTGAA 960  
 ACGATCTCTT CCCCATTGCC CCAAACCAT GTCTCCGCA CCCCACCTCC TGTGAAAGCC 1020  
 TCATTTCTCT CTCCACCGT GTCTGCCCTT GCGAATGTCA AACTACCAG CGCACCTCT 1080  
 GTCCAGACAG ACATCGTCAA CACGAGCAGT ATTTCTGATC TTGAGAACCA AGTGTTCAG 1140  
 ATGGAGAAGG CTCTGCTCTT GGGCAGCTG GAGCCTAACC TCGCAGGAGA AATGATCAAC 1200  
 CAAGTCAGCA GACTCCTTCA TTCCCGCCT GACATGCTGG CCCCCTGGC TCAAGATTG 1260  
 CTGAAAGTAG TGGATGACAT TGGCTACAG CTGAACCTTT CAAACACGAC TATAAGTCTA 1320  
 ACCTCCCTCT CTTTGGCTCT GGTGTGATC AGAGTGAATG CCAGTAGTTT CAACACACT 1380  
 ACCTTTGTGG CCCAAGACCC TGCAATCTT CAGGTTTCTT TGGAAACCCA AGCTCTGAG 1440  
 AACAGTATTG GCACAAATTAC TCTTCTTCA TCGCTGATGA ATAATTAC AGCTCATGAC 1500  
 ATGGAGCTAG CTTCCAGGCT TCAGTTCAT TTTTGTGAAA CACCTGCTTT GTTTCAGGAT 1560  
 CCTTCCCTGG AGAACCTCTC TCTGATCAGC TAGCTCATAT AGCACATCAA CCCGAGCCAG 1620  
 ACCGTCAGGA ACTTGACAGG AAACGTGACA GTCAATTAA AGCACATCAA CCCGAGCCAG 1680  
 GATGAGTTAA CAGTGAGATG TGTATTTGG GACTTGGGCA GAAATGTTGG CAGAGGAGGC 1740  
 TGGTCAGACA ATGGCTGCTC TGTCAAAGAC AGGAGATTGA ATGAAACCAT CTGTACCTGT 1800  
 AGCCATCTAA CAAGCTTCGG CGTCTGCTG GACCTATCTA GGACATCTGT GCTGCTGCT 1860

CAAATGATGG CTCTGACGTT CATTACATAT ATTGGTTGTG GGCTTTCATC AATTTTCTG 1920  
 TCAGTGACTC TTGTAAACCTA CATAGCTTTT GAAAGATCC GGAGGGATTA CCCTTCCAAA 1980  
 ATCCTCATCC AGCTGTGTGC TGCTCTGCTT CTGCTGAACC TGGTCTTCTT CCTGGACTCG 2040  
 TGGATTGCTC TGTATAAGAT GCAAGGCCTC TGCACTCTAG TGGCTGTATT TCTTCATTAT 2100  
 5 TTTCTCTTGG TCTCATTAC ATGGATGGGC CTAGAAGCAT TCCATATGTA CTGGGCCCTT 2160  
 GTCAAAGTAT TTAATACCTA CATCCGAAAA TACATCCTTA AATTCTGCAT TGTGGGTTGG 2220  
 GGGGTACCAG CTGTGGTTGT GACCATCATC CTGACTATAT CCCCAGATAA CTATGGGCTT 2280  
 GGATCCTATG GGAATATCCC CAATGGTTCA CCGATGACT TCTGCTGGAT CAACAACAA 2340  
 10 GCAGTATTCT ACATTACGGT GGTGGGATAT TTCTGTGTGA TATTTTGTCT GAACGTACAG 2400  
 ATGTTCAATTG TGGTCTGGT TCAGCTCTGT CGAATTAAGA AGAAGAAGCA ACTGGGAGCC 2460  
 CAGCGAAAAA CCAGTATTCA AGACCTCAGG AGTATCGCTG GCCTTACATT TTTACTGGGA 2520  
 ATAACTTGGG GCTTGGCCTT CTTTGCCTGG GGACCACTTA ACGTGACCTT CATGTATCTG 2580  
 TTTGCCATCT TTAATACCTT ACAAGGATTT TTCATATTCA TCTTTTACTG TGTGGCCAAA 2640  
 15 GAAAATGTCA GGAAGCAATG GAGGCGGTAT CTTTGTGTGT GAAAGTTACG GCTGGCTGAA 2700  
 AATTCTGACT GGAGTAAAC TGCTACTAAT GGTTTAAGA AGCAGACTGT AAACCAAGGA 2760  
 GTGTCCAGCT CTTCAAATTC CTTACAGTCA AGCAGTAACT CCCTAACTC CACCACACTG 2820  
 CTAGTGAATA ATGATTGCTC AGTACACGCA AGCGGGAATG GAAATGCTTC TACAGAGAGG 2880  
 AATGGGCTCT CTTTGTAGTT TCAGAAATGA GATGTGTGCC TTCACTGATT CACTGGAAAA 2940  
 20 CAGCACATGT TTAACGAGAA GGAAGATTCC TGCAATGGGA AAGGCCGTAT GGCTCTCAGA 3000  
 AGGACTTCAA AGCGGGGAAG CTTACACTTT ATTGAGCAAA TGTGA

Seq ID NO: 492 Protein sequence  
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51  
 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEB DTDNSSLSPF PAKLSVVSPA 60  
 PSSNEVETTS LNDVTLISLLP SNETEKTKIT IVKTFNASGV KPQRNICNLS SICNDSAPFR 120  
 30 GEIMFQYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYP IMCATAEAQS 180  
 TLNCTFTIKL NNTMNAACAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240  
 VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSPFAEP DYSPVTHNVP SPIGEIQPLS 300  
 PQPSAPIASS PAIDMPPQSE TISSPMQTH VSGTTPPVKA SFSSPTVSAP ANVNTTSAPP 360  
 VQTDIVNTSS ISDLENQVLQ MEKALSLSL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL 420  
 35 LKVVDDIGLQ LNSPNTTISL TSPSLALAVI RVNASSFNTT TFVAODPANL QVSELTQAPE 480  
 NSIGTTITLS SLMNLPFAHD MELASRVQFN FETPALFQD PSLENLSLIS VVISSVANL 540  
 TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600  
 SHLTSFGVLL DLSTSVLPA QMMALTFITY IGCGLSIFL SVTLVTYIAF EKIRRDYPSK 660  
 ILIQLCAALL LNLNVLFLDS WIALYKMQGL CISVAVFLHY FLLVSFTWMG LEAFHMYLAL 720  
 40 VKVENTYIRK YILKFCIVGW GVPVVVTII LTISPENYGL GSYGKFPNGS PDDFCWINNN 780  
 AVFYITVVG YFCVIFLLNV MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840  
 ITWGAFFAW GPNVNTFMYL PAIFNTLQGF FIFIPYCVAK ENVRKQWRRY LCCGKLRLAE 900  
 NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGNASTER 960  
 NGVSFSVQNG DVCLHDFTKG QHMFNEKEDS CNGKGRMALR RSKRGSLSHF IBQM

45 Seq ID NO: 493 DNA sequence  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241..1902

50 1 11 21 31 41 51  
 CGCAGAGGA GCCTGGGCCA GGCTAGCCAG GGGGCCCCCA GGGCCCTCCC AGGCCGOGAG 60  
 CGCCCTGCCC GGGGTGCTCG GCCTCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACCTG 120  
 CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180  
 55 GGGTCCGGCC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGGGAGA 240  
 ATGCTCTGCG CCGTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCGGTGGTGC AGGTGGTTTC 300  
 GGGAAOCCGG CCAGTGCAAG GCATCACGGG TTGTAGCAT CGGCACGTCA GCCTGGGGTC 360  
 TGTCACTATG GAACATAACT GCGCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420  
 TGTGAAGCTA CATGCGAAC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAATATG 480  
 60 AGATGCTTTC CAGGATACAC CGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGAATG 540  
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAG GAAGCTACAA GTGCTTTTGC 600  
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGSAC ATGTGCCATC 660  
 ATAACTGCT AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720  
 TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCTT 780  
 65 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840  
 AAATGTCACA TTGGTTTCCA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900  
 AATGAATGTA CTATGGATAG CCATAGTGC AGCCACCATG CCAATGTGCT CAATACCCAA 960  
 70 GGGTCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020  
 ATCCCTGAAA ATTCTGTGAA GGAAGTCTTC AGAGCACCTG GTACCATCAA AGACAGAAATC 1080  
 AAGAAGTTGC TTGCTACAAA AAACAGCATG AAAAAAGAG CAAAAATTAA AAATGTTACC 1140  
 CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200  
 ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260  
 GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320  
 75 AGCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380  
 CTGGTCCAAA GGAAGCGCT AACITCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440  
 GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGAATTTGAC 1500  
 TGGAAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA 1560  
 GGTCAACAGA AAGACATTGG CCGATTGAAA CTTCTCTAC CTGACCTGCA ACCCCAAAGC 1620  
 80 AACTTCTGTT TGCTCTTGA TTACCGGCTG GCGGAGACA AAGTCGGGAA ACTTOGAGTG 1680  
 TTTGTGAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCAAGAGTGA GGATGAAAAG 1740  
 TGGAGACAGC GGAATATCA GTTGATATCA GGAACATGAT CTACCAAAAG CATCATTTTT 1800  
 GAAGCAGAAC GTGGCAGGG CAAAACCGGC GAAATGSCAG TGGATGGCGT CTGCTTGT 1860  
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920  
 TTGACTTGT ATGTCACTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980  
 TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040



TCTTGTATAA GATATGCCAA TATTTGCTTT AAATATCAT TCACTGTATC TTCTCAGTCA 2100  
 TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCTCTCCT 2160  
 CAGTATATCT GATTGTGATA AGTAAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220  
 TAGAAAAAAA AGCACAGAGA AATGTTTAA TGTGTGACTC TTATGATACT TCTTGGAAAC 2280  
 5 TATGACATCA AAGATAGACT TTTGCCTAAG TSGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340  
 TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATA AAAAAAAA

Seq ID NO: 494 Protein sequence  
 Protein Accession #: NP\_056322

1 11 21 31 41 51  
 MPLPWSLALP LLLSWVAGGF GNAASARHGG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60  
 15 CEATCEPGCK PGECVGPKNK RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKCF 120  
 LSGHMLPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS 180  
 GKVICPNRR CVNTFGSYIC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240  
 GSPKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KLLLAHKNSM KKKAKIKNVT 300  
 20 PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360  
 SLRGDVFPPK VNEAGEPLI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WKQDREDDFD 420  
 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLDYDRL AGDKVGLKRV 480  
 FVKNSNALLA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERKGKGTG EIAVDGVLLV 540  
 SGLCPDLSLS VDD

Seq ID NO: 495 DNA sequence  
 Nucleic Acid Accession #: NM\_003506.1  
 Coding sequence: 259..2379

1 11 21 31 41 51  
 GCAGCTCCAG TCCCGGACGC AACCCCGGAG CCGTCTCAGG TCCCTGGGGG GAACGGTGGG 60  
 TTAGACGGGG ACGGGAAGGG ACAGCGGCTC TCGACCGCCC CCCGAGTAAT TGACCCAGGA 120  
 CTCATTTCAC GGAAAGCCTG AAAATGAGTA AAATAGTGAA ATGAGGAATT TGAACATTTT 180  
 35 ATCTTTGGAT GGGATCTTC TGAGGATGCA AAGAGTGATT CATCCAAGCC ATGTGGTAAA 240  
 ATCAGGAATT TGAAGAAAAT GGAGATGTTT ACATTTTGTG TGACGTGTAT TTTCTACCC 300  
 CTCCTAAGAG GGCACAGTCT CTTACCTGCT GAACCAATTA CTGTTCACAG ATGTATGAAA 360  
 ATGGCCTACA ACATGACGTT TTTCCCTAAT CTGATGGGTC ATTATGACCA GAGTATTGCC 420  
 GCGGTGGAAA TGGAGCATT TTTCTCTCTC GCAAATCTGG AATGTTTACC AAACATTGAA 480  
 40 ACTTTCTCTC GCAAAGCATT TGTACCAACC TGATAGAAC AAATTCATGT GGTTCACCT 540  
 TGTGTGTAAC TTTGTGAGAA AGTATATTCT GATTGCAAAA AATTAATTGA CACTTTTGGG 600  
 ATCCGATGGC CTGAGGAGCT TGAATGTGAC AGATTACAAT ACTGTGATGA GACTGTTCTT 660  
 GTAACTTTTG ATCCACACAC AGAATTTCTT GGTCTCTAGA AGAAACAGA ACAAGTCCAA 720  
 AGAGACATRG GATTTTGGTG TCCAAGGCAT CTTAAGACTT CTGGGGGACA AGGATATAAG 780  
 45 TTTCTGGGAA TTGACCATGT TGGCCTCCA TGCCCCAACA TGTATTTTAA AAGTGATGAG 840  
 CTAGAGTTTG CAAAAGTGT TATTGGAACA GTTTCATAT TTTGCTTTG TGCAACTCTG 900  
 TTCAATTTCC TTACTTTTTT AATTGATGTT AGAAGATTCA GATACCCAGA GAGACCAATT 960  
 ATATATTACT CTGTCTGTGA CAGCAITGTA TCTCTTATGT ACTTCATTGG ATTTTGTGCT 1020  
 GGGCATAGCA CAGCTGCTCA TAAGGCAGAT GAGAAGCTAG AACTTGGTGA CACTGTTGTC 1080  
 50 CTAGGCTCTC AAAATAAGGC TTGACCGGTT TGTTCATGCT TTTGTATTT TTTCAATG 1140  
 GCTGCACTGT TGTGTTGGGT GATTCTTACC ATTACTTGGT TCTTAGCTGC AGGAAGAAAA 1200  
 TGGAGTTGTG AAGCCATCGA GCAAAAAGCA GTGTGTTTC ATGCTGTGTC ATGGGGAACA 1260  
 CCAGGTTTCC TGACTGTTAT GCTTCTTGCT CTGAACAAAG TTGAAGGAGA CAACATTAGT 1320  
 GGAGTTTGCT TGTGTTGGCT TTATGACCTG GATGCTTCTC GCTACTTTGT ACTCTTGCCA 1380  
 55 CTGTGCTCTT GTGTGTTGTG TGGGCTCTCT CTTCTTTTAA CTGGCATTAT TTCTTAAAT 1440  
 CATGTTGAC AAGTCATACA ACATGATGGC CGGAACCAAG AAAAATAAAG GAAATTTATG 1500  
 ATTCGAATTG GAGTCTTCAG CGGCTTGAT CTGTGCTCAT TAGTGACACT TCTCGGATGT 1560  
 TACGTCATAG AGCAAGTGAA CAGGATTACC TGGGAGATAA CTGGGCTCTC TGATCATGTT 1620  
 60 CGTCAGTACC ATATCCCATG TCTTTATCAG GCAAAAGCAA AAGCTCGACC AGAATTGGCT 1680  
 TTATTTATGA TAAATACCT GATGACATTA ATTGTTGGCA TCTCTGCTGT CTCTGGGTT 1740  
 GGAAGCAAAA AGACATGCAC AGAATGGGCT GGGTTTTTAA AAGAAATCG CAAGAGAGAT 1800  
 CCAATCAGTG AAAGTCGAAG AGTACTACAG GAATCATGTG AGTTTCTCTT AAAGCACAA 1860  
 TCTAAAGTTA AACACAAAAA GAAGCACTAT AAACCAAGTT CACACAAGCT GAAGGTCATT 1920  
 TCCAAATCCA TGGGAACCAAG CACAGGAGCT ACAGCAATC ATGGCACTTC TGCAGTAGCA 1980  
 65 ATTACTAGCC ATGATTACCT AGGACAAGAA ACTTTGACAG AAATCCAAAC CTCACAGAA 2040  
 ACATCAATGA GAGAGGTGAA AGCGGACGGA GCTAGCACCC CCAGGTTAAG AGAACAGGAC 2100  
 TGTGTTGAAC CTGCTCTGCC AGCAGCATCC ATCTCCAGAC TCTCTGGGGA ACAGGTCGAC 2160  
 GGGAAAGGCC AGGCAGGCGAG TGTATCTGAA AGTGCGCGGA GTGAAGGAAG GATTAGTCCA 2220  
 AAGAGTGATA TTAATGACAC TGGCCTGGCA CAGAGCAACA ATTGTCAGGT CCCAGTTCT 2280  
 70 TCAGAACCAA GCAGCCTCAA AGGTTCCACA TCTCTGCTTG TTCACCCAGT TTCAGGAGTG 2340  
 AGAAAAGAGC AGGGAGGTGG TTGTCAATCA GATACTTGAA GAACATTTTC TCTGTTACT 2400  
 CAGAAGCAAA TTTGTGTTAC ACTGGAAGTG ACCTATGCAC TGTTTTGTAA GAATCACTGT 2460  
 TACGTTCTTC TTTTGCACTT AAAGTTGCAT TGCTTACTGT TATACGTGAA AAAATAGAGT 2520  
 TCAAGAATGA TATGATCAT TCCACAAAAA GGTTAATGAC AACAAATATC CTGAAAACAG 2580  
 75 AAATGTGCAG GTTAATAATA TTTTAAAAAT AGTGTGGGAG GACAGAGTTA GAGGAATCTT 2640  
 CCTTTCTAT TTATGAAGAT TCTACTCTTG GTAAGAGTAT TTTAAGATGT ACTATGCTAT 2700  
 TTTACCTTTT TGATATAAAA TCAAGATATT TCTTTGCTGA AGTATTAAAA TCTTATCCTT 2760  
 GTATCTTTT ATACATATT GAAAATAAGC TTATATGTAT TTGAACTTT TTGAAATCCT 2820  
 80 ATTCAAGTAT TTTTATCATG CTATTGTGAT ATTTAGCAC TTTGGTAGCT TTTACACTGA 2880  
 ATTCTAAGA AATTTGAAA ATAGTCTCTT TTTTACTGT AAAAAAAGAT ATACCAAAAA 2940  
 GTCTTATAAT AGGAATTTAA CTTTAAAAAC CCACCTATTG ATACCTTACC ATCTAAAAATG 3000  
 TGTGATTTT ATAGTCTCGT TTAGGAATT TCACAGATCT AAATATGTGA ACTGAAATAA 3060  
 GGTGCTTACT CAAGAGGTGT CCACATTTGA TTGTATTATG CTGCTCACTG ATCCTTCTGC 3120  
 ATATTTAAAA TAAATGTGCC TAAAGGGTTA GTAGACAAAA TGTAGTCTT TTGTATATTA 3180  
 GGCCAGTGCC AATTGACTTC CCTTTTAA TGTTCATGA CCACCCATTG ATTGTATTAT 3240

AACCACTTAC AGTTGCTTAT ATTTTITGTT TTAACCTTTG TTCTTAACA TTTAGAATAT 3300  
TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG

Seq ID NO: 496 Protein sequence  
Protein Accession #: NP\_003497.1

1 11 21 31 41 51  
MEMFTLLTLC IFPLLRGHS LPTCEPITVP RCMKMYNMT FFFNLMGHYD QSIAAVEMEH 60  
FLPLANLECS PNITFLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRWPPEE 120  
LECDRLQYCD ETVFVTFDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTSQG QGYKFLGIDQ 180  
CAPPCPNMYF KSDELEFAKS FIGTVSIFCL CATLPTFLTF LIDVRRFRYP ERPIIYYSVC 240  
YSIVSLMYFI GFLLDGSTAC NKADEKLELG DTVVLGSSQNK ACTVLFMLLY FFTMAGTVVW 300  
VILTITWFLA AGRKWSCEAI EQKAVWPHAV AWGTPGFLTV MLLALAKVEG DNISGVCVFG 360  
LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVROVI QHGRNQEKI KCFMIRIGVF 420  
SGLYLVLPLVT LLGCVYVEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELAFMIKY 480  
LMTLIVGIS A VFVWGSKKTC TEWAGFFKRN RKRDPISER RVLQBSCEFF LKHNSKVKHK 540  
KKHYKPSHHK LKVIKSMGT STGATANHGT SAVAITSHDY LGQETLTIQ TSPETSMREV 600  
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660  
TGLAQSNMLQ VPSSSEPSL KGSTSLLVHP VSGVRKEQGG GCHSDT

Seq ID NO: 497 DNA sequence  
Nucleic Acid Accession #: NM\_005046  
Coding sequence: 16..777

1 11 21 31 41 51  
GGATTTCGG GCTCCATGGC AAGATCCCTT CTCCTGCCCC TGCAGATCCT ACTGCTATCC 60  
TTAGCCTTGG AACTGCAGG AGAAGAAGCC CAGGSGTACA AGATTATTGA TGGCGCCCCA 120  
TGTGCAAGAG GCTCCACACC ATGGCAGGTG GCCCTGCTCA GTGGCAATCA GCTCCACTGC 180  
GGAGGCGTCC TGGTCAATGA GCGCTGGGTG CTCACTGCCG CCCACTGCAA GATGAATGAG 240  
TACACGTCG ACCTGGGCAG TGATACGCTG GCGACAGGA GAGCTCAGAG GATCAAGGCC 300  
TCGAAGTCAT TCGGCCACCC CGGCTACTCC ACACAGACCC ATGTTAATGA CTTCTATGCTC 360  
GTGAAGCTCA ATAGCCAGGC CAGGCTGTCA TCCATGGTGA AGAAAGTCAG GCTGCCCTCC 420  
CGCTGCGAAC CCCCTGGAAC CACCTGTACT GTCTCGGCT GGGGCACTAC CACGAGCCCA 480  
GATGTGACCT TTCCCTCTGA CCTCATGTGC GTGGATGTCA AGCTCATCTC CCCCAGGAC 540  
TGACGAAGG TTATCAAGGA CTTACTGGAA AATTCCATGC TGTGCGCTGG CATCCCCGAC 600  
TCCAAGAAA ACGCCTGCAA TGGTGACTCA GGGGACCGT TGGTGTGAG AGGTACCTGT 660  
CAAGGTCTGG TGTCTGGGG AACTTTCCCT TGGCGCCAAC CCAATGACCC AGGAGTCTAC 720  
ACTCAAGTGT GCAAGTTTAC CAAGTGGATA AATGACACCA TGAAGAAAGCA TGCTAACGC 780  
CACACTGAGT TAATTAAGTGT TGTGCTTCCA ACAGAAAATG CACAGGAGTG AGGACGCCGA 840  
TGACCTATGA AGTCARATT GACTTTACCT TTCTCAAAG ATATATTATA ACCTCATGCC 900  
CTGTGATAA ACCGATCAA TTGGTAAAGA CCTAAACCA AAACAATAA AGAAACACAA 960  
AACCTCAA

Seq ID NO: 498 Protein sequence  
Protein Accession #: NP\_005037

1 11 21 31 41 51  
MARSLLLPLQ ILLSLALET AGEBAQGDKI IDGAPCARGS HPWQVALLSG NQLHCGGVLV 60  
NERWVLTAAH CKMNEYTVHL GSDTLGDRRA QRIKASKSFR HPGYSTQTHV NDLMLVKLNS 120  
QARLSSMAVK VRLPSRCEPP GTTCTVSCWG TTTSPDVTFF SDLMCDVKL ISPDCTKVY 180  
KDLLENSMLC AGIPDSKINA CNGDSGGPLV CRGTQLGLVS WGTFFCGQPN DPGVYTQVCK 240  
FTKWINDTMK KHR

Seq ID NO: 499 DNA sequence  
Nucleic Acid Accession #: NM\_007196  
Coding sequence: 182..962

1 11 21 31 41 51  
GTTCCAGAA GCTCCCCAGG CTCTAGTGCA GGAGGAGAAG GAGGAGGAGC AGGAGGTGGA 60  
GATTCCAGT TAAAGGCTC CAGAATCGTG TACCAGGCAG AGAACTGAAG TACTGGGGCC 120  
TCCTCCACTG GGTCCGAATC AGTAGGTGAC CCCGCCCTG GATTCTGGAA GACCTCACCA 180  
TGGGACGCCC CCGACCTCGT GCGGCCAAGA CGTGGATGTT CCTGCTCTTG CTGGGGGGAG 240  
CCTGGGCAGG ACATCCAGG GCACAGGAGG ACAAGGTGCT GGGGGGTCAT GAGTGCCAAC 300  
CCCATTCGCA GCCTTGGCAG GCGGCCTTGT TCCAGGGCCA GCAACTACTC TGTGGCGGTG 360  
TCCTGTAGG TGGCACTGG GTCCCTACAG CTGCCCCACTG TAAAAAACCG AAATACACAG 420  
TAGCCCTGGG AGACCAAGC CTACAGAATA AAGATGGCCC AGAGCAGAA ATACCTGTGG 480  
TTCAGTCCAT CCCACACCCC TGCTACAACA GCAGCGATGT GGAGGACCAC AACCATGATC 540  
TGATGCTTCT TCAACTGCGT GACCAGGCAT CCTGGGGTTC CAAAGTGAAG OCCATCAGCC 600  
TGGCAGATCA TTGCACCCAG CTTGGCCAGA AGTGACCCGT CTCAGGCTGG GGCCTGTCA 660  
CCAGTCCCCG AGAAGATTTT CCTGACACTC TCAACTGTGC AGAAGTAAAA ATCTTTCCCC 720  
AGAAGAAAGT TGAGGATGCT TACCGGGGCG AGATCACAGA TGGCATGGTC TGTGAGGCA 780  
GCAGCAAAGG GGCTGACAG TGCCAGGGCG ATTCTGGAGG CCCCTGGTG TGTGATGGTG 840  
CATCCAGGG CATCATCC TGGGGCTCAG ACCCCTGTGG GAGGTCCGAC AAACCTGGCG 900  
TCTATACCAA CATCTGCCG TACCTGGACT GGATCAAGAA GATCATAGGC AGCAAGGGCT 960  
GATTCTAGGA TAAGCACTAG ATCTCCCTTA ATAAACTCAC AACTCTC

Seq ID NO: 500 Protein sequence  
Protein Accession #: NP\_009127

1 11 21 31 41 51

MGRPRPRAAK TWMFLLLGG AWAGHSRAQE DKVLGGHECQ PHSQPWQAAL FQGQQLLCGG 60  
 VLVGGNWLVT AAHCKKPKYT VRLGDHSLQN KDGPEQEIPV VQSIPHPCYN SSDVEDHNMHD 120  
 LMLQLLRDQA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPT LNCAEVKIFP 180  
 QKKCEDAYPG QITDGMVCAG SSKGADTCQG DSGGPLVCDG ALQGITSMGS DPGCRSDKPG 240  
 VYTINICRYLD WIKKIIGSKG

Seq ID NO: 501 DNA sequence  
 Nucleic Acid Accession #: NM\_006103  
 Coding sequence: 29..406

1 11 21 31 41 51  
 CACCTGCACC CGCCCGGGC ATAGCACCAT GCCTGCTTGT CGCCTAGGCC CGCTAGCCGC 60  
 CGCCCTCCTC CTCAGCCTGC TGCTGTTCGG CTTCACCCCTA GTCTCAGGCA CAGGAGCAGA 120  
 GAAGACTGGC GTGTGCCCGG AGCTCCAGGC TGACCAAGAC TGACGCAAG AGTGCGTCTC 180  
 GGACAGCGAA TGCGCCGACA ACCTCAAGTG CTGCAGCGCG GGCTGTGCCA CCTTCTGCCT 240  
 TCTCTGCCCA AATGATAAGG AGGGTTCTTG CCCCAGGTG AACATTAACT TTCCCCAGCT 300  
 CGGCCTCTGT CGGGACCACT GCCAGGTGGA CAGCCAGTGT CCTGGCCAGA TGAATGCTG 360  
 CGCAATGGC TGTGGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGGTC CAGCCACCAC 420  
 CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGGTT CCAGCCACC 480  
 TGCCCTCCCC TTTTTCGGGA CTCTGTATTC CCTCTTGGGC TGACCACAGC TTCTCCCTTT 540  
 CCAACCAAT AAAGTAACCA CTTTCAGCAA AAAAAAAAAA AAAA

Seq ID NO: 502 Protein sequence  
 Protein Accession #: NP\_006094

1 11 21 31 41 51  
 MPACRLGPLA AALLLSLLLP GFTLVSGTGA EKTGVCPQLQ ADQNTQECV SDSECADNLK 60  
 CCSAGCATFC LLCPNKKEGS CPQVWINFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC 120  
 VTFNF

Seq ID NO: 503 DNA sequence  
 Nucleic Acid Accession #: NM\_002407  
 Coding sequence: 65..352

1 11 21 31 41 51  
 CCTCCACAGC AACTTCCTTG ATCCCTGCCA CGCAGGACTG AACACAGACA GCAGCGCGCT 60  
 CGCCATGAAG CTGCTGATGG TCCTCATGCT GCGCGCCCTC CTCCTGCACT GCTATGCAGA 120  
 TTCTGGCTGC AAATCTCTGG AGGACATGGT TGAAGAGACC ATCAATTCCG ACATATCTAT 180  
 ACCTGAATAC AAGAGAGCTTC TTCAAGAGTT CATAGACAGT GATGCGCTG CAGAGGCTAT 240  
 GGGGAAATTC AAGCAGTGT TCCTCAACCA GTCACATAGA ACTCTGAAAA ACTTTGGACT 300  
 GATGATGCAT ACAGTGTACG ACAGCATTGG GTGTAATATG AAGAGTAATT AACTTTACCC 360  
 AAGGCGTTTG GCTCAGAGGG CTACAGACTA TGGCCAGAAC TCATCTGTTG ATTGTAGAAA 420  
 ACCACTTTTC TTCTGTGTGT TGTCTTTTA TGTGGAACCT GCTAGACAC TGTGAAACC 480  
 TCAATTCAAT TTCATTTCATA ATAACCTAAT GCAAATC

Seq ID NO: 504 Protein sequence  
 Protein Accession #: NP\_002398

1 11 21 31 41 51  
 MKLLMVLMLA ALLLHCYADS GCKLLEDMEV KTINSDISIP EYKELLQEFI DSDAAAEAMG 60  
 KFKQCFLNQS HRTLKQPLGM MHTVYDSIWC NMKSN

Seq ID NO: 505 DNA sequence  
 Nucleic Acid Accession #: NM\_014791.1  
 Coding sequence: 171..2126

1 11 21 31 41 51  
 TTGGCGGGCG GAAGCGGCCA CAACCCGGCG ATCGAAAAGA TTCTTAGGAA GCGCGTACCA 60  
 GCGCGTCTC TCAGGACAGC AGGCCCTGT CTCTCTGTG GCGCGCGCTC AGCGTGCCCC 120  
 TCCGCCCCCTC AGGTTCCTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180  
 ATGATGAATC TCTCAAATAT TATGAATTAC ATGAACTAT TGGGACAGGT GGCTTTGCAA 240  
 AGGTCAAATC TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300  
 AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAAC 360  
 TGAGACATCA GCATATATGT CAATCTTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420  
 TGGTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTC CAGGATCGCC 480  
 TGTCAAGA GAAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540  
 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600  
 ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGTAAC AAGGATTACC 660  
 ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAA 720  
 CATATCTTGG ATCAGAGGCA GATGTTTGA GCATGGGCAT ACTGTTATAT GTTCTTATGT 780  
 GTGGATTCTC ACCATTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840  
 GAAAATATGA TGTTCCTCAG TGGCTCTCTC CCAGTAGCAT TCTGCTCTCT CAACAATGSC 900  
 TGCAGGTGA CCCAAGAGAA CGGATTTCTA TGAATAATCT ATTGAACCAT CCTGGATCA 960  
 TCAAGATTA CAATATCTCT GTTGAAGTGC AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020  
 ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAACAA ATGGAGGATT 1080  
 TAATTTCACT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA 1140  
 AGGCTCGGGG AAAACCAAGT CGTTTAAGGC TTTCTTCTTT CTCTGTGGA CAAGCCAGTG 1200  
 CTACCCCATC CACAGACATC AAGTCAAATA ATTGGAGTCT GGAAGATGTG ACGCAAGTG 1260

5 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320  
 GTGCTGCTAC TCCCGCAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG 1380  
 AATCTAAATC ATTAACCTCA GCCTTATGCA GAACACCTGC AAATAAAATTA AAGAACAAG 1440  
 AAAATGTATA TACTCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCCTGAGC 1500  
 CAAAGACTCC AGTTAATAAG AACCAACATA AGAGAGAAAT ACTCACTACG CCAATTCGTT 1560  
 ACACCTACACC CTCAAAAGCT AGAAACCACT GCCTGAAAGA AACTCCAATT AAAATACCAAG 1620  
 TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC 1680  
 GCTCAGTGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG 1740  
 10 CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800  
 GCAAAGGAA GGGTCTGCC AGAGACGGGC CCAGAAGACT AAAGCTTAC TATAATGTGA 1860  
 CTACAACCTAG ATTAGTGAAT CCAGATCAAC TGTTGAATGA AATAATGTCT ATTTCTCCAA 1920  
 AGAAGCATGT TGACTTTGTA CAAAGGGGTT ATACACTGAA GTGTCAACA CAGTCAGATT 1980  
 TTGGGAAAGT GACAATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAAAA CCGATGTGG 2040  
 TGGGTATCAG GAGGAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAGA TTAGTGAAG 2100  
 15 ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCTGCCG GATGAGTGTG 2160  
 GGTGTGATAC AGCCTACATA AAGACTGTGA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220  
 CTACCAACTT GTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280  
 GATATTATT TTGTGTGAA TCTAAATCAA GCCCATCTGT CATTATGTGA CTGTCTTTT 2340  
 20 TAATCATGTG GTTTGTGATA TTAATAATTG TTGACTTCT TAGATTCACT TCCATATGTG 2400  
 AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAATT TCTTTCTGAA ATAAACCAT 2460  
 TTGTGAATAT

Seq ID NO: 506 Protein sequence  
 Protein Accession #: NP\_055606.1

25 1 11 21 31 41 51  
 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60  
 LKHLRQHIC QLVHVLLETAN KIFMVLEYCP GGELEFDYIIS QDRLSEEBTR VVFRQIVSAV 120  
 30 AYVHSQGYAH RDLKPENLLF DEYHKLKID FGLCAKPKGN KDYLQTCQG SLAYAAPALI 180  
 QGKSYLGSEA DVMSMGLILY VLMCGFLPFD DDNVMAlyK IMRGKYDVPK WLSPPSILL 240  
 QQMLQVDPK RISMKNLLNH PWIMQDYNYP VEWQSKNPFH HLDLDCVTEL SVHHRNRQT 300  
 MEDLISLWQY DHLTATYLL LAKKARGKPV RLRLSSFSQG QASATPFPTDI KSNHWSLEDV 360  
 TADSKNVVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL 420  
 35 KNKENVYTPK SAVKNEEYFM FPEPKTPVNK NQHKREILT PNYRTTSPKA RNQCLKETPI 480  
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAQVFGSL ERGLDKVITV 540  
 LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLNEIMS ILPKKHVDFV QGYTLKQCT 600  
 QSDFGKVTMQ FELEVQLQK PDVVGIRRRQ LKGDWVYKR LVEDILSSCK V

40 Seq ID NO: 507 DNA sequence  
 Nucleic Acid Accession #: NM\_000582  
 Coding sequence: 88..990

45 1 11 21 31 41 51  
 GCAGAGCACA GCATGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60  
 AACGCGGACC AAGGAAAAT CACTACCATG AGAATTGCAG TGATTGCTT TTGCCCTCCTA 120  
 GGCATCACT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAGAGCAG 180  
 50 CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240  
 CAGAATCTCC TAGCCCCACA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCATG 300  
 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360  
 AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420  
 TCTGATGAAT TGATGAACCT GGTCACTGAT TTTCCCAACG ACCTGCCAGC AACCGAAGTT 480  
 55 TTCACTCCAG TTGTCCCACT AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540  
 GGACTGAGGT CAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600  
 GACGAGGACA TCACCTCACA CATGGAAAAC GAGGAGTTGA ATGTGTCATA CAAGGCCATC 660  
 CCGGTGCCCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720  
 GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAGCA GTCCAGATTA 780  
 60 TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCOG ATGTGATGTA TAGTCAGGAA 840  
 CTTTCCAAG TCAGCGGTGA ATTCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900  
 GTTGTAGACC CCAAAAGTAA GGAAGAGAT AAACACCTGA AATTTCTGAT TTCTCATGAA 960  
 TTAGATAGTG CATCTTCTGA GTTCAATTAA AAGGAGAAAA AATACAATT CTCACCTTGC 1020  
 ATTTAGTCAA AAGAAAAAT GCCTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080  
 65 CTGAGTTTAT TGGTTGAATG TGATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140  
 ATTAGTTTAT TTTGTGGCTT CATGGAAACT CCCTGTAAC TAAAGCTTC AGGGTTATGT 1200  
 CTATGTTCAT TCTATAGAAG AAATGCAAC TATCACTGTA TTTTAATATT TGTATTCTC 1260  
 TCATGAATAG AAATTTATGT AGAAGCAAC AAAATACTTT TACCACCTTA AAAAGAGAAT 1320  
 70 AATACTTTT ATGTCACTAT AATCTTTTGT TTTTAAAGT AGTGATATAT TTGTTGTGAT 1380  
 TATCTTTTG TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAAAT TGGTGGTGTG 1440  
 AATTGCTTAT TTGTTTCCG ACGTTTGTCC AGCAATTAAT AAAACATAAC CTTTTTACT 1500  
 CCTAAAAA AAAAAAAA AAAA

Seq ID NO: 508 Protein sequence  
 Protein Accession #: NP\_000573

75 1 11 21 31 41 51  
 MRIVAVICFL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60  
 PSKSNESHDI MDDMDDEDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDESDELVT 120  
 80 DFPTDLPAE VPTPVPTVD TYDGRGDSV YGLRSKSKKF RRPDIQYFDA TDEDITSHME 180  
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240  
 NEHSDVDSQ ELSKVSREFH SHEPHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN

Seq ID NO: 509 DNA sequence  
Nucleic Acid Accession #: AB051390.1  
Coding sequence: 34..2457

5 1 11 21 31 41 51  
AGCGGCGCGG GCACAAAGTT GGGGGCGCGG AAGATGAGGC TGTCCCGCGG GCCCCTGAAG 60  
CTGAGCCGGA CTCGGGCACT GCTGGCCCTG GCGCTGCCCG TGGCGCGCGG GCTGGCCTTC 120  
TCCGACGAGA CCTGGGACAA AGTGGCCCAAG TCAGAGGGCT ACTGCAGCCG TATCCTGCCG 180  
10 GCCAGGGGCA CGCGCGCGGA GGGCTACACC GAGTTCAGCC TCCGCGTGGA GGGCGACCCC 240  
GACTTTCACA AGCGGGGAAC CAGCTACCGC GTAACTTTT CAGCTGCTCC TCCCTCCTAC 300  
TTCAGAGGAT TCACATTAAT TGCCCTCAGA GAGAACAGAG AGGGTGATAA GGAAGAAGAC 360  
CATGTCTGGA CCTTCCAGAT CATAGACGAA GAAGAACTC AGTTTATGAG CAATTGCCCT 420  
15 TTGCAAGTCA CTGAAGCAC TCCACGGAGG AGGACCCGGA TCCAGGTGTT TTGGATAGCA 480  
CCACCAGCGG GAACAGGCTG CGTGATTCTG AAGGCCAGCA TCGTACAAAA ACGCATTATT 540  
TATTTTCAAG ATGAGGGCTC TCTGACCAAG AAATTTTGTG AACAAAGATC CACATTTGAT 600  
GGGGTGACTG ACAAACCCAT CTTAGACTGC TGTGCTGCGG GAATGCCCAA GTACAGACTC 660  
ACATTTTATG GGAATTTGGT CGAGAAGACA CACCAAAGG ATTACCCCTG TCGGGCCNAC 720  
20 CACTGGTCTG CGATCATCGG AGGATCCAC TCCAAGAAAT ATGTACTGTG GGAATATGGA 780  
GGATATGCCA GCGAAGCGCT CAACAAGTT GCAGAATTGG GCTCACCCTG GAAATATGGA 840  
GAAGAAATTC ATGAGGAGCT GTATGAGGTC CTCACCGTCA TCAAGGCCAA AGCCCAATGG 900  
CCAGCTGGCG AGCCTCTCAA CGTGAGAGCA GCACCTTCAG CTGAATTTTC CGTGGACAGA 960  
ACGCGCCATT TAATGTCTTT CCTGACCATG ATGGGCCCTA GTCCCGACTG GAACGTAGGC 1020  
25 TTATCTCGAG AAGATCTGTG CACCAAGGAA TGTGGCTGGG TCCAGAAGGT GGTGCAAGAC 1080  
CTGATTCCCT GGGACGCTGG CACCGACGCG GGGGTGACCT ATGAGTCACC CAACAAACCC 1140  
ACCATTCCTC AGGAGAAATC CCGGCCCTGG ACCAGCCTGG ACCATCTCTA GAGTCTTTTC 1200  
TATGACCCAG AGGGTGGGTC CATCACTCAA GTAGCCAGAG TTGTCTATCGA GAGAATCGCA 1260  
CGGAAGGGTG AACATGCAA TATTGTACCT GACAATGTCT ATGATATTGT AGCTGACTGT 1320  
30 GCTCCAGAGG AGAAAGATGA AGATGACACC CTGAAACCT GCATCTACTC CACTGTGTTC 1380  
CCATGTGTCG CCTGACGCTC CTCACCTCTG GACAAAGGCA AGAGGATGCG ACAGGCGATG 1440  
CTGAAGCAC AGCTGGACCT CAGCGTCCCC TGCCCTGACA CCCAGGACTT CCAGCCCTGC 1500  
ATGGGCCCTG GCTGACGTGA CGAAGACGGC TCCACCTGCA CCATGTCOGA GTGGATCACC 1560  
TGGTTCGCCCT GCAGCATCTC CTGCGGCATG GGCATGAGGT CCGGGGAGAG GTATGTGAAG 1620  
35 CAGTTCCCGG AGGACGGCTC CGTGTGCAAG CTGCCCACTG AGGAAACGGA GAAGTGACAG 1680  
GTCAAGCGCG AGTGTCTTCC CAGCAGCTGC CTGATGACCG AGTGGGGCGA GTGGGACGAG 1740  
TGCAAGCGCA CTGCGGCAT GGGCATGAAG AAGCGGCACC GCATGATCAA GATGAACCCC 1800  
GCAGATGGCT CCATGTGCAA AGCCGAGACA TCACAGGCAG AGAAGTGATC GATGCCAGAG 1860  
TGCCACACCA TCCCATGCTT GCTGTCCCA TGGTCCGAGT GGAGTGACTG CAGCGTGACC 1920  
40 TGCGGGAAGG GCATGCGAAC CCGACAGCGG ATGCTCAAGT CTCTGGCAGA ACTTGGAGAC 1980  
TGCAATGAGG ATCTGGAGCA GGTGGAGAAG TGCAATGCTC CTGAATGCCC CATTGACTGT 2040  
GAGCTCAGCG AGTGTGCGCA GTGGTCCGAA TGTAAACAGT CATGTGGGAA AGGCCACGTG 2100  
ATTGAAACCC GGATGATCCA AATGGAGCCT CAGTTTGAGG GTGCACCTGG CCCAGAGACT 2160  
GTGCAGCGAA AAAAGTGCCG CATCCGAAAA TGCCCTTCGAA ATCCATCCAT CCAAAAGCTA 2220  
45 CGCTGGAGGG AGGCCGCGG GAGCGGGCGG AGTGAGCAGC TGAAGGAAGA GTCTGAAGGG 2280  
GAGCAGTTCC CAGGTTGTAG GATGCGCCCA TGGACGGCCT GGTGAGAATG CACCAAACTG 2340  
TGCGGAGGTG GAATTCAGGA ACGTTACATG ACTGTAAAGA AGAGATTCAA AAGCTCCAG 2400  
TTTACCAGCT GCAAAGACAA GAAGGAGATC AGAGCATGCA ATGTTCACTC TTGTAGCAA 2460  
GGGTACGAGT TCCCGAGGGC TGCACTCTAG ATTCCAGAGT CACCAATGGC TGGATTATTT 2520  
50 GCTTGTTTAA GACAATTTAA ATTTGTACG CTAGTTTACA TTTTTCAGT GTGGTTGCGC 2580  
CAGTAGTCTT GTGGATGCCA GAGACATCCT TTCTGAATAC TTCTGTATGG GTACAGGCTG 2640  
AGTGGGGGCG CTTCACTCTC AGCCAGCCTC TTCTGCGAGA GGAGTAGTGT GAGCCACCTT 2700  
GTACTAAGCT GAAACATGTC CCTCTGGAGC TTCCACCTGG CCAGGGAGGA CGGAGACTTT 2760  
GACCTACTCC ACATGGAGAG GCAACCATGT CTGGAAGTGA CTATGCTGTA GTCCAGGGT 2820  
55 GCGGCAGGTA GGAACCATTC ACAGATGAAG ACAGCAGATT CCCCACATTC TCATCTTTGG 2880  
CCTGTTCATG GAAACCATTT TTTGCCATC TCTTCTTAGT GGAACCTTAG GTCTCTTTTC 2940  
AAGTCTCTCT AGTCATCAAT AGTTCTCTGG GAAAAACAGA GCTGGTAGAC TTGAAGAGGA 3000  
GCATGTATGT TGGGTGGCTT TTGTCTTTC ACTGAGAAAT TCGGAATACA TTTGTCTCAC 3060  
CCCTGATATT GGTCTCTGAT GCGCCGCCAA CAAAAATAAA TAAATAAATT ATGGCTGCTT 3120  
60 TATTTAATA TAAGGTAGCT AGTTTITACA CCGAGATAAA ATATAAGCT TAGAGTGTAT 3180  
TTTTCCCTTG CTTTGGGGGG TTCAGAGGAG TATGTACAAT TCTTCTGGGA AGCCAGCCTT 3240  
CTGAACCTTT TGGTACTAAA TCCTTATTGG AACCAAGACA AAGGAAGCAA AATTGGTCTC 3300  
TTTAGAGACC AATTGGCTTA AATTTAAAA TCTTCTACA CACATCTAGA CGTTCAGTT 3360  
TGCAATACAG TTTTATGCAA GAAACATTT TTGCTATACA AACATTTTGC TAAGTCTGCC 3420  
65 CAAAGCCCC CCAATGCATT CCTCAACAA AATACAATCT CTGTACTTTA AAGTTATTTT 3480  
AGTCATGAAA TTTTATATGC AGAGAGAAAA AGTTACCGAG ACAGAAAAA AATCTAAGGG 3540  
AAAGGAATAT TATGGGATTA AGCTGAGCAA GCAATTTCTG TGGAAAGTCA AACCTGTGAG 3600  
TGCTCCACAC CAGGGCTGTG GTCTCCCGAG ACATGCTATG GAATGGCCAC AGGTTTACAC 3660  
TGCCCTCCCA GCAATTATTA GCACACCAGA TTCAGGGAGA CTGACCACCA AGGGATAGTG 3720  
70 TAAAAGGACA TTTTCTCAGT TGGGTCCATC AGCAGTTTTT CTTCCTGCAT TTATGTGTA 3780  
AACTATTGT TTAATTTCTT CTTTATAGG CCTTATTACT GCTTAATCCA AATGTGTACC 3840  
ATTGGTGAGA CACATACAA GCTCTGAATA CACTACGAAT TTGTATTAAA CACATCAGAA 3900  
TATTTCCAAA TACAACATAG TATAGTCTGT AATATGTACT TTTAACCAA GAGAGACTAT 3960  
TCAATAAAA CTCACCTGGT CTTTCAATG TTAAGCTAA GTAAGTGTCT AGAAGGTTCT 4020  
75 TTTTATATT GTCTCCACC TCCATCATTT TCAATAAAG ATAGGGCTTT TGCTCCCTTG 4080  
TTCTTGGAGG GACCATTTT ACATCTCTGA ACTACCTTTG TATCCACAT GTTTTAAATC 4140  
CTTAAATGAA TTGCTTTCTC CCAAAAAAAG CACAATATAA AGAAACACAA GATTTAATTA 4200  
TTTTTCTACT TGGGGGGAAG AAAGTCTCTA TGTAGAAGCA CCCACTTTTG CAATGTTGTT 4260  
CTAAGCTATC TATCTAATCT TCAGCCCATG ATAAAGTTCC TTAAGCTGGT GATTCTAAT 4320  
80 CAAGGACAAG CCACCTTAGT GTCTCATGTT TGTATTGGT CCCAGTGGG TACATTTTAA 4380  
AATCCTGATT TTGAGACTT AAAACAGGT TAATGGCTAA GAATGGGTAA CATGACTCTT 4440  
GTGGGATTGT TATTTTGTG TTGCAATGGG GAATTTATAA GAAGCATCAA GTCTCTTTCT 4500  
TACCAGATC TTGTAGGTT GTTTATAGTT CTTTGGCTA ACAAATCATT TTGGAATAAA 4560  
AGATTTTTTA CTACAAAAAT G

Seq ID NO: 510 Protein sequence  
Protein Accession #: BAB18461.1

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MRLSPAPLKL SRTPALLALA LPLAALAFS DETLDKVPKS EGYCSRILRA QGTRREGYTE 60
FSLRVEGDDP FYKPGTSYRV TLSAAPPSTYF RGFTLIALRE NREGDKEDDH AGTFQIIDE 120
ETQFMSNCPV AVTESTPRRR TRIQVFWIAP PAGTGCVLK ASIVQKRIIY FQDEGSLTKK 180
LCEQDSTFDG VTDKPIIDCC ACGTAKYRLT FYGNWSEKTH PKDYPRRANH WSAIIGGSHS 240
10  KNYVLWEYGG YASEGVKQVA ELGSPVKMEE EIRQSSDEVL TVIKAKAQWP AWQPLNVRAA 300
PSAEFSVDRT RHLMSFLTMM GPSPDMNVGL SAEDLCTKEC GWVQKVVDL IPWDAGTDSG 360
VTYESPNKPT IPQEKIRPLT SLDHPQSPFY DPEGGSTQV ARVVIERAR KGEQCNIVPD 420
NVDDIVADLA PEEKEDDTP ETCIYSNWSP WSACSSSTCD KGRMRQRL KAQLDLSVPC 480
15  PDTQDFPQCM GPCCSDEDSG TCTMSEWITW SPCSISCGMG MRSRERYVKQ FPEDGVSCTL 540
PTEETKCTCV NECSFSSCL MTEGSEWDEC SATCGMGMKK RHRMIKQNP DGSCKAETS 600
QAEKCMPEFC HTIPCLLSPW SEWSDCSVTC GKGMRTQRQM LKSLAELGDC NEDLEQVEKC 660
MLPECPIDCE LTEWSQWSEC NKSCGKHVI RTRMIQMEPQ FGGAPCPETV QRKCKRIRKC 720
LRNPSIQKLR WREARESRRS EQLKEESEGE QPFGCRMRFW TAWSECTKLC GGGIQERYMT 780
20  VKGRFKSSQF TSCKDKKEIR ACNVHPC

```

Seq ID NO: 511 DNA sequence  
Nucleic Acid Accession #: NM\_003108.1  
Coding sequence: 76..1401

```

25      1      11      21      31      41      51
|      |      |      |      |      |
GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA 60
GCCCTGCAAC GATCATGTGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCC 120
30  CGGGAGGCGC TGGACACGSA GGAGGGCGAA TTCATGGCTT GCAGCCGGT GGCCCTGGAC 180
GAGAGCGACC CAGACTGGTG CAAGACGGCG TCGGGCCACA TCAAGCGGCC GATGAACGCG 240
TTCATGTAT GGTCCAAGAT CGAACGCGAG AAGATCATGG AGCAGTCTCC GGACATGCAC 300
AACCCGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAAA TGTGAAGGA CAGCGAGAAG 360
ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC 420
35  TACAAGTACC GGCCCGGAA AAAGCCCAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC 480
CAGAGCCAG AGAAGAGCGC GGCCGGCGGC GCGCGGGGGA GCGCGGGCG AGGCGCGGCG 540
GGTGCCAGA CTTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCGCGCGGCC 600
GCGGCGGCA AGGCGGGCGC GGGCAAGGCG GCCAGTCCG GGGACTACGG GGGCGCGGCG 660
40  GACGACTACG TGCTGGCAG CTTGGCGTG AGCGCTCGG GCGCGGGCG GCGGGCGAAG 720
ACGGTCAAGT GCGTGTCTT GGATGAGGAC GACGACGAGC ACCAGCAGCA CGACGAGCTG 780
CAGCTGCAGA TCAACAGGA GCCGACGAG GAGGACGAGG AACACCGCA CAGCAGCTC 840
CTGCAAGCGC CGGGGAGCA GCGCTGCGAG CTGCTGAGAC GCTACAACT CGCCAAAGTG 900
CCCGCAGCC CTACGCTGAG CAGCTCGCG GAGTCCCCCG AGGAGCGAG CTTCTACGAC 960
45  GAGGTGCGGG CCGGCGGAC CTGCGGCGCC GGGGGCGCA GCGGCTCTA CTACAGCTTC 1020
AAGAACATCA CCAAGCAGCA CCGCGCGCG CTGCGGCGC CCGGCTGTC GCCCGGTC 1080
TCGCGCTCGG TGTCCACCTC CTGCTCCAGC AGCAGCGGCA GCAGCAGCG CAGCAGCGC 1140
GAGGACGCGC AGCAGCTGAT GTTGCACCTG AGCTTGAATT TCTCTCAAAG CGCGCACAGC 1200
GCCAGCGAGC AGCAGCTGAG GGGCGGCGC GCGGCGGGA ACCTGTCCCT GTGCTGGTG 1260
50  GATAAGGATT TGGATTCTGT CAGCGAGGCG AGCCTGGGCT CCCACTTGA GTTCCCGGAC 1320
TACTGCAGCG CGGAGCTGAG CGAGATGATC GCGGGGACT GCGTGGAGC GAACCTTCTC 1380
GACCTGGTGT TCACATATG AAAGGCGGCC GCTGCTGCT CTTTCTCTG GAGGGTGCAG 1440
AGCTGGGTTC CTTGGGAGGA AGTTGTATGT GTGATGATG TGATGATGAT AATGATGATG 1500
ATGATGGTGG TGTGTATGTT GCGGTGGTA GGGTGGAGGG GAGAGAAAG GATGCTGATG 1560
55  ATATTGATAA GATGTCGTA CGCAAGAAA TTGAAAGAA TGATGAAAT TTTGGTGGAG 1620
TTAAGTGAA ATGAGTAGTT TTTAAACATT TTTCTGTGCT TTTTGTGTC CCCCTCCCT 1680
TCCTTTATCG TGTCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCA 1740
AAAATGTGTT TTTGTAATTA CTATTTCTTT TTCTGAAAT TCGTGATTGC AACAAAGGCA 1800
GAGGGGGCGC CGCGGCGGAG GGGAGGTAGG ACCGCTCCG GAAGGCGCTG TTTGAAGCTT 1860
60  GTCGCTCTTT GAAGTCTGGA AGACGCTGC AGAGGACCTT TTTGGCAGCA CAACGTGTAC 1920
TCTAGGAGAT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAGAAC TGGTGATT 1980
TTTTTAACAA AAAAAGG

```

Seq ID NO: 512 Protein sequence  
Protein Accession #: NP\_003099.1

```

65      1      11      21      31      41      51
|      |      |      |      |      |
MVQQAESLEA ESNLPREALD TEEGEPMACS PVALDESDPD WCKTASGHK RPMNAPMWS 60
70  KIERRKIMEQ SPDMEAEIS KRLGKRWKML KDSEKIPFIR EAERLRLKHM ADYDPYKYRP 120
RKPKMDPSA KPSASQSPER SAAGGCGGSA GGGAGGAKTS KGSKKCGKL KAPAAAGAKA 180
GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGTKVKCV FLDEDDDDDD DDELDLQLIK 240
QEPDEEDEEP PHQQLQPPG QPQSLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVAD 300
ATSGAGGGR LYYSFKNITK QHPPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD 360
75  LMPDLNLNPS QSAHSASEQQ LGGAAAGNL SLSLVDKDL D SFESEGLGSH FEFPDYCTPE 420
LSEMIAGDWL EANFSDLVFT Y

```

Seq ID NO: 513 DNA sequence  
Nucleic Acid Accession #: CAT Cluster

```

80      1      11      21      31      41      51
|      |      |      |      |      |
GGTCGACCTA AATCTGATAA CTGGCTTATT ATGTAATTTA TTGGTGTAT TATAGTAGAG 60
ATTGGTAATC TACAGTAAGA TTTTCAGTTA GGATTGAGA TTATGATAAT AACTAATAGA 120
ATATTTCTAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTG 180

```

5  
 GCAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA 240  
 AAGGATATCT GTTGTCTCCG AATGAAACAA TTTTCTGAA ATAGAGGGCC CAGAATTGGT 300  
 CTCTGACAAAT TAATAAGAC ATCAAAGATA GCAAATGAT TTTTATATCT TAGGGCCAAT 360  
 ACTACCAATT TAATAATTAA ACAAATTCTT GGTGAGCTCT GAACCTTGGA GAATTGGTGG 420  
 CAACATAGAC TTGGATTCTT CCAAATTCCC CACATAAAAC AAAGGGGATC AACTAGATAG 480  
 AAAAACCCGA AACCTTTGGA AATATCTGTT TAAAAAATAA AAAAAGTCTGA CGCGGGGCC

Seq ID NO: 514 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

10

15  
 1 11 21 31 41 51  
 GGAGCCACAG TGAAAGTCAA GAATGTCAGT GATTCCACAT TTAATATCTA CATTTTTCGA 60  
 GGGCAGTTAC TCTTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTA GACAAGTGAA 120  
 TACAGGATTCT TCTGGGTTGT ATTCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC 180  
 CTGGCTTCA CTCTGACTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT 240  
 CCTGCAGTC TTAAGAAGAC CTITCCAAAC TATGAACAG CCCAGCAGCA CTGAGTTAGA 300  
 GGTAAATTCT GAACCTTGA AACTAAAAC TATTCTAAT GCACATAGAA TTGGCAAGTA 360  
 GCATTCTATG TCTATGAACA GTATGTCTTT TCTATATAAC AGAGAAATC TTTTAAAGCA 420  
 AACTACTCAG TTTAAAACCT AATTCTTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA 480  
 TCAATGCAAC AGTACACTCT TATTCAAGCA TTTGAAAGAA AGAATTCGAG ATCTAGTTTG 540  
 TATCAGATAT TATAAATTAG TATGGTTTAG TCTTTGTCTA GAAATTCCTAC TTAATTTTGG 600  
 GACTATAGT TTAAGAATGT AAGCAGAAGT TCTGCACCAA TCAGAATAAG CTACATTATG 660  
 25  
 CTGAGTGAAC AACTACTGTA ATGACAAAAT ATCAGTGGCT TAATACAATG GTTTTCTCT 720  
 CATACTTGTT CATAAAGAGT CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG 780  
 GGTGTGTGA AGCTCCACCA TTTTAGATAG CTCCTTCAA AGTCAGCCAT CTTTGGCAGT 840  
 CCATGTCCCC CACAGGCTG GCAAATTG GCTCTGGATG GCTTCAAGGA TTGAGCATCG 900  
 GGCAGTTTAA ATGCTTTCAA CATGGAAGT GGACACCGGC CACTCCCACT CACATCCCTT 960  
 30  
 GGGCCAGAAC TAGGTCAGTG GGGCCGGACC TAACCTGGGA GGGTTGGGGA ATTGTAAATC 1020  
 CTCCATGTAC CCAAGTGGA GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG 1080  
 AAATCCATTG TACCATTCCT TTGCCTAAA GTGAAAAGAT GAGTACTTTC ATCAATTTTG 1140  
 AAATCTGACT TTTGAAGTAA ATCCTGGTAG CTGTCATGGG GGCTGGATT TCCAGAAAGCC 1200  
 35  
 ATATGTAATT TGGGAATGAC ATTCACCTAA GCTCATAGAA TATCATTATT TGATGTAAA 1260  
 TGCCCTCAT TTGCAATACG GACCAAAATG CACTAACAC AAAACCCCC TCCCCACGGG 1320  
 GCCCGGGTCC CCAATTCCTC TCCATCCCTT TAAATGAGGC ATTCTATGAT TTGGAATGGA 1380  
 AGCCAGTGTG TAGTCGTAGG AATTTTACTT AATTCAAGAA TTATTCTCAC TGAATATGTG 1440  
 CCAATCTGTA AAGCAATGCA AAGTCAAAAT TTGCATCTTC TTGCTCAAG GGCCTTTAGA 1500  
 40  
 TGTAACAACA CAGACATGAT ACAAGGCTGA CAATGACATT ATGATTAAAA TATGTTAAAC 1560  
 AACTTATTAA ATTGTGAATC AACAAAAAAT TATGTTCTTT ATTTTATGGT TTTGCAATAGT 1620  
 CCTGACTCAC TGCCTACATA CCCCTCTTGT TCCTCAGTTC TTATCCCTGA TTTCTTACAG 1680  
 GATGGCCTAA GACAGCTGTA GATGTTTTTA TTAGCAAAA AAAAAAATAA AAAAGTCGAC 1740  
 CGCGCCCGGA ATTTAGTAG

45

Seq ID NO: 515 DNA sequence  
 Nucleic Acid Accession #: NM\_012427  
 Coding sequence: 43..924

50  
 1 11 21 31 41 51  
 CTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGCTAC AGCAAGACCC 60  
 CCCTGGATGT GGGTCTCTG TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT 120  
 GTTCTCGCCA ACAATGATGT TTCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180  
 55  
 AACCAGGACC TGGGAGCTGG GGGCGGGGAA GACGCCCGGT CGGATGACAG CAGCAGCCGC 240  
 ATCATCAATG GATCCGAGTG CGATATGCAC ACCCAGCCGT GGCAGGCCGC GCTGTGCTA 300  
 AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGGTGATC CACAGTGGCT GCTCACGGCC 360  
 GCCCACTGCA GGAAGAAAGT TTTCAGATGC CGTCTCGGCC ACTACTCCCT GTCAACAGT 420  
 TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAAATCA TCCCCACCC TGGCTACTCC 480  
 60  
 CACCCCTGGC ACTCTAACGA CCTCATGCTC ATCAAACTGA ACAGAAGAAT TCGTCCCACT 540  
 AAAGATGTCA GACCCATCAA CGTCTCCTCT CATTGTCCCT CTGCTGGGAC AAAGTGCTTG 600  
 GTGTCTGGCT GGGGGACAA CAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC 660  
 TTGAATATCA GCGTGCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720  
 GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG 780  
 65  
 GGGCCTGTGG TCTGCAATGG CTCCTGCAG GGAATGCTGT CCTGGGAGGA TTACCTTTGT 840  
 GCCCGGCCCA ACAGACCGGG TGCTACAGG AACCTCTGCA AGTTCACCAA GTGGATCCAG 900  
 GAAACCATCC AGGCCAACTC CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCCACCT 960  
 GCTGCAGGGA CAGCCCTGAC ACTCCTTTCA GACCCCTATT CCTTCCAGGA GATGTTGAGA 1020  
 70  
 ATGTTACTCT CTCACGCCCC TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCCCCAC 1080  
 ATTGGGCTGA CGGTGCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCCAGGG 1140  
 CGGGGGTTGC GTCTCAATCT CCTTGGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT 1200  
 TCTCTGACGC TCTGACCCAA ATTTAGTCCC AGAATAAACA TGAGAAGTGG AAAAAAATAA

75

Seq ID NO: 516 Protein sequence  
 Protein Accession #: NP\_036559

80

1 11 21 31 41 51  
 MATARPPWML VLCALITALL LGVWEHVLN NDVSCDHPSN TVPSGNSQDL GAGAGEDARS 60  
 DDSSSRIRNG SDCDMHTQPW QAALLLRPNQ LYCGAVLVHP QNLLTAARCR KKVFRVRLGH 120  
 YLSLSPVYESG QQMPQGVKSI PHPGYSHPHG SNDLMLIKLN RRIIPTKQDVR PINVSSHCP 180  
 AGTKCLVSGW GTTKSPQVHP PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS 240  
 CQDSSGGPVV CNGSLQLVLS WGDYPCARPV RPGVYTNLCK FTKMIQETIQ ANS

Seq ID NO: 520 Protein sequence  
Protein Accession #: Eos sequence



1 11 21 31 41 51  
 5 MLTEVMEVWH GLVIAVVSFL LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH 60  
 HPPAVKENKE TQTERDIPMS DSYLRHSDT PSDSLDSSCS SPPACQATED VDYTVVFS 120  
 PGELKNDSP L DYENKEITD YVNVNPERHK PSFVYFVNPA LSEPAEYDQV AM

Seq ID NO: 521 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 107..328

1 11 21 31 41 51  
 15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCCA AATATTTTAA 60  
 ATGGGGTCCA GTTCTCTATG GATTCTTACA TTTAATTGTG AGGGAATGCG CATTTTTCCT 120  
 CCTTAAACAA GGCATGGGCG TCACAAGTCT ATGGAGACAG GCCAAAAGA ATGTGGAGAA 180  
 GAAATCTGAT AATATCACAG AGGTCTCTCA GACCCATGGA CTCTGGTCT GTACCCAAAA 240  
 AAGCTGTTCG TTCTCTCAAA ACAAAAACAA GGCTTGGCTG GGAAAACAGG CCAATGCCCC 300  
 20 GGCAAGAAAG GTTGAGATCA GATGTAGGA AGAATCTTCA GGTAAAGTAT GAGAACTATG 360  
 GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCCAGG GAAAAATTTA AAAAGGTTGA 420  
 ATCAGCTGTT GTAGAGTCTT ATTTGGCAAT CTCATGGTTA AATGACTTCC CTTTGAGCTC 480  
 TTTAATTATT GGCAATAAAC AACTTCTTTA AAAGTTTAA ATAAAAATAGC AACCACCACC 540  
 A

25 Seq ID NO: 522 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 30 MPFFPLKQGM GLTSLWRQAK KNVEKKTDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK 60  
 QANAPARKVE IRC

35 Seq ID NO: 523 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 211..1895

1 11 21 31 41 51  
 40 GGATCTGAGG GGCGCCAGT CACTTCTCTC ACGTCTCTGT GCTGGGCGGG AGGAGCGGAT 60  
 GGGGCTTGGG AGGCAGCGCT CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTGGGA 120  
 GAGGAATTAT CTGATAAAAT TCTGGGTTA ATATTTTAA AAAACGGAGAG TTTTAAAAA 180  
 TGATTTTTT CCCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGT CAAACAGCATA 240  
 GTGCTTTTTC TTTTCTCTTC TTTTCTTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300  
 45 CACAGGTTCC TTGAACAGCT GGATCTGAT GGCAACATTA CTATAGAGGA GCAGATTGTC 360  
 CTTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCAACT CCAGGAGGGA 420  
 GAAGGTAATT GTTTCCCTGA ATGGGATGGA CTCATTGTGT GGCCAGAGG AACAGTGGGG 480  
 AAAATATCGG CTGTTCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540  
 TTCCGACACT GTAAACCCAA TGGAAACATGG GATTTTATGC ACAGCTTAAA TAAACATGG 600  
 50 GCAATATTAT CAGACTGCTC TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660  
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGCTACT CCATCTCTTT TGGTCTCTG 720  
 GCTGTGGCTA TTCTCATCAT TGGTACTTTC AGACGATTGC ATTGCACTAG GAATATATC 780  
 CACATGCACT TATTTGTGTC TTTCATGCTG AGAGCTACAA GCATCTTTGT CAAAGACAGA 840  
 GTAGTCCACT ATGCATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900  
 55 CAAAATTTCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960  
 GTTGTGATGT TTATTTACTT CTTGGCTACA AATTATTATT GSATCCTGTT GGAAGTCTCT 1020  
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAATACCT GTGGGCTTTC 1080  
 ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTTGAG CATGGGCTGT GGCACGAGCA 1140  
 ACTCTGGCTG ATGCGAGGTT CTGGGAACTT AGTGTGGAG ACATCAAGTG GATTATCA 1200  
 60 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TCTGAATAC GGTTAGAGTT 1260  
 CTAGTACCA AATCTGGGA GACCAATGCA GTTGGCATG ACACAAGGAA GCAATACAGG 1320  
 AAATCGGCA AATCGACACT GGTCTGGTC CTAGTCTTTG GAGTGCATTA CATCGTGTTC 1380  
 GTATGCTGCT CTCACTCCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440  
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500  
 65 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCGTGA CTGGAAGAGG 1560  
 ACACCGCAT GTGGCAGCG CAGATGCGC TCAGTGCTCA CCACGTGAC GCACAGCACC 1620  
 AGCAGCCAGT CACAGGTGGC GGCAGCACA GCATGGTGC TTAATCTTGG CAAAGCTGCC 1680  
 AAGATCGCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740  
 TCAGAGCAGG ACTGCTGCC ACATCTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800  
 70 CAGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCTTA TGAATCTAA CCCAGACACT 1860  
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 524 Protein sequence  
 Protein Accession #: Eos sequence

75 1 11 21 31 41 51  
 MLRSSLSSTSI VLFLFSSFSI INESISSRRK HRFLEQLDSD GTTIEBQIV LVLKAKVQCE 60  
 LNTAQLQEG EGNCFFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120  
 80 DFMSLNKWT ANYSDCLRFL QPDISIGQKE FFERLYVMT VGYISFSGSL AVAILIIGYF 180  
 RRLHCTRYNI HMHLFVSFML RATSIFVKOR VVHAHIGVKE LESLIMQDDP QNSIEATSDV 240  
 KSQYIGCKIA VVMFIYFLAT NYWILVEGL YLHNLIFVAF PSDTKYLWGF ILIGWGFPA 300  
 PVAAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILPLNTRV LATKIWETNA 360  
 VGHDTKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FPNFQGFV 420  
 SIIICYCNGE VQAEVKQWMS RWNLSVDWKR TPPOGSRRCG SVLTITVTHST SSQSQAAS 480

RMVLISGKAA KIASRQPD SH ITLPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540  
SRPMESNPDT EGCGQETEDV L

Seq ID NO: 525 DNA sequence  
Nucleic Acid Accession #: NM\_005048  
Coding sequence: 143..1795

1 11 21 31 41 51  
10 | | | | | |  
GGCCGCTGGC CCGGGCCCCA CCACCCACG TCGCGCTCGT TACTGGCCAC AAGTTTGCTC 60  
TGGGCCAGCC AAGTTGGCAA CTCTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120  
TCTTCTTACA GCCGTTCCCG GCATGGCCGG GCTGGGGGGC TCGCTCCACG TCTGGGGTGT 180  
GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCACAGCT GATTCTGATG GCACCATTAC 240  
TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300  
15 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTG 360  
GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGC CCTCCTTATA TTTATGACTT 420  
CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAAACATGGG ATTTTATGCA 480  
CAGCTTAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGCG AGCCAGATAT 540  
CAGCATAGGA AAGCAAGAA TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600  
20 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTACTTCA GAGATTGCA 660  
TTGCACTAGG AACTATATCC ACATGCACCT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720  
CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780  
AATAATGCGA GATGACCCAG AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840  
TATCGGCTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATATTG 900  
25 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCT TTTGGACAC 960  
CAATATCCTG TGGGCTTCA TCTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020  
ATGGGCTGTG CACGAGAGCA CTCTGGCTGA TCGAGGCTGC TGGGAACCTA GTGCTGGAGA 1080  
CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140  
TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200  
30 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG 1260  
AGTGCATTAC ATCGTGTTCG TATGCTGCCC TCACCTCTTC ACTGGGCTCG GGTGGGAGAT 1320  
CCGCACTGAC TGTGAGCTCT TCTTCAACTC CTTCAGGGT TCTTTTGTGT CTATCATCTA 1380  
CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440  
CTCCGTGGAC TGGAAAGGA CACCGCCATG TGGCAGCCGC AGATGCGGCT CAGTGTCTAC 1500  
35 CACCGTGACG CACAGCACA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560  
TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACCTTACC 1620  
TGGCTATGTC TGGAGTAATC CAGAGCAGGA CTGCTGCCA CACTCTTCC ACAGGAGAC 1680  
CAGGAAGATG AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740  
GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800  
40 CATTGTGGC TGACTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860  
ATACTCTTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920  
TTTTAGGCTC CATGAATTCG CTCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980  
GGAGTAGTTC ATTACCTTCT ATTGGCATCA AGTTTCTCTC TAAATTAATG TATGGTATT 2040  
45 GCTCTGTGAT TGTTCTATTT TTTCTGTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100  
GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160  
ATTTCTCTTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220  
ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280  
GATCTAAGAA CAAGTACTTG CTGGAATAAT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340  
50 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAAATT CTCAAAAAG AATATTTTAC 2400  
ACATCCCTTC TTTTGAATGG CCTCTTGTG ACCAGCCAGA CCTCAGTCT TCACCTTTTC 2460  
TTCTTTGTA ACCATGTCTAT GTGGAAAGAT TTCTCTAGTT AGTGAGCTTG TGTCTGCAAA 2520  
TTGATTTTGT TTGTAATGTA TTTGATAGC AAATCATGCT GCATCTATAT CTTTCTCTG 2580  
TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTAAAAA 2640  
T

Seq ID NO: 526 Protein sequence  
Protein Accession #: NP\_005039

1 11 21 31 41 51  
60 | | | | | |  
MAGLGASLHV WGLWMLGSL LARAQLDSG TITIEEQIVL VLKAKVQCEL NITAIQLEGE 60  
GNCFPEWDGL ICWPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120  
NYSDCRLRFLQ PDISIGKQEP FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYYH 180  
MHLFVSFMLR ATSFIVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240  
65 VMFIYFLATN YWILVEGLY LHNLIQVAF SDTKYLWGF IIGWGFPAF VAAWAVARAT 300  
LADARCWELS AGDIKWYQA PILAAIGLNF ILPLNTVRVL ATKIWETNAV GHDTRKQYRK 360  
LAKSTLVVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELP FNSFQGFVVS IICYCNGEV 420  
QAEVKMWSR WNLSDWKRT PPGSRRRCS VLTTVTHSTS SQSQVAASR MVLISGKAAK 480  
70 IASRQPD SHI TLPGYVWSN SEQDCLPHSF EETKEDSGRQ GDDILMEKPS RPMESNPDT 540  
GCQGETEDVL

Seq ID NO: 527 DNA sequence  
Nucleic Acid Accession #: XM\_036683  
Coding sequence: 38..3655

1 11 21 31 41 51  
75 | | | | | |  
GCTTTGCCCA GTAGTTGGAA AGTGAACCTG ACTCGTGATG GTTCTCCTGT CACTTTGGTT 60  
GATAGCAGCC GCTCTGGTAG AGGTTAGGAC TTCAGCTGAT GGACAAGCTG GTAATGAAGA 120  
80 AATGGTGCAA ATAGATTTAC CAATAAGAG ATATAGAGAG TATGAGCTGG TGACTCCAGT 180  
CAGCACAAT CTAGAAGGAC GCTATCTCTC CCATACCTCT TCTGCGATC ACAAAAAGAG 240  
GTCAGCGAGG GACGTGTCTT CCAACCTCTG GCAGTGTGTC TTTAACAATA CGGCATTGG 300  
AAAAGATTTT CATCTGCGAC TAAAGCCCAA CACTCAACTA GTAGCTCTG GGGCTGTGTT 360  
GGAGTGGCAT GAGACATCTC TGGTGCTCG GAATATAACC GATCCCATTA ACAACCATCA 420

	ACCAGGAAGT	GCTACGTATA	GAATCCGGAA	AACAGAGCCT	TTGCAGACTA	ACTGTGCTTA	480
	TGTTGGTGAC	ATCGTGGACA	TTCCAGGAAC	CTCTGTTGCC	ATCAGCAACT	GTGATGGTCT	540
	GGCTGGAATG	ATAAAAAGTG	ATAATGAAGA	GTATTTTCATT	GAACCCCTGG	AAAGAGGTAA	600
	ACAGATGGAG	GAAGAAAAG	GAAGGATTCA	TGTTGTCTAC	AAGAGATCAG	CTGTAGAACA	660
5	GGCTCCCAT	GACATGTCCA	AAGACTTCCA	CTACAGAGAG	TCGGACCTGG	AAGGCCTTGA	720
	TGATCTAGGT	ACTGTTTATG	GCAACATCCA	CCAGCAGCTG	AATGAAACAA	TGAGACGCCG	780
	CAGACACGGG	GGAGAAAACG	ATTACAATAT	CGAGGTACTG	CTGGGAGTGG	ATGACTCTGT	840
	GGTCCGTTTC	CATGGCAAAG	AGCACGTCCA	AAACTACCTC	CTGACCCTAA	TGAACATTGT	900
	GAATGAAATT	TACCATGATG	AGTCCCTCGG	AGTGCATATA	AATGTGGTCC	TGGTGCGCAT	960
10	GATAATGCTG	GGATATGCAA	AGTCCATCAG	CCTCATAGAA	AGGGGAAACC	CATCCAGAAG	1020
	CTTGGAGAAT	GTGTGTGCGT	GGGCGTCCCA	ACAGCAAAGA	TCTGATCTCA	ACCACTCTGA	1080
	ACACCATGAC	CATGCAATTT	TTTAAACCAG	GCAAGACTTT	GGACCTGCTG	GAATGCAAGG	1140
	ATATGCTCCA	GTACCGGCA	TGTGTCTATC	AGTGAGAAGT	TGTACCTCTG	ATCATGAGGA	1200
	TGGTTTTTCA	TCGTCTTTTG	TAGTAGCCCA	TGAAACGGGC	CATGTGTGGG	GAATGGAGCA	1260
15	TGATGGACAA	GGCAACAGGT	GTGGTGATGA	GACTGCTATG	GGAAGTGTCA	TGGCTCCCTT	1320
	GGTACAAGCA	GCAATTCATC	GTTACCACCTG	GTCCCGATGC	AGTGGTCAAG	AAGTGAAGAG	1380
	ATATATCCAT	TCTATGACT	GTCTCCTTGA	TGACCCCTTT	GATCATGATT	GGCCTAAACT	1440
	CCCAAGACTT	CCTGGAATCA	ATTATTCTAT	GGATGAGCAA	TGTCTTTTGG	ATTTTGGTGT	1500
	TGGCTATAAA	ATGTGCAACG	CGTTCCGAAC	CTTTGACCCA	TGTAACACGC	TGTGGTGTAG	1560
20	CATCCTGAT	AATCCCTACT	TTTGTAAAGC	TAAAAAGGGA	CCTCCACTTG	ATGGGACTGA	1620
	ATGTGCTGCT	GGAAATATGT	GCTATAAGGG	TCATTGTCATG	TGGAAGAATG	CTAATCAGCA	1680
	AAAACAAGAT	GGCAATTGGG	GGTCATGGAC	TAAATTGTCG	TCCTGTTCTC	GGACATGTGG	1740
	AACCTGGTTT	CGTTTCAGAA	CAGCCAGTGC	CAATAATCCC	ATGCCCATCA	ATGGTGGTCA	1800
	GGATTGTCTT	GGTGTAAATT	TTGAGTACCA	GCTTTGTAA	ACAGAAGAA	GCCAAAACAA	1860
25	CTTTGAGGAC	TTGAGAGCAC	AGCAGTGTCA	GCAGCGAAAC	TCCCACTTTG	AATACCGAA	1920
	TACCAAAACAC	CATCTGTTGC	CATATGAACA	TCCTGACCCC	AAGAAAAGAT	GCCACCTTTA	1980
	CTGTGAGTCC	AAGGAGACTG	GAGATGTTGC	TTACATGAAA	CAACTGTTGC	ATGATGGAA	2040
	GCACTGTTCT	TACAAAGATC	CATATAGCAT	ATGTGTGCGA	GGAGAGTGTG	TGAAAGTGGG	2100
	CTGTGATAAA	GAATTTGGTT	CTAATAAGGT	TGAGGATAAG	TGTGGTGTCT	GTGGAGGAGA	2160
30	TAATTCGCCAC	TGCCGAACCG	TGAAGGGGAC	ATTTACCAGA	ACTCCAGGA	AGCTTGGGTA	2220
	CCTTAAGATG	TTTGATATAC	CCCTGGGGC	TAGACATGTG	TTAATCCAAG	AAGACGAGGC	2280
	TTCTCTCAT	ATTCTTGCTA	TTAAGAACCA	GGCTACAGGC	CATTATATTT	TAAATGGCAA	2340
	AGGGAGGAAA	GCCAACTGCG	GGACCTTCAT	AGATCTTGGT	GTGGAGTGGG	ATTATAACAT	2400
	TGAAGATGAC	ATTGAAAGTC	TTACACCGA	TGGACCTTTA	CATGATCCTG	TTATTGTTTT	2460
35	GATTATACCT	CAAGAAAATG	ATACCCGCTC	TAGCCTGACA	TATAAGTACA	TCATCCATGA	2520
	AGACTCTGTA	CCTACAAATCA	ACAGCAACAA	TGTCTCCAG	GAAGAATTAG	ATACTTTTGA	2580
	GTGGGCTTTG	AAGAGCTGGT	CTCAGTGTTC	CAAAACCTGT	GGTGGAGGTT	TCCAGTACAC	2640
	TAAATATGGA	TCCGATAGGA	AAAGTGATAA	TAAATGGTTC	CATCCGAGCT	TCTGTGAGGC	2700
	CAACAAAAG	CCGAAACCTA	TTAGACGAAT	GTGCAATATT	CAAGAGTGTG	CACATCCACT	2760
40	CTGGGTAGCA	GAAGAAATGG	AACACTGCAC	CAAAACCTGT	GGAAGTCTCT	GCTATCAGCT	2820
	TGCGACTGTA	CGCTGCCTTC	AGCCACTCCT	TGATGGCACC	AACCGCTCTG	TGCACAGCAA	2880
	ATACTGCTAG	GGTGACCGTC	CCGAGAGCCG	CCGGCCCTGT	AACAGAGTGC	CCTGCCCTGC	2940
	ACAGTGAGAA	GCCAGACCTC	GGAGTGAGTG	TTCACTGACC	TGCGGTGAAG	GAACGGAGGT	3000
	GAGGCAGGTC	CTCTGACGGG	CTGGGGACCA	CTGTGATGGT	GAAAAGCCTG	AGTCGGTCAG	3060
45	AGCCTGTCAA	CTGCCTCCTT	GTAATGATGA	ACCATGTTTG	GGAGACAAGT	CCATATTCTG	3120
	TCAAATGGAA	GTGTTGGCAC	GATACCTGCT	CATACCAGGT	TATAACAAGT	TATGTTGTGA	3180
	GTCTGTCAGC	AAGCGCAGTA	GCACCTGCCC	ACCACCATAC	CTTCTAGAAG	CTGCTGAAAC	3240
	TCAATGATG	TCATCTCTGA	ACCCTAGTGA	CCTCCCTAGA	TCTCTAGTGA	TGCTATACATC	3300
	TTTGGTTCCT	TATCATTCAG	AGACCCCTGC	AAAGAAGATG	TCTTTGAGTA	GCATCTCTTC	3360
50	AGTGGGAGGT	CCAATATGAT	ATGCTGCTTT	CAGGCCAAAC	AGTAAACCTG	ATGTTGCTAA	3420
	TTTACGCCAG	AGGAGTGTCT	AGCAAGCAGG	AAGTAGACT	GTGAGACTGG	TCACCGTACC	3480
	ATCCTCCCCA	CCCACCAAGA	GGGTCCACCT	CAGTTCAGCT	TCACAAATGG	CTGCTGCTTC	3540
	CTTCTTTGCA	GCCAGTGATT	CAATAGGTGC	TTCTTCTCAG	GCAAGAACCT	CAAGAGAAAG	3600
	TGAAAGATC	ATTGACAACA	GACGTCCGAC	AAGATCATCC	ACCTTAGAAA	GATGAGAAAG	3660
55	TGAACCAAAA	AGGCTAGAAA	CCAGAGGAAA	ACCTGGACAA	CCTCTCTCTT	CCCATGGTGC	3720
	ATATGCTTGT	TTAAAGTGGG	AATCTCTATA	GATCGTCAGC	TCATTTTATC	TGTAATTGGA	3780
	AGAACAGAAA	GTGCTGGCTC	ACTTCTAGT	TGCTTTTCATC	CTCCTTTTGT	TCTGCATTGA	3840
	CTCAATTTACC	AGAAATTCATT	GGAAGAAATC	ACCAAAGATT	ATTACAAAAG	AAAAATATGT	3900
	TGCTAAGATT	GTGTTGGTGC	CTCTCTGAAG	CAGAAAAGGG	ACTGGAAACA	ATTGTGCATA	3960
60	TCAGCTGACT	TTTTGTTTGT	TTTAGAAAAG	TTACAGTAAA	AATTAAGAA	AGTAAACCAAT	4020
	GGTTTACACT	TTAAACAAGAA	ATTTTGGATA	TGGAACAAAG	AATCTTAGA	CTTGTATTCC	4080
	TATTTATCTA	TATTAGAAAT	ATTGTATGAG	CAAAATTGCA	GCTGTTGTGT	AAATACTGTA	4140
	TATTTGMAAA	ATCAGTATTA	TTTTAAGAGA	TGTGTTCTCA	AATGATTGTT	TACTATATTA	4200
	CATTTCTGGA	TGTTCTAGGT	GCTGTCTGTT	GAGTATTGCC	TGTTTGGACA	TTCTATAGGT	4260
65	TAATTTTCAA	AGCAGAGTAT	TACAAAAGAG	AAGTTAGAA	TACAGCTACT	GACAATATAA	4320
	AGGGTTTTGT	TGAATCAACA	ATGTGATACG	TAAATTATAG	AAAAAGAAAA	GAAACACAAA	4380
	AGCTATAGAT	ATACAGATAT	CAGCTTACCT	ATTGCCCTCT	ATACTTATAA	TTTAAAGGAT	4440
	TGGTGTCTTA	GTACACTTGT	GGTCACAGGG	ATCAACGAAT	AGTAAATAAT	GAACCTCGTC	4500
	AAGACAAAAC	TGAACCCCTC	TTTCCAGGAC	CTCAGTAGGC	ACCGTTGAGG	TGTCCTTTGT	4560
70	TTTTGTGTGT	GTGTGTTCTT	TTTTAATTTT	CGCATTTGTT	ACAGATACAA	ACAGTTATAC	4620
	TCATGTACT	GTAATAATCG	CAAAAGGAAA	AGTTTGGGGA	TAACTTATTT	GTATGTTGGT	4680
	AGCTGAGAAA	AATATCATCA	GTCTAGAAAT	GATATTGAG	TATAGTAGAG	CTTTGGGGCT	4740
	TTGAAGGCAG	GTTCAGAAAA	GCAATATGCG	ATGGTTGAGA	TATTTATTTT	CCATATGTTT	4800
	CATGTTCAAA	TGTTCAACAC	CACATGCAAT	CTGACTGCAA	TAAATGCTTA	ATAATTTATG	4860
75	TCAGTAGTCA	CCTTGCTCAC	AGCAAGGCCA	GAAATGCTCT	CTCCAGGGAG	TAGATGTAAA	4920
	GTACTGTATC	ATAGAATTCA	GAACTGAAGA	TATTTATTTA	AAGTTGATTT	TTTTTTCTTG	4980
	ATAGTATTTT	TATGACTTAA	ATATTACAC	TAATATCAAT	TACATATTTT	GGTAAACTAG	5040
	AGAGACATAA	TTAGAGATGC	ATGCTTTGTT	CTGTGCATAG	AGACCTTTAA	GCAAACTACT	5100
	ACAGCCAACT	CAAAAGCTAA	AACCTGAACAA	ATTGATGTTT	ATGCAAAACAT	CTTGCAATTT	5160
80	TAGTAGTTGA	TATTAAGTTG	ATGACTTGT	TCCCTTCAAG	GAAACATTAA	ATTGTATGGA	5220
	CTCAGCTAGC	TGTTCAATGA	AATTGTGAAT	TAGAAACATT	TTTTAAAGTT	TTTGAAGAG	5280
	ATAAGTGCAT	CATGAATTAC	ATGTACATGA	GAGGAGATAG	TGATATCAGC	ATAATGATTT	5340
	TAGGTCAGT	ACCTGAGCTG	TCTAAAAATA	TATTATACAA	ACTAAAAATG	AGATGAATTA	5400
	ACCTCTCAAA	GCACAGAATG	TGCAAGAACT	TTTGCAATTT	AATCGTTGTA	AACCTAACGC	5460

5 TTAACACTATT GACTCTATAC CTCTAAAGAA TTGCTGCTAC TTTGTGCAAG AACTTTGAAG 5520  
 GTCAAATTAG GCAAAATCCA GATAGTAAAA CAATCCCTAA GCCTTAAGTC TTTTTTTTTT 5580  
 CCTAAAAAT CCCATAGAAT AAAATTCTCT CTAGTTTACT TGTGTGTGCA TACATCTCAT 5640  
 CCACAGGGGA AGATAAGAT GGTACACAAA ACAGTTTCCA TAAAGATGA CATATTTCATT 5700  
 ATACTTCTGA CCTTTGGGCT TTCTTTTCTA CTAAGCTAAA AATTCTTTT TATCAAAGTG 5760  
 TACACTACTG ATGCTGTTTG TTGTACTGAG AGCACGTACC AATAAAAATG TTAACAAAAT 5820  
 AT

10 Seq ID NO: 528 Protein sequence  
 Protein Accession #: XP\_036683

15 1 11 21 31 41 51  
 | | | | |  
 MVLSSLWLIA AALVEVRTSA DQAGNEEMV QIDLPIKRYR EYELVTPVST NLEGRYLSHT 60  
 LSASHKKRSA RDVSSNPQL FFNITAFKGD FHLRLKPNTQ LVAPGAVVEW HETSLVPGNI 120  
 TDPINNHPFG SATYRIKTE PLQTNCAVVG DIVDIPGTSV AINSCDGLAG MIKSDNEEYF 180  
 IEPLERGRQM EEEKGRIHVY YKRSAVEQAP IDMSKDFHYR ESDLEGLDDL GTVYGNHQQ 240  
 LNETMRRRRH AGENDYNIEV LLGVDDSVVR FHGKEHVQNY LLTLMNIVNE IYHDESLGVH 300  
 INVVLVRMIM LGYAKSISLI ERGNPSRSLE NVCRWASQQQ RSDLNHSEHH DHAIPLTRQD 360  
 FGPAGMGGYA PVTGMCHPVR SCTLNHEDGF SSFVVAHET GHVLGMEHDG QGNRCGDETA 420  
 MGSVMAPLQV AAFHYHWSR CSGQELKRYI HSYDCLLDDP FDHWPKLPE LPGINYSMDE 480  
 QCRFDGFGVY KMCTAFRTFD PCKQLNCWSP DNPYFCKTKK GPPLDGTCA AGKWCYKGHC 540  
 MWKNNANQKQ DGNWGSWTKF GSCSRTCGTG VRFRTQCMN PMPINGGQDC PGVNFYQLC 600  
 NTEECQKHFE DFRAGCQQR NSHFEYQNTK HHLPLPEHPD PKKRCHLYCQ SKETGDVAYM 660  
 KQLVHDGTHC SYKDPYSICV RGECKVKGCD KEIGSNKVED KCGVCGGDNH HCRTVKGTFT 720  
 RTPRKILGLK MFDIPGARH VLIQDEASP HILAINKQAT GHYILNGKE EAKSRTFIDL 780  
 GVEWDYNIED DIESLHTDGP LHDPIVILII POENDTRSSL TYKIIHEDS VPTINSNNVI 840  
 QEELDTFEWA LKSWSCSKP CGGFGYQTKY GCRKSDNKM VHSFCEANK KPKPIRRMCN 900  
 IQECTHPLWV AEWEEHCTKT CGSSGYQLRT VRLCLPLLDG TNRSVHSKYC MGDREPESRRP 960  
 CNRVPCPAQV KTFWSECSV TCGEGTEVRQ VLCRAGDHCD GEKPEVRAC QLPPCNDEPC 1020  
 LGDKSIFCQM EVLARYCSIP GYNKLCCESC SKRSSTLPPP YLLEAAETHD DVISNPSDLP 1080  
 RSLVMTSLV PYHSETPAKK MSLSSIISVG GPNAYAAFRP NSKPDGANLR QRSQAQAGSK 1140  
 TVRLVTPVPS PPTKRVHLSS ASQMAAASFF AASDSIGASS QARTSKKDGK IIDNRRPTRS 1200  
 STLER

35 Seq ID NO: 529 DNA sequence  
 Nucleic Acid Accession #: NM\_002774  
 Coding sequence: 246..980

40 1 11 21 31 41 51  
 | | | | |  
 AGGCGGACAA AGCCCGATTG TTCTGGGGCC CTTTCCCAT CGCGCTGGG CCGCTCCCC 60  
 AGCCCGGGGC AGGGCGGGG GCCAGTGTGG TGACACACGC TGTAGCTGTC TCCCCGGCTG 120  
 GCTGGCTCGC TCTCTCTCTG GGACACAGAG GTCCGGCAGGC AGCACACAGA GGGACCTACG 180  
 GGACGCTGTT CTTTCCCGCG ACTCAAGAA CCCCAGGAGC CCGGAGGCGT CGAGCAGGAG 240  
 CGGCCATGAA GAAGCTGATG GTGGTGCTGA GTCTGATTGC TGCAGCTGGG CGACAGGAGC 300  
 AGAATAAGTT GGTGCATGGC GGACCCTGGG ACAAGACATC TCAACCTAC CAAGCTGCC 360  
 TCTACACCTC GGGCCACTTG CTCTGTGGTG GGGTCTTAT CCATCCACTG TGGGTCTCTCA 420  
 CAGCTGCCCA CTGCCAAAAA CCGAATCTTC AGGTCTTCTT GGGGAAGCAT AACCTTCGGC 480  
 AAAGGGAGAG TCCCCAGGAG CAGAGTTCTG TTGTCCGGGC TGTGATCCAC CCGTACTATG 540  
 ATGCCGCGAG CCATGACCAG GACATCATGC TGTTCGGGCT GGCAGGCCCA GCCAAACTCT 600  
 CTGAACCTAT CCAGCCCTTT CCCCTGAGGA GGGACTGCTC AGCCAACACC ACCAGCTGCC 660  
 ACATCCTGGG CTGGGGCAAG ACAGCAGATG GTGATTTCCT TGACACCATC CAGTGTGCAT 720  
 ACATCCACCT GGTGTCCCGT GAGGAGTGTG AGCATGCCTA CCCTGGCCAG ATCACCACGA 780  
 ACATGTTGTG TCGTGGGGAT GAGAAGTACG GGAAGGATTC CTGCCAGGCT GATTCTGGGG 840  
 GTCCGCTGGT ATGTGGAGAC CACCTCCGAG GCCTTGTGTC ATGGGGTAAC ATCCCTCTGT 900  
 GATCAAGGA GAAGCCAGGA GTCTACACCA ACGTCTGCAG ATACAGAAC TGGATCCAAA 960  
 AAACCAATCA GGCCAAAGTA CCCTGACATG TGACATCTAC CTCCGACCT ACCACCCAC 1020  
 TGGCTGGTTC CAGAACGTCT CTCACTAGA CCTTGCCTCC CCTCTCTCC TGCCAGCTC 1080  
 TGACCTGAT GCTTAATAAA OGCAOGACG TGAGGGTCTT GATTCTCCCT GTTTTACCC 1140  
 CAGCTCCATC CTTCATCAC TGGGAGGAG GTGATGAGT AGGACTTGGG TCCTCGGTCT 1200  
 TACCCCCACC ACTAAGAGAA TACAGGAAAA TCCCTCTAG GCATCTCCTC TCCCAACCC 1260  
 TTCCACAGT TTGATTCTT CCTGCAGAG CCCAGCCAG TGTCTGGAAT CCCAGCTCCG 1320  
 CTGCTTACTG TCGGTGTCCC CTTGGGATG ACCTTTCTTC ACTGCAGATT TCTCACCTGT 1380  
 AAGATGAAGA TAAGGATGAT ACAGTCTCCA TCAGGCAGTG GCTGTTGGAA AGATTTAAGA 1440  
 TTTCACACT ATGACATACA TGGGATAGCA CCTGGGCCG CATGCACTCA ATAAAGAAAT 1500  
 TATTTT

70 Seq ID NO: 530 Protein sequence  
 Protein Accession #: NP\_002765

75 1 11 21 31 41 51  
 | | | | |  
 MKKLMVVL SL IAAAWAEQN KLVHGGPCDK TSHPYQAALY TSGHLLCGGV LIHPLVLT 60  
 AHCKKPNLQV FLGKHNLQR ESSQEQQSVV RAVIHPDYDA ASHDQDIML RLARPARKLSE 120  
 LIQPLPLERD CSANTTSCHI LGWGTADGD FPDITIQAYI HLVSRECEH AYPQITQNM 180  
 LCAGDEKYKG DSCQSDSGGP LVCGDHLRGL VSWGNIPGS KEKPGVTVNV CRYTNWIKQT 240  
 IQAK

80 Seq ID NO: 531 DNA sequence  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43..1104

1 11 21 31 41 51

5  
 10  
 15  
 20

CTTCTTTAAA	TTTCTTTCTA	GGATGTTTAC	TTCTTCTCCA	CAATGAATGA	GTGTCACTAT	60
GACAAGCACA	TGGACTTTT	TTATAATAGG	AGCAACACTG	ATACTGTGCA	TGACTGGACA	120
GGAACAAAGC	TTGTGATTGT	TTTGTGTGTT	GGGACGTTTT	TCTGCCTGTT	TATTTTTTTT	180
TCTAATTCTC	TGTCATCGC	GGCAGTGATC	AAAAACAGAA	AATTTCAATT	CCCCTTCTAC	240
TACCTGTGG	CTAATTAGC	TGCTGCCGAT	TTCTTCTGCTG	GAATTGCCTA	TGTATTCTCTG	300
ATGTTTAAAC	CAGGCCCACT	TTCAAAAACT	TGACTGTGCA	ACCGCTGGTT	TCTCCGTCAG	360
GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTACCAACT	TGCTGGTTAT	CGCGTGGAG	420
AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTATGG	GGGCGGTCCC	CACACTGGGC	540
TGGAATTGCC	TCTGCACAT	CTCTGCCCTG	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
TACCTTGT	TCTGGACAGT	GTCCAACCTC	ATGGCCTTCC	TCATCATGGT	TGTGGTGTAC	660
CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAACGTCT	TGTCTCCGCA	TACAAGTGGG	720
TCCATCAGCC	GCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
GCGTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTCTGCG	TCCTCGACGG	CCTGAACTGC	840
AGGCAGTGTG	GCGTGACAGA	TGTGAAAAGG	TGGTTCCTGC	TGCTGGGCTC	GCTCAACTCC	900
GTCTGAAACC	CCATCATCTA	CTCTTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
ATGATCTGCT	GCTTCTCTCA	GGAGAAACCA	GAGAGGGGTC	CCTCTCGCAT	CCCCTCCACA	1020
GTCCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
GTCTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCCTCT	GGCCACCCA	GGTGATGACT	1140
GTCTTAGG						

Seq ID NO: 532 Protein sequence  
 Protein Accession #: NP\_036284

25  
 30

1	11	21	31	41	51	
MNECHYDKHM	DFFYNRNTD	TVDDWTGKL	VIVLCVGTFF	CLFIFFSNL	VIAAVIKNRK	60
PHFFPYLLA	NLAADFPAG	IAYVLFMENT	GPVSKLTIVN	RWFLRQGLLD	SSLTASLTNL	120
LVIIVERHMS	IMRMVHSNL	TKKRVTLIL	LWVAIAIFMG	AVPTLGNL	CNISACSSLA	180
PIYSRSYLVP	WTVSNLMAFL	IMVVVYLR	YVYKRKTINV	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CWPTGLVLL	LDGLNCRQCG	VOHVKRWFLL	LALLNSVVP	IYYSYKDEDM	300
YGTMKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

35  
 Seq ID NO: 533 DNA sequence  
 Nucleic Acid Accession #: NM\_002821  
 Coding sequence: 150..3362

40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

1	11	21	31	41	51	
AACTCCCGCC	TCGGGACGCC	TCGGGGTCGG	GCTCCGGCTG	CGGCTGCTGC	TGCGGGCCCC	60
GCGCTCCGGT	GCGTCCGGCT	CCTGTGCCCG	CCGCGGAGCA	GTCTGGGGCC	GCGCGTGGCC	120
CCTCAGCTCC	TTTTCCTGAG	CCGCGCGCGA	TGGGAGCTGC	GCGGGGATCC	CCGCGCAGAC	180
CCGCGCGGTT	GCCTCTGCTC	AGCGTCTCTG	TGCTGCCGCT	GCTGGGCGGT	ACCCAGACAG	240
CCATTGTCTT	CATCAAGCAG	CCGTCTCTCC	AGGATGCACT	GCAGGGGCGC	CGGGCGCTGC	300
TTGCTGTGA	GGTTAGGGCT	CCGGGCGCGG	TACATGTGTA	CTGGCTGCTC	GATGGGGCCC	360
CTGTCCAGGA	CACGGAGCGG	CGTTTCGCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG	420
ACCGGCTGCA	GGACTCTGGC	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAAG	480
AAGCCCGCAG	TGCCAACGCC	TCCTTCAACA	TCAAATGGAT	TGAGGCAGGT	CCTGTGGTCC	540
TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGGTCA	CTTGGTTGCC	600
ACATTGATGG	GCACCTCGG	CCCACCTACC	AATGGTTCG	AGATGGGACC	CCCCTTCTG	660
ATGGTCAGAG	CAACCAACA	GTCAGCAGCA	AGGAGCGGAA	CCTGAGCTCT	CGGCCAGCTG	720
GTCTCAGCA	TAGTGGGCTG	TATTCCTGCT	GCGCCACAG	TGCTTTTGGC	CAGGCTTGCA	780
GCAGCCAGAA	CTTCACCTTG	AGCATTGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
CCCAGGACGT	GGTAGTAGCG	AGGTATGAGG	AGGCCATGTT	CCATTGCCAG	TTCTCAGCCC	900
AGCCACCCCC	GAGCCTGCAG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCGCAGTC	960
GCCTCCCAACA	CCTCCGAGCA	GCCACAGTGT	TGCGCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
TCCGCGCCAG	CAATGCAGGG	ATCTACCGCT	GCATTGGCCA	GGGGCAGAGG	GGCCCAACCA	1080
TCATCTTGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
GGGTGTTTAC	AGCTGGCAGC	GAGGAGGCTG	TGACCTGCTT	TCCCCCAAG	GGTCTGCCAG	1200
AGCCACGCGT	GTGGTGGGAG	CACGCGGGAG	TCCGGCTGCC	CACCCATGGC	AGGGTCTACC	1260
AGAAGGGCCA	CGAGCTGGTG	TTGGCCAATA	TTGCTGAAAG	TGATGCTGGT	GTCTACACCT	1320
GCCACGGGCG	CAACCTGGCT	GGTCAGCGGA	GACAGGATGT	CAACATCACT	GTGGCCACTG	1380
TGCCCTCCTG	GCTGAAGAAG	CCCCAAGACA	GCCAGCTGGA	GGAGGGCAAA	CCCGGCTACT	1440
TGGATTGCTT	GACCCAGGCG	ACACCAAAAC	CTACAGTTGT	CTGGTACAGA	AACCCAGATGC	1500
TCATCTCAGA	GGACTCACGG	TTCCAGGTCT	TCAAGATGG	GACCTTGC	ATCAACAGCG	1560
TGGAGGTGTA	TGATGGGACA	TGGTACCGTT	GTATGAGCAG	CACCCAGGCC	GGCAGCATCG	1620
AGGGGCAAGC	CCGTGTCCAA	GTGCTGGAAA	AGCTCAAGTT	CACACCACCA	CCCCAGCCAC	1680
AGCAGTGCAT	GGAGTTTGAC	AAGGAGGCCA	CGGTGCCCTG	TTCAGCCACA	GGCCGAGAGA	1740
AGCCCACTAT	TAAGTGGGAA	CGGCGAGATG	GGAGCAGCCT	CCAGAGTGG	GTGACAGACA	1800
ACGCTGGGAC	CCTGCATTTT	CCCCGGGTGA	CTCGAGATGA	CGCTGGCAAC	TACACTTGCA	1860
TTGCTCCCAA	CGGGCGGAG	GGCCAGATTCT	GTGCCCATGT	CCAGCTCACT	GTGGCAGTTT	1920
TTATCACTTT	CAAAAGTGAA	CCAGAGCGTA	CGACTGTGTA	CCAGGGCCAC	ACAGCCCTAC	1980
TGCAGTGCGA	GGCCAGGGGG	GACCCCAAGC	OGCTGATTCA	GTGGAAGGCG	AAGGACCGCA	2040
TCCTGGACCC	CACCAAGCTG	GGACCCAGGA	TGCACATCTT	CCAGAAATGG	TCCTGGGTGA	2100
TCCATGACGT	GGCCCTGAG	GACTCAGGCC	GCTACACCTG	CAITGCAGGC	AACAGCTGCA	2160
ACATCAAGCA	CAGCGAGGCC	CCCCTCTATG	TGCTGACAAA	GCCTGTGCGG	GAGGAGTCCG	2220
AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGGT	2280
CGCTGTGGC	CTACATCAT	GCGTGTGCTG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
AAGCCAAAGC	GCTGCAGAA	CAGCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAAAG	2400
GAGGGCCCTT	GCAGAAACGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
GCTTGGGCTC	CGGCCCGCGG	GCCACCAACA	AAGCCACAG	CACAAGTGAT	AAGATGCACT	2520
TCCACGGCTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGAGGTGT	2580
TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTGGTA	CTTGTGAAGA	2640

5 GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG 2700  
 GGAAGCTGAA CCACGCCAAC GTGGTGCGGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC 2760  
 ACTACATGCT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA 2820  
 AGAGCAAGGA TGAAAAATTG AAGTCACAGC CCCTCAGCAC CAAGCAGAAG GTGGCCCTAT 2880  
 GCACCCAGGT AGCCCTGGGC ATGGAGCACC TGTCCAACAA CCGCTTTGTG CATAAGGACT 2940  
 TGGCTGCGCG TAACATGCTG GTCAGTGCCC AGAGACAAGT GAAGGTGTCT GCCCTGGGCC 3000  
 TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCTGGG GTGCCGCTGC 3060  
 GCTGGATGTC CCCCGAGGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCTGGG 3120  
 CCTTCGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCAT GGTGGGCAGG 3180  
 10 CAGATGATGA AGTACTGSCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG 3240  
 GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GGCCCTCAGC CCCAAGGACC 3300  
 GGCCCTCCTT CAGTGAGATT GCCAGCGCCC TGGGAGACAG CACCGTGGAC AGCAAGCCGT 3360  
 GAGGAGGGAG CCCCTCAGG ATGGCCTGGG CAGGGGAGGA CATCTCTAGA GGGAGGCTCA 3420  
 CAGCATGATG GGCAGATCC CTGTCTCTCT GGGCCTTAG GTGCCCTAGT GCAACAGGCA 3480  
 15 TTGCTGAGGT CTGAGCAGGG CCTGGCCTTT CCTCCTCTTC CTCACCTCA TCCTTTGGGA 3540  
 GGCTGACTTG GACCCAAACT GGGCGACTAG GGCTTTGAGC TGGGCAGTTT CCCTGCCCAC 3600  
 CTCTCTCTCT ATCAGGAGCA GTGTGGGTGC CACAGGTAAC CCCAATTCTT GGCTTCAAC 3660  
 TTCTCCCTCT CACCGGCTCC AACTCTGCCA CTCATCTGCC AACTTTGCC TGGGAGGGCT 3720  
 AGGCTTGGGA TGAGCTGGGT TTGTGGGGAG TTCTTAATA TTCTCAAGT CTGGGCACAC 3780  
 20 AGGGTTAATG AGTCTCTTGC CCACCTGGTCC ACTTGGGGGT CTAGACCAGG ATTATAGAGG 3840  
 ACACAGCAAG TGAGTCTCTC CCACCTGGG CTGTGCACA CTGACCCAGA CCCAGCTCTT 3900  
 CCCACACCTT CTCTCTTTC CTCATCTTAA GTGCCCTGCA GATGAAGGAG TTTTCAGGAG 3960  
 CATTGTGACAC TATATAAACC GCCCTTTTGT TATGCACCAC GGGCGGCTTT TATATGTAAT 4020  
 25 TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG 4080  
 GCCATCCTTA CCCACACTT TTAATGTGTG CGTTTTTGTG TTGTTTTGTT TTTTGTGTTT 4140  
 TGTTTTTGTT TTACACTCG CTGCTCTCAA TAAATAAGCC TTTTITA

Seq ID NO: 534 Protein sequence

Protein Accession #: NP\_002812

30 1 11 21 31 41 51  
 MGAARGSPAR PRRLPLLSVL LLPLLGTTQT AIVFIKQPS QDALQRRAL LRCEVEAPGP 60  
 35 VHVYLLDGA PQVQDTERFA QSSLSFAAV DRLQDSGTFQ CVARDVDTGE EARSANASFN 120  
 IKWIEAGPVV LKHPASEAEI QPQTQVTLRC HIDGHPRTY QWFRDGTPLS DQGSNHTVSS 180  
 KERNLTLRPA GPEHSLGLYC CAHSAPGQAC SSQNFSLISA DESFARVULA PQDVVVARYE 240  
 EAMFHCQFSA QPPPSLQWLF EDETPIITNS RPHLLRRATV FANGSLLLTQ VRPRNAGIYR 300  
 CIGQGQRGPP ILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG 360  
 40 VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGOR RQDVNITVAT VPSWLKKPQD 420  
 SQLEEGKPGY LDCILTQATPK PTVVVYRNQM LISEDSRFEV FKNGTLRINS VEVIDGTWYR 480  
 CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QOCMEFDKEA TVPCSATGRE KPTIKNERAD 540  
 GSSLPEWYTD NAGTLHFARV TRDDAGNYTC IASNGPQQI RAHVQLTVAV PITFKVEPER 600  
 TTVYQGHVAL LQCEAGGDPK PLIQWKGKDR ILDPKLGPR MHIPQNGSLV IHDVAPEDSG 660  
 45 RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPSPPPFYK MIQTIGLSVG AAVAYIIAVAL 720  
 GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780  
 KRHSTDKMH FPRSLQPIIT TLGKSEFGEV FLAKAQGLEB GVAETLVLVK SLQTKDEQQQ 840  
 LDFRELEMF GKLHNANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ 900  
 PLSTKQKVAL CTQVALGMEH LSNRNFVHKD LAARNCLVSA QRQVKVSLG LSKDVYNSY 960  
 50 YHERQAWVPL RWSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLDLQ 1020  
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP

Seq ID NO: 535 DNA sequence

Nucleic Acid Accession #: NM\_013952

Coding sequence: 161..1357

55 1 11 21 31 41 51  
 TTCAGAAGGA GGAGAGACAC CGGGCCCGAG GCACCCCTGC GGGCGGGCGG ACCCAAGCAG 60  
 60 TGAGGGCCTG CAGCGGCGCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGAGGGA 120  
 AGCCCGGAGC CCTCGCGCGG CTGCGAGCSA CTCCCGGCGG ATGCCTCACA ACTCCATCAG 180  
 ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGCTTTT GTGAATGGCA GACCTCTGCC 240  
 GGAAGTGGTC CGCCAGCGCA TCGTAGACCT GGCCCAACAG GGTGTAAGGC CTGCGGCAT 300  
 CTCTCGCCAG CTCCGCGTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA 360  
 65 GACTGGCAGC ATCCGCGCTG GAGTGATAGG GGGCTCCAAG CCCAAGGTGG CCACCCCAAA 420  
 GGTGGTGGAG AAGATTGGGG ACTACAAACG CCAGAACCTT ACCATGTTTG CTGGGAGAT 480  
 CCGAGACCGG CTCTGGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCACTC 540  
 CATTAATAGA ATCATCCGGA CCAAAGTGCA GCAACCATTC AACCTCCCTA TGGACAGCTG 600  
 OGTGGCCACC AAGTCCCTGA GTCCCGGACA CACGCTGATC CCCAGCTCAG CTGTAACCTC 660  
 70 CCGGAGTCA CCCAGTCGG ATTCCCTGGG CTCCACCTAC TCCATCAATG GGCTCCTGGG 720  
 CATCGCTCAG CCTGGCAGCG ACAAGAGGAA AATGGATGAC AGTGATCAGG ATAGCTGCCG 780  
 ACTAAGCATT GACTCACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC 840  
 CTTACGCCAG CACCACCTCG AGCCGCTCGA GTGCCCATTT GAGCGGCAGC ACTACCCAGA 900  
 GGCCATATGG TCCGCCAGCC ACACCAAGG CGAGCAGGGC CTCTACCCCG TGCCCTTGGT 960  
 75 CAACAGCACC CTGACGACG GGAAGGCCAC CTGACCCCT TCCAACACGC CACTGGGGCG 1020  
 CAACCTCTCG ACTCACCAGA CCTACCCCTG GGTGGCAGCT CCGCCCTTTT GGATCTGCAG 1080  
 CAAGTGGCTT CGGGGTCCC GCCCTTCAAT GCCTTTCCCC ATGCTGCGCTC CGTGTACGGG 1140  
 CAGTTACCGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCACG GCTGCCCGGA 1200  
 TACCCACCCC ACATCCCCAC CAGCGGACAG GGCAGCTATG CCTCTCTGCG CATCGCAGCG 1260  
 80 ATGGTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCTTA CTCTCTCTAC 1320  
 AGCGAGGCCCT GGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC 1380  
 ACATCAAGGC CGAGTGCAAC GCCCACCCTT GCCAAGGCTT TTGACCATCT GTAGTTGCCA 1440  
 TGGGACAGT G

Seq ID NO: 536 Protein sequence  
Protein Accession #: NP\_039246

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQPPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD SDQDSCLSLI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
10  ERQHYPEAYA SPSHTKGBQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAA 300
PPFWICSKSA PGRSPMPFP MLPPCTGSSR ARPSSQGERW WGPRCPDTHP TSPPADRAAM 360
PLPLSQANWQ EVNTLAMPMA TPPTPTARP GASPTPAC

```

Seq ID NO: 537 DNA sequence  
Nucleic Acid Accession #: NM\_003466.1  
Coding sequence: 11..1363

```

20      1      11      21      31      41      51
      |      |      |      |      |      |
GAATTCGGCG ATGCTCTACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG 60
AGGGGGCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
GGCCACCAAG GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCGCGCTCA GCCATGGTTG 180
GGTCAGCAAG ATCCTTGGCA GGTACTACGA GACTGGCAGC ATCCGGCCTG GAGTGATAGG 240
GGGCTCCAAG CCCAAGGTGG CCACCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAACG 300
25  CCAGAACCCT ACCATGTTTG CCTGGGAGAT CCGAGACCGG CTCCTGGCTG AGGGGCTCTG 360
TGACAATGAC ACTGTGCCCA GTGTACAGTC CATTAATAGA ATCATCCGGA CCAAGTGCA 420
GCAACCATTC AACCTCCCTA TGGACAGCTG CGTGCCACCC AAGTCCCTGA GTCCCGGACA 480
CAGCTGATC CCAGCTCAG CTGTAACTCC CCGGAGTCA CCCCAGTCGG ATTCCTGGG 540
CTCCACCTAC TCCATCAATG GGCTCCTGGG CATCGCTCAG CTGGCAGCG ACAAGAGGAA 600
30  AATGGATGAC AGTGATCAGG ATAGCTGCCG ACTAAGCATT GACTCACAGA GCAGCAGCAG 660
CGGACCCCGA AAGCACCTTC GCACGGATGC CTTACGCCAG CACCACCTCG AGCGCGCTCGA 720
GTGCCCATTT GAGCGGCGAG ACTACCCAGA GGCCTATGCC TCCCCCGACC ACACCAAAGG 780
CGAGCAGGCG CTCTACCGCG TGCCCTTGCT CAACAGCACC CTGGACGACG GGAAGGCCAC 840
CCTGACCCCT TCCACACGCG CACTGGGCGG CAACCTCTCG ACTACCCAGA CCTACCCCGT 900
35  GGTGGCAGAT CCTCACTCAC CCTTGCCCAT AAAGCAGGAA ACCCCGAGG TGTCCAGTTC 960
TAGCTCCACC CCTCTCTCTT TATCTAGCTC CGCCTTTTTC GATCTGCAGC AAGTCGGCTC 1020
CGGGGTCCCG CCCTTCAATG CCTTTCCCCA TGCTGCCTCC GTGTACGGGC AGTTACGGG 1080
CCAGGCCCTC CTCTCAGGCG GAGAGATGGT GGGGCCCAAG CTCGCCGAT ACCCAACCCA 1140
CATCCCAACC AGCGGACAGG GCAGCTATGC CTCTCTGCC ATCGCAGGCA TGGTGGCAGG 1200
40  AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCTTAC TCCTCTACA GOGAGGCCGT 1260
GCGCTTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1320
GAGTGACCG CCCACCACTG CCACGGCCTT TGACCATCTG TAGTTGAGC TT

```

Seq ID NO: 538 Protein sequence  
Protein Accession #: NP\_003457

```

50      1      11      21      31      41      51
      |      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQPPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD SDQDSCLSLI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGBQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAD 300
55  PHSPPAIKQE TPEVSSSSST FSSLSSSAFL DLQVGVSGVP PFNAFPAAAS VYGQFTGQAL 360
LSGREMVQFT LPGYPPHIFT SGQGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP 420
NSSLLSSPY YSSTSRPSAP PTTATAFDHL

```

Seq ID NO: 539 DNA sequence  
Nucleic Acid Accession #: NM\_006799  
Coding sequence: 19..963

```

65      1      11      21      31      41      51
      |      |      |      |      |      |
GCCGCGGGAG AGGAGGCCAT GGGGCGCGCG GGGGCGCTGC TGCTGGGCTG GCTGCTGGCT 60
CGGGCTGGAC TCAGGAAGCC GGAGTCGAG GAGGCGGCGC GGTATCAGG ACCATGCGGC 120
CGACGGGTCA TCACGTCGCG CATCGTGGGT GGAGAGGACG CGAAGCTCGG GCGTGGCCG 180
TGGCAGGGGA GCCTGCGCCT GTGGGATTC CACGTATGCG GAGTGAGCCT GCTCAGCCAC 240
CGCTGGGCAC TCACGGCGCG GCACCTGCTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
GGGTGGATG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTTCTGGAG CCTGCAGGCC 360
70  TACTACACC GTTACTTCGT ATCGAATATC TATCTGAGCC CTGCTACCT GGGGAATTCA 420
CCCTATGACA TTGCCCTGGT GAAGCTGTCT GCACCTGTCA CCTACATAA ACACATCCAG 480
CCCATCTGTC TCCAGGCCTC CACATTTGAG TTTGAGAACG GGACAGACTG CTGGGTGACT 540
GGCTGGGGGT ACATCAAAGA GGATGAGGCA CTGCCATCTC CCCACACCT CCAGGAAGTT 600
CAGGTGCGCA TCATAACAA CTCTATGTGC AACCACTCT CTCTCAAGTA CAGTTTCCGC 660
75  AAGGACATCT TTGAGACAT GGTTTGTGCT GGCAATGCCA AAGGCGGAA GGATGCCTCG 720
TTCGGTGACT CAGGTGGACC CTTGGCCTGT AACAGAATG GACTGTGGTA TCAGATTGGA 780
GTGCTGAGCT GGGGAGTGGG CTGTGGTCGG CCATATCGCG CCGGTGTCTA CACCAATATC 840
AGCCACCACT TTGAGTGGAT CCAGAAGCTG ATGGCCAGA GTGGCATGTC CCAGCAGAC 900
CCCTCCTGGC CGCTACTCTT TTTCCCTCTT CTCTGGGCTC TCCACTCCT GGGGCGGCTC 960
80  TGAGCCTACC TGAGCCCATC CAGCCTGGGG CCACTGCCAA GTCAGGCCCT GGTTCCTCTT 1020
TGCTCTGTTT GGTAAATAAC ACATTCCAGT TGATGCCCTG CAGGCACTTC TTCAAAA

```

Seq ID NO: 540 Protein sequence  
Protein Accession #: NP\_006790

1 11 21 31 41 51  
 5 MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWFWQGS LR 60  
 LWDSHVCGVS LLSHRWALTA AHCFTYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120  
 VSNIIYLSPRY LGNSPYDIAL VKLSAPVTYT KHIQPICLQA STFEFENRTD CNVTGWGYIK 180  
 EDEALPSPHT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACFGDSGG 240  
 PLACNKNGLW YQIGVVSQGW GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSWPLL 300  
 10 FFPLLWALPL LGPV

Seq ID NO: 541 DNA sequence  
 Nucleic Acid Accession #: NM\_014344  
 Coding sequence: 131..1444

15 1 11 21 31 41 51  
 GCGGCCGCGA TGGGGCCGAA GCGCCCGAAG CCCCAGAGCC CACAAACTGC CGGGCCCGCC 60  
 TCGCCGCGCG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGGCGC ACCGGCAGAC 120  
 CCGCGGGAGC ATGGGCAGGA GGATGCGGGG CGCCGCCGCC ACCGCGGGGC TCTGGCTGCT 180  
 20 GCGCTGGGG TCGCTGCTGG CGCTGTGGGG AGGCTCCTG CCGCGCGGA CCGAGCTGCC 240  
 CGCTCCCGG CGCCCGAAG ACCGACTCCC ACGGCGCCCG GCCCGGAGCG GCGGCCCGCG 300  
 GCGCCGCGCT CGCTTCCCTC TGCCCCCGCC CCTGGGCTGG GACGCCCGCG GCGGCTCCCT 360  
 GAAAACCTTC CGGGCGCTGC TCACCCCTGG GCGCGGCGCG GACGGCCGCG CCGGCGAGTC 420  
 CCGGAGCGAG CCCAGGTGGC AGTGTCAGC CAGGCGAGCC CGGCGGAGG AGAGCGCGCG 480  
 25 GGTGCACGG GCGCTCTTCT GGAGCGCGCG CCTGGAGGAG CAGGTGCCCC CGGGCTTTTC 540  
 GGAGGCCAG GCGGCGGCGT GGCTGGAGGC GGCTCGCGGC GCCCGGATGG TGGCCCTGGA 600  
 GCGCGGGGGT TCGGGCGGCA GCTCCAAACG ACTGGCCCGT TTTGCGGAG GCACCGCGCG 660  
 CTGCGTGCGC TACGCGATCA ACCCGGAGCA GATTGAGGCG GAGGCCCTGT CTTACTATCT 720  
 GCGCGCGCTG CTGGGCTTCC AGCGCCACGT GCGCGCGCTG GCACTGGCTC GGGTGGAGGC 780  
 30 TCGGCGCGCG CAGTGGGCGC AGGTGCAGGA GGAGCTGCGC GCTGCGCACT GGACCGAGGG 840  
 CAGCGTGGT AGCCTGACAC GCTGGCTGCC CAACCTCACG GACGTGGTGG TGCCCGCGCC 900  
 CTGGCGCTCG GAGGACGCGC GTCTGCGCCC CCTCCGGGAT GCGGGGGGTG AGCTGGCCAA 960  
 CCTCAGCCAG GCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTCGACTA 1020  
 35 CTGACGCGCC AACTTCGACC GGCTCGTAAG CAACCTCTTC AGCTCGAGT GGGACCGCG 1080  
 CGTCATGCAG CTGTGCCACG CCAACCTGCA CCGCGGTCCG GCGGGGGCGC TGGTCTTTCT 1140  
 GGACAATGAG GCGGGCTTGG TGCAACGGTA CCGGTAGCA GGCATGTGGG ACAAGTATAA 1200  
 CGAGCGCGCT GTGAGTCAG TGTGCGTGT CCGGAGCGCG ACCGCGCGGC GCGTCTCTGA 1260  
 GCTGACAGCG GCGGAGGAG CCGCGGCGCG GCTGCTGCGC CTCTACCGCG GCCACGAGCC 1320  
 40 TGCTTTCCCG GAGCTGGCGC CCCTTGCGA CCCCCACGCT CAGCTGTAC AGCGCGCGCT 1380  
 CGACTTCTCT GCGACGACA TTTTGCACTG TAAGGCCAAG TACGGCGCGC GGTCTGGGAC 1440  
 TTAGTGTAC CCGGAGGAAA AGAGAGAGAT CTGGGCGTGG GGTATGGATG ATGGGGGAAA 1500  
 GGGCGGTGCG CTCTGCCACT GTCAGGAGCC AGCGCGCCAA CGCCACCGCG CAAAGGTGTC 1560  
 TAAAACTTC AGCTTTTCAC CCACCTGCCC CTTTCTTTCA ATCCACGCT GTTTCCTTTC 1620  
 45 AAAGTTCTGG GAGGACGAAC TCACCGAGGC GAGAAGTGTA ACATTCTCTC CACCAGCTT 1680  
 ATAAAAGATG TCCTTCTGT GCGAGCAGCG GGATTGGATC CGAAGAACT GGCTACTGGG 1740  
 GTTTGGCCCC CGAGTGGCG TCCCTGTGGG AGATGACCC CATTTCTGGG CCCCCTCAT 1800  
 TCCTTTCCCG AAAAAGGAAA ACTTGCCTTT GAGCGGTGTA GCTAATTCTG CAATTTTCTA 1860  
 CCAACAGAG CCGTGTGGCG CCGGAGCAG GGCTGTGACA TTGGCTGGTG GAGCCCTTC 1920  
 50 CTGTGTTCTC CCTTGTTC AGCGCCCGCA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC 1980  
 GGCTCGCGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG 2040  
 ACAATTGGCC TGACTCATTC CTGACCTCT GTCATTTTGG CCTGAAGGCT ACAATTGAG 2100  
 GGTGAGCTGT ATGCACTAAG TCAATAATG AATTTCTTCC TCCCTCTCGC AACCGACCA 2160  
 AATTTTGACA ACAGATATGT TCACCAGAAG GAAAAAATAA TCAGTTTTAT GCACTTTATT 2220  
 55 TTGTTTGTAT TTTTATTTT TATTAAGAAA AAATTTTATT TTACAGAAAT TACCTTCTCT 2280  
 GTATATATGT GCATAAAGTG TGGTGTAAAT ATACTAAACA AACTTATATT TCAATAAAG 2340  
 GGAGTTTAAA ATTTAAAAA AAAAAA

Seq ID NO: 542 Protein sequence  
 Protein Accession #: NP\_055159

60 1 11 21 31 41 51  
 MGRMRGAAA TAGLWLLALG SLLALWGLL PPRTELPASR PPEDRLPRRP ARSGGPAPAP 60  
 RFPPLPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHSARQP RPEESAAVHG 120  
 65 GVFWRSGLLE QVPPGFSEAQ AAAMLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180  
 YGINPEQIQG EALSYYLARI LGLQRHVPPL ALARVEARGA QMAQVOEELR AAEWTEGSVV 240  
 SLTRWLPNLT DVVWFAPWRS EDGRRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLT 300  
 NFDRLVSNLF SIQWDPRVMQ RATSNLHRGP GGALVFLDNE AGLVHGIRVA GMDKYNEPL 360  
 70 LQSVCFRFR TARRVLEHR GQDAARLLR LYRRHEPRFP ELAALADPHA QLLQRLDLFL 420  
 AKHILHCKAK YGRRSGT

Seq ID NO: 543 DNA sequence  
 Nucleic Acid Accession #: XM\_007652.4  
 Coding sequence: 1..1290

75 1 11 21 31 41 51  
 ATGGCGCGCT CTGGCGCGTG GAAGCGCCTC AAATCTATGC TAAGGAAGGA TGATGCGCGG 60  
 CTGTTTTTAA ATGACACAG CGCCTTTGAC TTCTCGGATG AGGCGGGGGA CGAGGGGCTT 120  
 80 TCTCGGTACA ACAAACTTCG AGTTGTGGTG GCGGATGACG GTTCCGAAGC CCGGAAAGG 180  
 CCTGTTAACG GGGCGCACCC GACCTCCAG GCCGACGATG ATTCTTACT GGACCAAGAC 240  
 TTACCTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CTTGTGACAA CTGCAGCAAA 300  
 CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAGCCAGGTG TGACCATTGC TGCCGTTCTG 360  
 TACTTGCTTT TCATGATTGG AGAACTTGTA GGTGGATACA TTGCAATAG CCTAGCAATC 420



ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480  
TTGTGGCTAT CATCAAAATC ACCAACCAGG AGATTACCTT TTGGATTTC TCGCTTAGAG 540  
GTTTTGTGAG CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT 600  
GAAGCTGTGC AAAGAAGTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660  
ACCGCAGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGGT TTCTGTTGAA CCAGTCTGGT 720  
CACCGTCACT CCCATTCCCA CTCCTGCGCT TCAAATTCCT CTACCAGAGG TTCTGGGTGT 780  
GAACGTAAAC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTGTGACA TGCTTTGGGA 840  
GATTGTGTAC AGAGTGTGG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA 900  
TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA 960  
TTTGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTGGAAT 1020  
GTAGACTATA TCAAGAAGC CTGTATGAAA ATAGAAGATG TATATTGAGT CGAAGATTTA 1080  
AATATCTGGT CTCTCACTTC AGGAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140  
GGAAGTTTCA TAAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTATT ATTGAACACA 1200  
TTTGGCATGT ATAGATGTAC TATTGAGCT CAGAGTTACA GGCAAGAAGT GGACAGAAGT 1260  
TGTGCAAAAT GTCAGAGTTC TAGTCCCTGA

Seq ID NO: 544 Protein sequence  
Protein Accession #: XP\_007652.1

1 11 21 31 41 51  
MAGSGAWKRL KSMRLKDDAP LFLNDTSAPD PSDEAGDEGL SRFNKL RVVV ADDGSEAPER 60  
PVNGAHP TLQ ADDSLLDQD LPLTNSQLSL KVDSCDNCSK QREILKQKRV KARLTIAAVL 120  
YLLFMIGELV GGYIANSLAI MTDALHMLTD LSAILLTLA LMLSSKSPKT RPTFGFHRLE 180  
VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDIHLI TAAVGVA VNV IMGFLLNQSG 240  
HRHSHSHSLP SNPTTRGSGC ERNHGQDSL A VRAAFVHALG DLVQSVGLVI AAYIRFKPE 300  
YKIDPICYT VPSLIVAF TT FRIIWDTVVI ILEGVPSHLN VDYIKEALMK IEDVYSEVDL 360  
NIWSLTSGKS TAIVHIQLIP GSSSKWEEVQ SKANHL LLNT FGM YRC TIQL QSYRQEVDRD 420  
CANCQSSSP

Seq ID NO: 545 DNA sequence  
Nucleic Acid Accession #: AB037765.1  
Coding sequence: 1..2478

1 11 21 31 41 51  
ATGTTTTCGG GCTTCAATGT CTTTAGAGTT GGGATCTCTT TTGTCATAAT GTGCATTTTT 60  
TACATGCCAA CAGTAAACTC TTTACCAGAA CTGAGTCTCT AGAAATATTT TAGTACATTG 120  
CAACCAGGAA AAGCCTCTTT AGCTTATTTT TGTCAGCTG ATTCCCAAG AACATCTGTA 180  
TTTCTTGAAG AACTGAATGA GGCTGTTAGA CCTCTGCAGG ACTATGGAAT TTCAGTTGCC 240  
AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAAA GGATTGTATG 300  
AAAGCATATT TATTCAAGGG CAACATATGT CTCAGAGAA TCCCTACTGA CACCTTGTTT 360  
GATGTGAATG CCTTGTGCG CCAATGTTCT TTTGCTCTTC TTTTAGTGA AGTGAAATAT 420  
ATTACCAACC TGAAGACCTC TCAGAACATA GAAATGCTC TGAAGGAAA AGCAATATTT 480  
ATATTCTCAT ATGTAAGAGC CATGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCCGCT 540  
TTTGTGTATG GGAATACATA CCAATTGTC TTAACACAG AAATTGCCCT TTTGAAAGT 600  
ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCATTGTA ACTAGTCTTG 660  
GACTTGACCC AGCAATGTAG AAGAACATA ATGGAACAGC CATTGACTAC ACTGAACATT 720  
CACCTGTTTA TTAAGACAT GAAAGCACCT CTGTGACTG AAGTTGCTGA AGATCCTCAA 780  
CAAGTTTCAA CTGTCCATCT CCAACTGGGC TTACCACTGG TTTTATTTGT TAGCCACAG 840  
GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG CTGCGCTCT TCTGGGAAA 900  
GCAGGAGTTC TACTCTGTT AAGGGACTCT TTGGAAGTGA ACATTCTCTA AGATGCTAAT 960  
GTGGTCTTCA AAGAGCAGCA AGAGGAGTT CCAATGGAAT TTTTGTGATT ACATGATGTT 1020  
GATTTAATAA TATCTCATGT GGAATAAAT ATGCACATTG AGGAAATACA AGAAGATGAA 1080  
GACAATGACA TGAAGAGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAACTGTT 1140  
TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACCTACAG TGGAACTAAC AGAAGAAACA 1200  
TTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260  
GTATCCATGG CATTTTGGCA ATCCTATATT GATGTGGCAG TTAAACTGAA AGGCACATCT 1320  
ACTATGCTTC TACTAGAAAT AAAGTGTGCA GATTGCTCTG ATGTATGTAC TAAGCAAAAT 1380  
GTTACTGAAT TTCTATCAT AAAGATGTAC AAGAAAGCG AGAAGCCAGT ATCTTATGCT 1440  
GGAATGTTAG GAACCGAAGA TCTCCTAAAA TTTATCCAGC TCAACAGGAT TTCATATCCA 1500  
GTGAATATAA CATCGATCCA AGAAGCAGAA GAATATTTAA GTGGGGAATT ATATAAGAC 1560  
CTCATCTTCA ATTCTAGTGT GTCAGTATTG GGACTATTTA GTCCAACCAT GAAAACAGCA 1620  
AAGAAAGATT TTAGTGAAGC AGGAACTAC CTAAAGGAT ATGTATCAC TGAATTTTAT 1680  
TCTGAAGAAG ATGTTTTGCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCCTGCTG 1740  
CTTGCAGAGC ACACAGAAGG CAAAATAGAG AGCATCCCAC TAGCTAGCAC ACATGCACAA 1800  
GACATAGTTC AAATAATAAC AGATGCATA CTGGAATGT TTCCGGAAT CACTGTGGAA 1860  
AATCTTCCCA GTTATTTTCA ACTTCAGAAA CCATTATTGA TTTTGTTCAG TGATGGCACT 1920  
GTAAATCTCT AGTATAAAA AGCAATATTG ACCTGTTAA AGCAGAAATA CTGGAATCA 1980  
TTTACTCCAT GCTGTTTAAA TCTAAAGAA ACTCCAGTGG GGAGAGGAAT CTTGAGGGCA 2040  
TATTTGTATC CTCTGCTTCC CCTTCTCTT CTGTGTTTGG TGAATCTGCA TTCAGTGGC 2100  
CAAGTATTTG CATTTCTTCT AGACCAGGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160  
AAGAAATTAG AAGCAGGACT AGAAATCAT ATCACAATTT TACCTGCTCA AGAATGGAAA 2220  
CCTCTCTTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280  
ACTAGGAAAG TTCCCAAGTG TATGAAAGAA ACAGATGTGC AGGAGAAATGA TAAGGAACAA 2340  
CATGAAGATA AATCGGAGT CAGAAAAGAA CCGATTGAAA CTCTGAGAA ATAGCATTGG 2400  
AATAGAAGTA ATTGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA 2460  
TGCTCAAAG TGAACATA

Seq ID NO: 546 Protein sequence  
Protein Accession #: BAA92582.1

1 11 21 31 41 51  
| | | | | |

5 MFSGFNVRV GISFVIMCIF YMPTVNSLPE LSPQKYFSTL QPGKASLAYF CQADSPRTSV 60  
 FLEELNEAVR PLQDYGISVA KVNCKVEEIS RYCGKEKDLN KAYLFPKGNIL LREFPTDTLF 120  
 DVNAIVAHVL FALLFSEVKY ITNLEDLQNI ENALKGKANI IPSYVRAIGI PEHRAVMEAA 180  
 FVYGTITYQFV LTTEIALLES IGSEDVEYAH LYFFHCKLVL DLTQQCRRTL MEQPLTTLNI 240  
 HLFIKTMKAP LLEVAEDPO QVSTVHLQLG LPLVFIVSQQ ATYEADRRTA ENVAWRLLGK 300  
 AGVLLLLRDS LEVNIQPDAN VVFKRAEEGV PVEPLVLHDV DLIISHVENN MHIEEIQEDE 360  
 DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTEET FNATVMASDS IVLFYAGWQA 420  
 VSMAPLQSYI DVAVKLKGTS TMLLRINCA DWSDVCTKQN VTEFPPIKMY KKGPNVSYA 480  
 10 GMLGTEDLLK FIQLNRISYP VNITSIQEAE EYLSGELYKD LILYSSVSVL GLFSPTMKTA 540  
 KEDFSEAGNY LKGYVITGIY SEEDVLLIST KYAASLPALL LARHTEGKIE SIPLASTHAQ 600  
 DIVQIITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKKAIL TLVKQKYLDS 660  
 FTPCWLNLKN TFPVGRGILRA YFDPLPLPL LVLVNLHSGG QVFAFPSDQA IIEENLVLWL 720  
 KLEAGLENH ITILPAQEWK PPLPAYDPLS MIDAATSQRG TRKVPKCKME TDVQENDKEQ 780  
 15 HEOKSAVRKE PIETLRIKHW NRSNWFKEAE KSFRDRKELG CSKVN

Seq ID NO: 547 DNA sequence  
 Nucleic Acid Accession #: NM\_033102.1  
 Coding sequence: 1..1662

20 1 11 21 31 41 51  
 | | | | |  
 ATGGTCCAGA GGCTGTGGGT GAGCGGCTG CTGCGGCACC GGAAAGCCCA GCTCTTGCTG 60  
 GTCAACCTGC TAACTTTGG CCTGGAGGTG TGTTTGGCOG CAGGCATCAC CTATGTGCCG 120  
 25 CCTCTGCTGC TGGAGTGGG GGTAGAGGAG AAGTTTCATGA CCATGGTGCT GGGCATTTGT 180  
 CCAGTGCTGG GCCTGGTCTG TGTCCGCTC CTAGGCTCAG CCAGTGACCA CTGGCGTGA 240  
 CGCTATGGCC GCGCGCGGCC CTTCATCTGG GCACGTGTCT TGGGCATCCT GCTGAGCCTC 300  
 TTTCTCATCC CAAGGGCCGG CTGGCTAGCA GGGCTGTCTG GCGCGGATCC CAGGCCCCCTG 360  
 GAGCTGGCAG TGCTCATCCT GGGCGTGGGG CTGCTGGA CTCTGTGGCA GGTGTGCTTC 420  
 30 ACTCCACTGG AGGCCCTGCT CTCTGACCTC TTCCGGGACC CGGACCACTG TCGCCAGGCC 480  
 TACTCTGTCT ATGCGCTTCT GATCAGTCTT GGGGCTGCTG TGGGCTACTC CTGCGCTGCC 540  
 ATTGACTGGG ACACCACTGC CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCCCTCTT 600  
 GGCTGTCTCA CCTCATCTT CTTCACCTGC GTAGCAGCCA CACTGCTGCT GGCTGAGGAG 660  
 GCAGCGCTGG GCGCCACCGA GCCAGCAGAA GGGCTGTGCG CCCCCTCCTT GTGCGCCAC 720  
 35 TGCTGTCCAT GCGCGGCGCG CTGGCTTTC CGGAACCTGG GCGCCTGCT TCCCGGCTG 780  
 CACCAGCTGT GCTGCGCAT GCGCCGACCT CTGGCGGCG TCTTCTGTC TGAGCTGTGC 840  
 AGCTGGATGG CACTCATGAC CTTCACGCTG TTTTACACGG ATTTCTGTGG CGAGGGGCTG 900  
 TACCAGGGCG TGCCAGAGG TGAGCGGGCG ACGAGGCCCC GGAGACACTA TGATGAAGGC 960  
 GTTCGGATGG GCAGCTGGG GCTGTTCTG CAGTGGCGCA TCTCCTGCTT CTCTCTCTG 1020  
 40 GTCATGGACC GGCTGGTGA GCGATTGGC ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080  
 GCTTTCCCTG TGCTGCGCG TGCCACATGC CTGTCCCA GTGTGGCGT GGTGACAGT 1140  
 TCAGCGGCC TCACCGGTTT CACCTTCTCA GCGCTGCAGA TCCGTGCCCTA CACACTGGCC 1200  
 TCCCTCTACC ACCGGAGGAA GCAGGTGTTT CTGCCCAAT ACCGAGGGGA CACTGGAGGT 1260  
 GCTAGCAGTG AGGACAGCT GATGACCACT TTCTGCGCAG GCGCTAAGCC TGGAGCTGCC 1320  
 45 TTCCCTAATG GACACGTGGG TGCTGGAGG AGTGGCCTGC TCCCACTCC ACCCGGCTC 1380  
 TGCGGGGCTT CTGCTGTGA TGCTCCGTA CGTGTGGTGG TGGGTGAGCC CACCGAGGCC 1440  
 AGGTGGTTC CCGGCGGGG CATCTGCTG GACCTCGCCA TCCGTGGATG TGCTTCTCTG 1500  
 CTGTCCAGG TGCGCCATC CCTGTTTATG GGCTCCATTG TCCAGCTCAG CCACTCTGTC 1560  
 50 ACTGCTATA TGGTGTCTG CGCAGGCTG GGTCTGGTGC CCATTACTT TGCTACACAG 1620  
 GTAGTATTG ACAAGAGCA CTGGCCAAA TACTCAGCT GA

Seq ID NO: 548 Protein sequence  
 Protein Accession #: NP\_149093.1

55 1 11 21 31 41 51  
 | | | | |  
 MVQRLWVSR LRRHKAQLLL VNLITFGLV CLAAGITYVP PLLLEVGVVE KFTMTVLGIG 60  
 PVLGLVCPVL LGSASDHWG RYRRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120  
 ELALLILGV LLLFCQVCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180  
 60 IDMDTSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGTEPAE GLSAPSLSPH 240  
 CCPCRLARL RNLGALLPRL HQLCCRPRT LRRLFVAELC SMALMTFTL FYTDFVGEGL 300  
 YQGVPRAEFG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG TRAVYLASVA 360  
 APPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420  
 ASSEDSLMTS FLPGPKPGAP PPNGHVAGG SGLLPPPPAL CGASACDVS RVVVGEPTEA 480  
 65 RVVPGRGICL DLAILDSAF LSQLVPSLFM GSIVQLSQSV TAYMVAAGL GLVAIYFATQ 540  
 VVFDKSLAK YSA

Seq ID NO: 549 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1389

70 1 11 21 31 41 51  
 | | | | |  
 ATGGGCTACC AGAGGCAGGA GCCTGTCTAT CCGCGCAGG GAGATTAGA TGACAGAGAA 60  
 ACCCTTGTTC CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120  
 75 GTTGTCACT CGATTATAG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180  
 GGGTTTCTTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTACCGA CTTTCCCTT 240  
 GTTTTATGTA TAAAGAGAG GCGCCTCTCT GGAACAGATA CCTACCAGTC TTGTGTCAT 300  
 AAAACTTTG GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTAGTTTCTT GTATCTTTT 360  
 80 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420  
 ATCCAGGAG TTATCTCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480  
 ACAGTTACCT TTAGTCTGCC TTTATCTTGT TACCGAAATA TAGCAAGCT TGGAAAGTTC 540  
 TCCCTCATCT CTACAGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600  
 TCACCTGGTC CACACATACC AAAACAGAA GACGCTTGGG TATTTCGAAA GCCCAATGCC 660  
 ATTCAGCGG TCGGGGTAT GTCTTTTGA TTTATTGTC ACCATAACTC CTCTTAGT 720

5 TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTATCCA TATGTCCATC 780  
 GTGATTTCCTG TATTATCTCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840  
 TTCAACCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900  
 AGATTTTGTG ATGGTGTCAC TGTCATTTTG ACATACCCTA TGGAAATGCTT TGTGACAAGA 960  
 GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCTA CATTGTTGTA 1020  
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTTGATTG CCTCGGGATA 1080  
 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTATCAT TCCATCAGCC 1140  
 TGTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTC 1200  
 ATGCTTCCCA TTGGTGCTGT GGTGATGGTT TTTGGATTCC TCATGGCTAT TACAAATACT 1260  
 CAAGACTGCA CCCATGGCA GGAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA 1320  
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC 1380  
 TTTCAATGA

15 Seq ID NO: 550 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 20 MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60  
 GFPLGILLFP WVSYVTFDFSL VLLIKGGALS GTDTYQSLVN KTFGFPYGLL LSVLQFLYPF 120  
 IAMISYNIIA GDTLSKVQFR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIKLGKV 180  
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKFA IQAVGVMSFA FICHNSFLV 240  
 YSSLEETVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLFENY CRNDLVTFG 300  
 RFCYGVTVIL TYPMECFVTR EVIANVFVFG NLSSVFHIV TVMVITVATL VSLIDCLGI 360  
 25 VLELNGVLCA TPLIFIPSA CYLKLSEEP THSDKIMSCV MLPIGAVMV FGFVMAITNT 420  
 QDCTHGQEMF YCFPDNPSLT NTSESHVQQT TQLSTLNISI PQ

30 Seq ID NO: 551 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1284

1 11 21 31 41 51  
 35 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGA GAGGATTGCC TTATTCAATG 60  
 AAGCAAGCTG GGTTCCTTT GGAATATTG CTTTATTCT GGGTTTCATA TGTACAGAC 120  
 TTTCCCTCTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180  
 TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG 240  
 TATCCTTTTA TAGCAATGAT AAGTTACAAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300  
 TTTCAAGAA TCCAGGAGT TGATCCTGAA AACGTGTTA TTGGTCGCCA CTTCATTATT 360  
 40 GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTGT ACCGAAATAT AGCAAAGCTT 420  
 GGAAAGGTCT CCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGAAT TGTAAATGGCA 480  
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540  
 CCAATGCGA TTCAAGCGGT CGGGGTTATG TCTTTGCTT TATTGCGCA CCATAACTCC 600  
 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660  
 45 ATGTCATCTG TGAATCTCTG ATTTATCTGT ATATTCTTG CTACATGTGG ATACTTGACA 720  
 TTTACTGGCT TCACCAAGGG GACTTATTG GAAATTAAT CTACAAATGA TGACCTGGTA 780  
 ACATTGGGAA GATTTTGTTA TGGTGTCACT GTCATTTGA CATACCTAT GGAATGCTTT 840  
 GTGACAAGAG AGGTAATGCG CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900  
 50 ATTGTGTAG CAGTGTGTT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960  
 CTCGGGATAG TCTTAGAAT CAATGGTGTG CTCTGTGCA CTCCCTCAT TTTTATCATT 1020  
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCGA TAAGATTATG 1080  
 TCTTGTGCTA TGCTTCCAT TGGTGTCTGT GTGATGGTTT TTGATTTCGT CATGGCTATT 1140  
 ACAAACTACT AAGACTGCAC CCAATGGGCG GAAATGTTCT ACTGCTTTCC TGACAATTTT 1200  
 55 TCTCTCACA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260  
 ATTAGTATCT TTCAACTCGA GTAA

Seq ID NO: 552 Protein sequence  
 Protein Accession #: Eos sequence

60 1 11 21 31 41 51  
 MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVSYVD FSLVLLIKGG ALSGDTDYQS 60  
 LVNKTGFPFG YLLSVLQFL YPFIAMISYN IAGDTLSKV PQRIPGVDP NVPIGRHFII 120  
 65 GLSTVTFLEP LSLYRNIKIL KSVSLISTGL TTLILGIVMA RAISLGHPIP KTEDAWVFAK 180  
 PNAIQAVGVN SFATICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240  
 FTGFTQGDLE ENYCRNDLV TFGRCYGVV VILTYPMECF VTREIVANVF FGNLSSVPH 300  
 IVVTVMVITV ATLVSLIIC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360  
 SCVMLPIGAV VMVFGPVMAT TATQDCTHQ EMFYCFPDNP SLTNTSESHV QQTTLSTLN 420  
 70 ISIPQLE

75 Seq ID NO: 553 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1203

1 11 21 31 41 51  
 80 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGT TTTCCCTTGT TTTATTGATA 60  
 AAAGGAGGGG CCTCTCTGG AACAGATACC TACCACTCTT TGGTCAATAA AACTTTCGGC 120  
 TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTGT ATCCTTTTAT AGCAATGATA 180  
 AGTTCAACATA TAATAGCTGG AGATACTTGG AGCAAAGTTT TTCAAAGAAT CCAGGAGTTT 240  
 GATCCTGAAA ACGTGTGTTT TGGTCGCCAC TTCATTATG GACTTTCCAC AGTTACCTTT 300  
 ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGCTTC CCTCATCTCT 360  
 ACAGGTTTAA CAGTCTGAT TCTTGAATG GTAATGGCAA GGGCAATTTT ACTGGGTCCA 420  
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

GGGGTTATGT CTTTTCGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCCTCT 540  
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTTCGTGA 600  
TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660  
GACTTATTGG AAATATTACTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTTGTAT 720  
GGGTCACTG TCATTTTGAC ATACCCCTATG GAATGCITTG TGACAAGAGA GGTAAATTGCC 780  
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTGTAAAC AGTGATGGTC 840  
ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAAGTC 900  
AATGGTGTGC TCTGTGCAAC TCCCCTCAT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
CTGTCTGAAG AACCAAGGAC ACACCTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020  
GGTGTGTGG TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCAGAAA TACCTCAGAG 1140  
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200  
TAA

Seq ID NO: 554 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPIAMI 60  
SYNIIAGDTL SKVQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLLS 120  
TGLTTLILGI VMARAIISLP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180  
EPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY 240  
GVTVILTYPM ECFVTRVIA NVFPGNLS VFIHVVTVMV ITVATLVSL IDCLGIVLEL 300  
NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVGFV MAITNTQDCT 360  
HGQEMFYCFP DNFLTNTSE SHVQQTQLS TLNISIFQLE

Seq ID NO: 555 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1140

1 11 21 31 41 51  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGCGAG TCAATAAAAC TTTCCGGCTTT 60  
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120  
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180  
CCTGAAAACG TGTATTATGG TCGCCACTTC ATTATTGGAC TTTCACAGT TACCTTTACT 240  
CTGCCCTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300  
GGTTTAACAA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360  
ATACCAAAAA CAGAAGACGC TTGGGTATT GCAAAGCCCA ATGCCATTCA AGCGTCCGGG 420  
GTTATGCTTT TTGCATTAT TGGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480  
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATT 540  
ATCTGTATAT TCTTGTCTAC ATGTGGATAC TTGCATTATA CTGGCTTCAC CCAAGGGGAC 600  
TTATTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660  
GTCACGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720  
GTGTTTTTGG GTGGGAATCT TTCATCGGT TTCCACATTG TTGTAACAGT GATGGTCATC 780  
ACTGTAGCCA CGCTGTGTC ATTGCTGATT GATTGCCCTG GGATAGTTCT AGAACTCAAT 840  
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCCAT CAGCCGTGTA TCTGAAACTG 900  
TCTGAAGAAC CAAGGACACA CTCGATTAAG ATTATGTCT GTGTGATGCT TCCATTGGT 960  
GCTGTGTGA TGGTTTTTGG ATCGTCAAT GCTATTACAA ATACTCAAGA CTGCACCAT 1020  
GGGCAGGAAA TGTTCTACTG CTTTCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080  
CATGTTACAG AGACACACA ACTTTCTACT TTAATATTA GTATCTTCA ACTCGAGTAA

Seq ID NO: 556 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
60  
65  
70  
75  
80

MGYQRQEPVI PPQVNKTFG FGYLLLSVLQ FLYPIAMIS YNIIAGDTLS KVFQRIPGVD 60  
PENVFIRH IIGLSTVTF LPLSLYRNI KLKVSLLS GLTTLILGIV MARAISLGP 120  
IPKTEDAWV AKPNAIQAV VMSFAFICH NSFLVYSSLE EPTVAKWSR LIHMSIVISV 180  
ICIFFATCGY LTFTGFTQGD LFNENYCRND LVTFRFCY VTIIVTYPM ECFVTRVIA 240  
VFFGGNLSV FHIHVVTMVI TVATLVSLI DCLGIVLEL NVLCATPLI FIIPSACYLK 300  
SEEPRTSD KIMSCVMLPI GAVVMVGFV MAITNTQDCT HGQEMFYCFP DNFLTNTSE 360  
HVQQTQLS TLNISIFQLE

Seq ID NO: 557 DNA sequence  
Nucleic Acid Accession #: XM\_057188.1  
Coding sequence: 769..4269

1 11 21 31 41 51  
70  
75  
80

ATGGGATGCT CTCTCCCTCT CACTCTGGGC TTCTGTCCCA CTCTTATCTT AGTTCAGTC 60  
CTCCCCCAAG TCTGTGTCCT TCTCTCTCCC CTAATCTCT GGGCCCTCCT TTCTGAGTTC 120  
CTGCCCTTCC CCAATCTCT TGGTTTTGTC ATCCCCCTCT GCGCCCTGCC TCAGTCAAGT 180  
CTCCCTCTGT TGTCTCTCTC CCCCCGCGCC GACCTCTGCG ACCCCCGAGG TCGTGTCC 240  
TCTGTCCCTT TATCGCGGCC TGGGACCGCG CCTCTCCCG CCTCCCGCTT TGGCGTCTCC 300  
AAGACTCCCC GCGCCCGAGA CCTCGCCCG CCGCAGGCTA GGTGGGAAG TGGAGGATCC 360  
GGTTTGTCTT GGGCGGGTCT GGAAGCAGAG CCGGCGGAGG GAGCGCGGG GCGCTGGGCT 420  
GCAGGAGGTT GCGGCGGCG CGGAGCATG GTGGTCCCG AGAAGGAGCA GAGCTGGATC 480  
CCCAAGATCT TCAAGAAGAA GACCTGCACG ACGTTCATAG TTGACTCCAC AGATCCGGGG 540  
GATGGGGTCT CGCTCTATAT CCCAGGCTGT TCTCAAATC CTGGGCTCAA GAGTCTCTTC 600  
TGCCCTGACC TCCCAAGTGT CTTGGATTGT GCCCAGCGGT CTTGAAGT TTGCTCAGAA 660  
GAGCAAACCT TCTGGGAGT AGCTGCAGGT GTTGAAGTA GCTGCAGGG AACTAGGGGA 720

5 TTCAAGGATG GAGCTGAAAT GGGTGAACGG ACAAGATCGG TAAACTGAAT GGAGGATGCC 780  
 TTGGGGGCG CCGTGGTGAC CCGTGTGGGAC AGCGATGCAC ACACCAACGGA GAAGCCACCC 840  
 GATGCCCTACG GAGAGCTGGA CTTACGCGGG GCCGGCCGCA AGCAGACGAA TTTCTCTCCG 900  
 CTCTCTGACC GAACCGGATCC AGCTGCAATT TATAGTCTGG TCACACGCAC ATGGGGCTTC 960  
 CGTGCCCGGA ACCTGGTGGT GTCACTGCTG GGGGATCGG GGGGCCCCGT CCTCCAGACC 1020  
 TGGCTGCAGG ACCTGCTCGG TCGTGGGCTG GTGCGGGCTG CCCAGAGCAC AGGAGCCTGG 1080  
 ATTGTCACTG GGGGTCTGCA CACGGGCATC GGGCGGCATG TTGGTGTGGC TGTACGGGAC 1140  
 CATCAGATGG CCAGCACTGG GGGCACCAG GTGGTGGCCA TGGGTGTGGC CCCCTGGGGT 1200  
 GTGGTCCGGA ATAGAGACAC CCTCATCAAC CCCAAGGGCT CGTTCCTGCG GAGGTACCGG 1260  
 10 TGGCGGGTGG ACCCGGAGGA CGGGGTCCAG TTTCCCTGG ACTACAACTA CTGGCCCTTC 1320  
 TTCTGTGGTG ACAGACGGC CACAGCGCTG CTGGGGGGCG AGAACCGCTT CCGCTTGGCG 1380  
 CTGGAGTCTT ACATCTCACA GCAGAAGAGC GGGCTGGGAG GGACTGGAAT TGACATCCCT 1440  
 GTCTGTCTCC TCTGATTGA TGGTGTAGAG AAGATGTTGA CGCGAATAGA GAACGCCACC 1500  
 15 CAGGCTCAGC TCCATGTCTT CCTGTGGCTT GGCTCAGGGG GAGCTGCGGA CTGGCTGGGG 1560  
 GAGACCTGGG AAGACACTCT GGGCCAGGG AGTGGGGGAG CCAGGCAAGG CGAAGCCCGA 1620  
 GATCGAATCA GGGCTTTCTT TCCCAAGGG GACCTTGAGG TCTGCAAGGC CCAGGTGGAG 1680  
 AGGATTATGA CCGGGAAGGA GCTCCTGACA GTCTATTCTT CTGAGGATGG GTCTGAGGAA 1740  
 TTCGAGACCA TAGTTTGTAA GGGCTTGTG AAGGCTGTG GAGCTCGGA GGGCTCAGCC 1800  
 20 TACCTGGATG AGTGGCTTTT GGCTGTGGCT TGGAAACCGG TGGACATGCG CCAGAGTGAA 1860  
 CTCTTTGCGG GGGACATCCA ATGGCGGTCC TTCCATCTCG AAGCTTCCCT CATGGAAGCG 1920  
 CTGCTGAATG ACCGGCTTGA GTTCTGTGCG TTGCTCATTT CCCACGGCTT CAGCTTGGGC 1980  
 CACTTCTGCA CCCGATGGG CCTGGCCCAA CTCTACAGCG CGGCGCCCTC CAACTCGCTC 2040  
 ATCCGCAACC TTTTGGACCA GGGCTCCAC AGCGCAGGCA CCAAGGCCCT AGCCCTAAAA 2100  
 25 GGGGGAGCTG CGGAGCTCGG GGGCCCTGAC GTGGGGCATG TGCTGAGGAT GCTGCTGGGG 2160  
 AAGATGTGGG CGCCGAGGTA CCGCTCGGG GGGCTGGGG ACCCTCACCC AGGCCAGGGC 2220  
 TTCGGGGAGA GCATGTATCT GCTCTCGGAC AAGGCCACCT CGCGCTCTC GCTGGATGCT 2280  
 GGGCTCGGGG AGGCCCCCTG GAGCGACCTG CTCTTTGGG CACTGTGTCT GAACAGGGCA 2340  
 CAGATGGCCA TGACTTCTG GAGATGGGT TCCAAATGAG TTTCTCAGC CTTTGGGGCC 2400  
 30 TGTTTGCTCG TCCGGGTGAT GGCACGCGTG GAGCCTGACG CTGAGGAGGC AGCAGGAGG 2460  
 AAGAAGCTGG GCTTCAAGTT TGAGGGGATG GGGCTTGACC TCTTTGGCGA GTGCTATGCG 2520  
 AGCAGTGAGG TGAGGGCTGC CGGCTCTCTC CTCCGTGCTT GCGCGCTCTG GGGGATGCC 2580  
 ACTTGCCTCC AGCTGGCCAT GCAAGCTGAC GCGCGTGCCT TCTTTGCCA GGATGGGGTA 2640  
 35 CAGTCTCTGC TGACACAGAA GTGGTGGGA GATATGGCCA GCATACACC CATCTGGGCC 2700  
 CTGGTCTCGC CCTTCTTTG CCGTCCACTC ATCTACACCC GCCTCATCAC CTTACGAGAA 2760  
 TCAGAAAGAG AGCCGACACG GAGGAGCTA GAGTTTGACA TGGATAGTGT CATTAAATGG 2820  
 GAAGGGCTG TCGGAGCGG GAGCCAGCC GAGAAGACGC CGCTGGGGGT CCGCGCCAG 2880  
 TCGGGCGCTC CGGGTGTCTG CGGGGGCGCG TCGGGGGGGC GCGGTGTGCT ACGCCGTGG 2940  
 TTCCACTTCT GGGGGCGGCG GTGACCATC TTCATGGGCA ACGTGTGCTG CTACCTGCTG 3000  
 40 TTCTGTGCTG TTTTCTCGCG GGTGCTGCTG GTGGATTTC AGCGCGGCCG GCGCGGCTCC 3060  
 CTGGAGCTGC TGCTCTATTG CTGGGCTTTC ACGCTGCTGT GCGAGGAAC TCGCCAGGGC 3120  
 CTGAGCGGAG GCGGGGCGAG CCTCGCCAGC GGGGGCCCCG GGCTGGCCA TGCTCACTG 3180  
 AGCCAGCGCC TGCGCTCTA CCTCGCCGAC AGCTGGAACC AGTCCGACCT AGTGGCTCTC 3240  
 45 ACCTGCTTCC TCTGGGGCTT GGGCTGCGG CTGACCCCGG GTTGTACCA CCTGGGCGCG 3300  
 ACTGTCTCTT GCATGCACTT CATGGTTTTC ACGGTGCGGC TGCTTCACAT CTTACGCGTC 3360  
 AACAAACAGC GCTTCAAGTT GATCGTCATC GTGAGCAAGA TGATGAAGGA CGTGTCTTC 3420  
 TTCTCTCTCT TCTCTGGCGT GTGGCTGGTA GCCTATGGCG TGGCCACGA GGGGCTCCTG 3480  
 AGGCCACGGG ACAGTGACTT CCCAAGTATC CTGCGCCGCG TCTTCTACCG TCCCTACCTG 3540  
 CAGATCTTGG GGCAGATTCC CCAGAGGAC ATGAGCGTGG CCTCATGGA GCACAGCAAC 3600  
 50 TGCTGCTGGG AGCCCGGCTT CTGGGACAC CCTCCTGGGG CCCAGGCGGG CACTGCGTC 3660  
 TCCAGTATG CCAACTGGCT GTGGTGTCTG CTCTCTGTCA TCTTCTGCT CGTGGCCAAC 3720  
 ATCTGCTGCT TCAACTTGCT CATTGCCATG TTCAGTTACA CATTCGCAA AGTACAGGGC 3780  
 AACAGCGATC TACTATGGAA GGGCAGCGT TACCGCTCA TCCGGGAAT CCACTCTCGG 3840  
 CCGCGCTGG CCGCGCCCTT TATGTCATC TCCCACTTGC GCCTCTGCT CAGGCAATTG 3900  
 55 TGCAAGCGAC CCGGAGCGCC CCAGCGCTCC TCCCGGCGCC TGAGCATT CCGGGTTTAC 3960  
 CTTTCTAAGG AAGCCGAGCG GAAGCTGCTA ACGTGGGAAT CGGTGCATA GGAGAACTTT 4020  
 CTGCTGGCAC GCGCTAGGGA CAAGCGGAG AGCGACTCCG AGCGTCTGAA GCGCACTGCC 4080  
 CAGAAAGTGG ACTTGGCACT GAAACAGCTG GGACACATCC GCGAGTACGA ACAGCGCTG 4140  
 60 AAGTGTCTGG AGCGGAGGT CCAGCAGTGT AGCGCGCTCC TGGGGTGGT GGGCGAGGCC 4200  
 CTGAGCGCTG CTGCTTGTCT GCGCCAGGT GGGCGGCCAC CCGCTGACCT GCCTGGGTCC 4260  
 AAGACTGAG CCTGCTGGC GGACTTCAAG GAGAAGCCCC CACAGGGGAT TTTGCTCTA 4320  
 GAGTAAGGCT CATCTGGGCC TCGGCCCGG CACTGTGTGG CTTTCTCTT GAGGTGAGCC 4380  
 CCATGTCCAT CTGGGCCACT GTCAGGACCA CCTTTGGGAG TGTCTCTT ACACACCA 4440  
 65 GCATGCGCGG CTCTCCAG AACCACTCC AGCGTGGGAG GATCAAGGCC TGGATCCCGG 4500  
 GCGGTATCAT ATCTGGAAGG TGCAAGGCTC TTGGGTAAC AGGAGACACA GACCCCTCAC 4560  
 CACTACACAGA TCTCTCACAC TGGGGAATA AAGCCATTTC AGAGGAAAAA AAAAAAAA 4620  
 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 558 Protein sequence  
 Protein Accession #: XP\_057188.1

70 1 11 21 31 41 51  
 MEDAFGAUV TVWSDAHT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAYVSLVTR 60  
 TWGFRAPNLV VSVLGGSGGP VLQTNLQDLL RRLVRAAQS TGAWIVTGGI HTGIGRHVGV 120  
 75 AVRDRQMAST GGTKVAMGV APWGVVRNRD TLINPKGSFP ARYRNRGDPE DGVQPLDYN 180  
 YSAFFLVDDG THGCLGGENR FRLRLSEYIS QKKTGVGGTG IDIPVLLLI DGDEKMLTRI 240  
 ENATQAQLPC LLVAGSGGAA DCLAETLEDT LAPGSGGARQ GEARDRIIRF FPKGDLEVLQ 300  
 AQVERIMTRK ELLTVYSSD GSEEFETIVL KALVKACGSS EASAYLDEL R LAVANRVDI 360  
 80 AQSELPFRDI QNRSHFLEAS LMDALLNDP EPVRLLSHG LSLGHFLTPM RLALYLSAAP 420  
 SNLSLRNLDD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480  
 PQQGFPGESMY LLSDKATSPF SLDAGLGQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540  
 ALGACLLLRV MARLEPDAEE AARRKDLAFK FEGMGVDLFG ECRYRSEVRA ARLLLRRCPL 600  
 WGDATCLQLA MQADARAFFA QDGVQSLITQ KMGDMASTT PIWALVLAF CPPLIYTRLI 660  
 TFRKSEBEPT REELEFDMDS VINGESPVT ADPAEKTPLG VPRQSGRPGC CGGRCGGRRR 720

LRRWFHFWGA PVTIFMGNV SYLLFLLFS RVLLVDFQPA PPGSLELLLY FWAFTLLCEE 780  
 LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840  
 HLGRTVLICD FMVFTVRLH IFTVVKQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT 900  
 EGLLRPRDSF PPSILRRVFI RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPPGAQA 960  
 GTCVSOYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQNSDLWY KAQRYRLIRE 1020  
 FHSRPAIAPP FIVISHRLRL LRQLCRRPRS PQSSPALEH FRVYLSKEAE RKLTLWESVH 1080  
 KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQQCSRVLGW 1140  
 VAEALSRSLAL LPPGGPPPPD LPGSKD

Seq ID NO: 559 DNA sequence  
 Nucleic Acid Accession #: NM\_006853.1  
 Coding sequence: 26..874

1 11 21 31 41 51  
 | | | | |  
 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTGTAGG TGGCTGCGGG ACTGGAAGTC 60  
 ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCCTCCAGGC 120  
 CATGAGGATT CTGAGATTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180  
 CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT 240  
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300  
 AGCCCACTGC CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA 360  
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCACCCCG GCTTCAACAA 420  
 CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATGCCAGT 480  
 CTCATCATCC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540  
 CAGCTGCCTC ATTTCGGGCT GGGGCGACAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC 600  
 CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAAGAG TGTGAGAAGC CCTACCCCGG 660  
 CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAAGAA GGGGGCAAGG ACTCCTGCCA 720  
 GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCTGGGG 780  
 CCAGAGTCGG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840  
 GGACTGGATC CAGGAGACGA TGAAGAACA TTAGACTGGA CCCACCCACC ACAGCCCATC 900  
 ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCATCTI GTTAATAAGA AACCTAAGC 960  
 CAAGACCTTC TAGCAACATT CTTTGGGCTT CCTGGACTAC AGGAGATGCT GTCACTTAAT 1020  
 AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080  
 GACTCTGGGA ATGACAACAC CTGGTTTGTI CTCTGTTGTA TCCCCAGCCC CAAAGACAGC 1140  
 TCCTGGCCAT ATATCAAGGT TTCATAAAT ATTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence  
 Protein Accession #: NP\_006844.1

1 11 21 31 41 51  
 | | | | |  
 MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60  
 AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV 120  
 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIIE HOKCENAYPG 180  
 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQIISWG QDPCAITRKP GYVTKVKXYV 240  
 DHIQETMKN

Seq ID NO: 561 DNA sequence  
 Nucleic Acid Accession #: AY046419.1  
 Coding sequence: 1..1743

1 11 21 31 41 51  
 | | | | |  
 ATGTTTACCT TCCTGTCTAT GTCACTGCT GCTGTCACTG GCCTCCTGGT GGGTTATGAA 60  
 CTGGGATCA TCTCTGGGGC TCTTCTTCTAG ATCAAAACCT TATTAGCCCT GAGCTGCCAT 120  
 GAGCAGGAAA TGGTGTGTAG CTCCCTCGTC ATTGGAGCCC TCCTTGCCCT ACTCACCGGA 180  
 GGGTCTCTGA TAGACAGATA TGAAGAAGG ACAGCAATCA TCTTGTCTAT CTGCTGTGCT 240  
 GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTTCTTAT AGTGGGACGC 300  
 ATTGCCATAG GGGTTTCCAT CTCCCTCTCT TCCATGCGCA CTGTGTGTTA CATCGCAGAG 360  
 ATTGCTCCTC AACACAGAAG AGGCCCTCTT GTGTCACTGA ATGAGCTGAT GATTGTCAATC 420  
 GGCATTCTTT CTGCTATAT TCAAAATTAC GCATTGCGCA ATGTTTTCCTA TGGCTGGAAG 480  
 TACATGTTTG GTCTGTGTAT TCCTTGGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT 540  
 CCTCCAAGCC CTCGTTTCTT GGTGATGAAA GGACAAGAGG GAGCTGCTAG CAAGGTTCTT 600  
 GGAAGGTTAA GAGCACTCTC AGATACAACT GAGGAATCA CTGTGATCAA ATCCTCCCTG 660  
 AAAGATGAAT ATGAGTACAG TTTTGGGAT CTGTTTGGT CAAAAGACAA CATCGGAGCC 720  
 CGAATAATGA TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACTGGCCA ACCAAACATA 780  
 TTGTCTATG CATCAACTGT TTTGAAGTCA GTTGGATTTC AAAGCAATGA GGCAGCTAGC 840  
 CTCGCTCCA CTGGGTTGG AGTCGTCAAG GTCAATTAGCA CCATCCCTGC CACTCTTCTT 900  
 GTAGACCATG TCGGCAGCAA AACATCTCTC TGCAATTGGCT CCTCTGTGAT GGCAGCTTGG 960  
 TTGGTGACCA TGGGCATGCT AAATCTCAAC ATCCACATGA ACTTCACCCA TATCTGCAGA 1020  
 AGCCACAATT CTATCAACCA GTCTTGGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080  
 TCAACCAACA ACATATCTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC 1140  
 TCACTCATGC CCTGAGAAA TGATGTGGAT AAGAGAGGGG AGACGACCTC AGCATCCTTG 1200  
 CTAAATGCTG GATTAAAGCA CACTGAATAC CAGATAGTCA CAGACCCCTG GGCAGTCCCA 1260  
 GCTTTTCTTA AATGGCTGTC CTTAGCCAGC TTGCTGTGTT ATGTTGTCTG TTTTCTAATT 1320  
 GGTCTAGGAC CAATGCCCTG GCTGGTCTC AGCGAGATCT TTCCTGGTGG GATCAGAGGA 1380  
 CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCCTCAT CTCGTGACA 1440  
 TTTTGTACTG TAATGATGCT TATTGGCTG CCATGGGTGT GCTTTATATA TACAATCATG 1500  
 AGTCTAGCAT CCTGTCTTT TGTGTATTAT TTTATACCTG AGACAAAGGG ATGCTCTTTG 1560  
 GAACAAATAT CAATGAGAGT AGCAAAAGTG AACTATGTGA AAAACAACAT TGTTTTATG 1620  
 AGTCATCACC AAGAAGAAAT AGTGCCAAA CAGCCTCAA AAAGAAAACC CCAGGAGCAG 1680  
 CTCTTGGAGT GTAACAAGCT GTGTGGTAGG GGCCAAATCA GGCAGCTTTC TCCAGAGACC 1740  
 TAA

Seq ID NO: 562 Protein sequence  
Protein Accession #: AAL02327.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      MFTFLSSVTA AVSGLLVGYE LGIISGALLQ IKTLALLSCH EQEMVVSSLV IGALLASLTG 60
      GVLIIDRYGRR TAILLSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSISLS SIATCVYIAE 120
      IAPQHRRLGLL VSLNELMIVI GILSAYISNY AFANVPHGWK YMFGLVIPLG VLQAIAMYFL 180
      PPSPRELVMK  GQEGASKVL  GRRLALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
10     RIMIGLTLVF FVQITQPNL LFYASTVLKS VGFQSNEMAS LASTGVGVVK VISTIPATLL 300
      VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMFTHICR SHNSINQSLD ESVIYGPNL 360
      STNNITLRDH FKGISHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDPV 420
      AFLKWLSLAS LLVYVAAFSI GLGPMPLVL SEIFPGGIRG RAMALTSSMN WGINLLISLT 480
15     FLTVDLIGL PWFCFIYTIM SLASLLFVVM FIPETKGC SL EQISMELAKV NYVKNNICFM 540
      SHQEELVFK QPQKRPQEQ LLECNKLCGR GQSRQLSPET

```

Seq ID NO: 563 DNA sequence  
Nucleic Acid Accession #: XM\_059466.1  
Coding sequence: 1..894

```

20     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCTGGGG 60
      CTGCTGTGTA CGGCCATCTT CACCGACCAC TGGTAOGAGA CCGACCCCGG GCGCCACAAG 120
25     GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CCGCCTGATG 180
      CCGCTGTGCG ACTTCGCGCT GCGGGACTCG CCCCCTGTGG GCGCCCGGCT GCTCCCGGGC 240
      GGCCCGGGCG GCGCCGACCC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
      GCGGAGTGGG GCGGGCCCTT CTTGCCACCC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
      CTGGGCATCG ACCGGGACAT CGACACCCCT ATCTCGAAGG GTATTGCGCA GCGATGCACG 420
30     GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCTCTT TAATTAAACC 480
      AAGACCATAC AGCAGATGAT GTGGCACCTG CTTCAATTAA GAAGAATCAC TGCTGGCTTC 540
      CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
      TGGAGAGATA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
      TGCACCATTT CCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
35     AAGCTAATT ATAGCCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
      GCCTGGTGCA GTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
      ATTAGCCGGA CCAAGATTGC ACAGCTAAG TCTGCAGAG ACTCCACGGT ATGA

```

Seq ID NO: 564 Protein sequence  
Protein Accession #: XP\_059466.1

```

40     1      11      21      31      41      51
      |      |      |      |      |      |
      MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
      PLSHLPLRDS PPLGRRLLPF GPRADPESW RSLGLGLD AEGRPLPAT YSLWRKCYF 120
45     LGIDRIDITL ILKGIAQRCT AIKYHFSQPI RLRNIPFNL KTIQDEWHL LHLRRITAGF 180
      LGMVAVLLC GCIVATVSFF WEESLTQHVA GLFLMTGIF CTISLCTYAA SISYDLNRLP 240
      KLIYSLPADV EHYGSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

```

Seq ID NO: 565 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3315

```

55     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGTCCTTTC GGGCAGCCAG GCTCAGCATG AGGAACAGAA GGAATGACAC TCTGGACAGC 60
      ACCCGGACCC TGTAATCCAG CGGCTCTCGG AGCACAGACT TGTCTTACAG TGAAGCGCAC 120
      TTGGTGAATT TTATTCAGAG AAATTTTAAG AAACAGAAAT GTGTCTTCTT TACCAAGAT 180
      TCCAGGCCCA CGGAGAATGT GTGCAAGTGT GGCTATGCCG AGAGCCAGCA CATGGAAGGC 240
60     ACCCAGATCA ACCAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCTTACC 300
      GAGSCCTTTG GGGATATTCA GTTTGAGACA CTGGGAAGA AAGGGAAGTA TATACGTCTG 360
      TCCTGGGACA CGGACGCCGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGAAA 420
      ACACCCAAAC TGGTCATTTC TGTGACCGGG GGCGCCAAGA ACTTGGCCCT GAAGCCGCGC 480
      ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATGCGCGAGT CCAAAGTGTC TTGGATTCTC 540
65     ACGGAGGCCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGGTGAG AGATAACACC 600
      ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGGCATGGTC 660
      TCCAACCGGG ACACCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTT AGCCCACTAC 720
      CTTATGGATG ACTTCACAAG AGATCCAAGT TATATCCTGG ACAACAACCA CACACATTTG 780
      CTGCTCGTGG ACAATGGCTG TCAATGGACAT CCCACTGTGG AAGCAAAAGT CCGGAATCAG 840
70     CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
      ATTGTGTGTT TTGCCCAAGG AGGTGGAAAA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
      AAAAAATAAA TTCTTGTGTT GGTGGTGAAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT 1020
      AGCCTGGTGG AGGTGGAGGA TGCCCTGACA TCTTCTGCGG TCAAGGAGAA GCTGGTGCAG 1080
      TTTTACCCCG GCACGTGTCT CCGGCTCGCT GAGGAGGAGA CTGAGAGTTG GATCAATGAG 1140
75     CTCAAAGAAA TTCTCGAATG TTCTCACCTA TTAACAGTTA TTAATGGA AGAAGCTGGG 1200
      GATGAAATTG TGAGCAATGC CATCTCTAC GCTCTATACA AAGCCTTCAG CACCACTGAG 1260
      CAAGACAAGG ATAACTGGAA TGGGCAGCTG AAGCTTCTGC TGGAGTGAA CCAGCTGGAC 1320
      TTAGCCAATG ATGAGATTTT CACCAATGAC CGCCGATGGG AGTCTGCTGA CCTTCAGAA 1380
      GTACGTGTTA CGGCTCTCAT AAAGGACAGA CCCAAGTTTG TCCGCTCTT TCTGGAGAA 1440
80     GGCTTGAAAC TACGGAAGTT TCTCACCCAT GATGCTCTCA CTGAACCTT CTCCAACACC 1500
      TTCAGCACGC TTGTGTACCG GAATCTGCAG ATGCCAAGA ATTCTATAA TGATGCCCTC 1560
      CTCACGTTTG TCTGGAAACT GGTGCGAAGC TTCCGAAGAG GCTTCCGAA GGAAGACAGA 1620
      AATGGCCGGG ACAGAGATGGA CATAGAACTC CACGACGTGT CTCCTATTAC TGGCACCCC 1680
      CTGCAAGCTC TCTTCATCTG GGCATTTCT CAGATAAGA AGGAACCTC CAAAGTCATT 1740

```

5  
10  
15  
20  
25  
30

TGGGAGCAGA CCAGGGGCTG CACTCTGGCA GCCCTGGGAG CCAGCAAGCT TCTGAAGACT 1800  
CTGGCCAAAG TGAAGAACGA CATCAATGCT GCTGGGGAGT CCGAGGAGCT GGCTAATGAG 1860  
TAGGAGACCC GGGCTGTGTA GCTGTTCACT GAGTGTACGA GCAGCGATGA AGACTTGGCA 1920  
GAACAGCTGC TGGTCTATTCT CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG 1980  
GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAAATT TCTTTCTAAG 2040  
CAATGGTATG GAGAGATTTC CCGAGACACC AAGAACTGGA AGATTATCCT GTGCTCTGTT 2100  
ATTATACCTT TGGTGGGCTG TGGCTTTGTA TCATTTAGGA AGAAACCTGT CGACAAGCAC 2160  
AAGAAGCTGC TTTGGTACTA TGTGGCGTTC TTCACCTCCG CCTTCGTGGT CTTCTCCTGG 2220  
AATGTGGTCT TCTACATCGC CTTCTCCTG CTGTTTGCTT ACGTGTCTGCT CATGGATTTC 2280  
CATTCGGTGC CACACCCCCC CGAGCTGGTC CTGTACTCGC TGGTCTTTGT CCTCTTCTGT 2340  
GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTAGTGACCT GTGGAATGTG 2400  
ATGGACACGC TGGGGCTTTT TTACTTCATA GCAGGAATTG TATTTCCGCT CCACCTCTCT 2460  
AATAAAGCT CTTTGATTTC TGGACGAGTC ATTTTCTGTC TGGACTACAT TATTTTCACT 2520  
CTAAGATTGA TCCACATTTT TACTGTAAGC AGAAACTTAG GACCCAGAT TATAATGCTG 2580  
CAGAGGATGC TGATCGATGT GTTCTTCTTC CTGTTCTCTT TTGCGGTGTG GATGGTGGCC 2640  
TTTGGCGTGG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCGCTGGAG GTGGATATTC 2700  
CGTTCGGTCA TCTACGAGCC CTACCTGGCC ATGTTGGGCC AGGTGCCAG TGACGTGGAT 2760  
GGTACCACTG ATGACTTTGC CCACTGCACC TTCACTGGGA ATGAGTCCAA GCCACTGTGT 2820  
GTGGAGCTGG ATGAGCAAA CCTGCCCGG TTCCCGGAGT GGATCACCAT CCCCCTGGTG 2880  
TGCATCTACA TGTATCCAC CAACATCCTG CTGGTCAACC TGCTGGTGC CATGTTTGGC 2940  
TACACGGTGG GCACCGTCCA GGAGAACAAAT GACCAGGTCT GGAAGTTCCA GAGGTACTTC 3000  
CTGGTGCGAG AGTACTCGAG CGGCTCAAT ATCCCTCTCC CCTTCATGCT CTTGCTTAC 3060  
TTCTACATGG TGGTGAAGAA GTGCTTCAAG TGTGTCTGCA AGGAGAAAAA CATGGAGTCT 3120  
TCTGTCTGCT GTTTCAAAAA TGAAGACAAT GAGACTCTGG CATGGGAGGG TGTGATGAAG 3180  
GAAAACTACC TTGTCAAGAT CAACACAAAA GCCAACGACA CCTCAGAGGA AATGAGGCAT 3240  
CGATTAGAC AACTGGATAC AAAGCTTAAT GATCTCAAGG GTCTTCTGAA AGAGATTGCT 3300  
AATAAATCA AATGA

Seq ID NO: 566 Protein sequence  
Protein Accession #: Eos sequence

35  
40  
45  
50

1 11 21 31 41 51  
MSFRAARLSM RNRNDTLDS TRTLYSSASR STDLSYSESD LVNFIQANFK KRECVFFTKD 60  
SKATENVCKC GYAQSQHMEG TQINQSEKWN YKHTKEFET DAFGDIQFET LGKKGYIYRL 120  
SCDIDAELLY ELLTQHWHLK TPNLVISVTG GAKNFALKPR MRKIFSRILIY IAQSKGAWIL 180  
TGGTHYGLMK YIGEVVRDNT ISRSSEENIV AIGIAAWGMV SNRDTLIRNC DAEGYFLAQY 240  
LMDDFTRDPL YLLDNHNLH LLVDNGCHGH PTVEAKLRNQ LEKYISERTI QDSNYGKIP 300  
IVCFAQGGGK ETLKAINTSI KNIKPCVVVE GSGQIADVIA SLVEVEDALT SSAVKEKLV 360  
FLPRTVSRLP EETESWIWK LKEILECSHL LTVIKMEEAG DEIVSNAIYS ALYKAFSTSE 420  
QDKDNWNGQL KLLLEWNQLD LANDEIFTND RRWESADLQE VMPTALIKDR PKFVRLPLEN 480  
GLNLKRFILTH DVLTELFNSH FSTLVYRNLO IAKNSYNDAL LTFVWKLIVAN FRRGFRKEDR 540  
NGRDEMDEL ELHDVSPITRHP LQALFIWAIL QNKKELSKVI WEQTRGCTLA ALGASKLLKT 600  
LAKVRMDINA AGESEELANE YETRAVELEF ECVSSDEDLA BQLLVYSCEA WGSNACLELA 660  
VEATDQHPA PGPQVNFLEK QNYGEISRDY KWKIILCLF IIPLVGCGFV SFRKKPVDKH 720  
KLLLYYVAF PTSPPVVSFV NVVFIYAFLL LPAYVLLMDF HSPVHPPELV LYSLVFVLFC 780  
DEVQRQYVNG VNYFTDLNVV MDTLGLFYFI AGIVFRLHSS NKSSLYSGRV IFCLDIYIFT 840  
LRLIHIFTVS RNLGPKIIML QRMLIDVFFF LFLFAVMMVA FGVARQGILR QNEQRWRWIF 900  
RSVIYEPYLA MFGQVPSVDV GTTYDPAHCT FTGNESEKPLC VELDERNLPR FFEWITIPLV 960  
CIYMLSTNLL LVNLLVAMPG YTVGTQENN DQVWKQRYF LVQEYCSRLN IFFPFIYFAY 1020  
FYMVVKCKFK CCKCKNMES SVCCFKNEDN ETLAWEGVMK ENYLKXINTK ANDTSEEMRH 1080  
RFRQLDTKLN DLKGLLKEIA NKIK

Seq ID NO: 567 DNA sequence  
Nucleic Acid Accession #: NM\_006911.1  
Coding sequence: 1..558

60  
65  
70

1 11 21 31 41 51  
ATGCGCTGCC TGTCTTGTG CCACCTGCTA GAATCTGTT TACTACTGAA CCAATTTTCC 60  
AGAGCAGTCG CGGCCAAATG GAAGGACGAT GTTATTAAAT TATGCGGCCG CGAATTAGTT 120  
CGCGCGCAGA TTGCCATTGG CGGCATGAGC ACCTGGAGCA AAAGGTCTCT GAGCCAGGAA 180  
GATGCTCCTC AGACACCTAG ACCAGTGCCA GAAATTGTAC CATCCTTCAT CAACAAAGAT 240  
ACAGAAACTA TAATTATCAT GTTGAATTTC ATTGCTAATT TGCCACCGGA GCTGAAGGCA 300  
GCCCTATCTG AGAGGCAACC ATCATTACCA GAGCTACAGC AGTATGTACC TGCATTAAG 360  
GATTCCAATC TTAGCTTTGA AGAATTTAAG AAACCTATTC GCAATAGGCA AAGTGAAGCC 420  
GCAGACAGCA ATCCTTCAGA ATTAAATAC TTAGGCTTGG ATACTCATT TCAAAAAAAG 480  
AGACGACCTC ACGTGGCACT GTTGAGAAA TGTGCGCTAA TTGGTTGTAC CAAAAGGTCT 540  
CTTGCTAAAT ATTGCTGA

Seq ID NO: 568 Protein sequence  
Protein Accession #: NP\_008842.1

75  
80

1 11 21 31 41 51  
MPRLFLFHLH EFCLLLNQFS RAVAAKWDD VIKLCGRELV RAQIAICGMS TWSKRLSQE 60  
DAPQTFRPVA EIVPSFINKD TETIIIMLEF IANLPPELKA ALSERQPSLP ELQYVPALK 120  
DSNLSFEFEK KLIIRNRQSEA ADSNPSELKY LGLDTHSQK RRPYVALPEK CCLIGCTKRS 180  
LAKYC

Seq ID NO: 569 DNA sequence  
Nucleic Acid Accession #: XM\_036453.1



Coding sequence: 1..3978

```

1      11      21      31      41      51
5      |      |      |      |      |
      ATGCTGCCCG TGTACCAGGA GGTGAAGCCC AACCCGCTGC AGGACGGGAA CCTCTGCTCA 60
      CGGGTGTCTT TCTGGTGGCT CAATCCCTTG TTTAAATTTG GCCATAAACG GAGATTAGAG 120
      GAAGATGATA TGTATTTCAGT GCTGCCAGAA GACCGCTCAC AGCACCTTGG AGAGGAGTTG 180
      CAAGGGTTCT GGGATAAAGA AGTTTAAAGA GCTGAGAATG ACGCACAGAA GCCTTCTTTA 240
      ACAAGAGCAA TCATAAAGTG TTAATGGAAA TCTTATTTAG TTTTGGGAAT TTTTACGTTA 300
      ATTGAGGAAA GTGCCAAAGT AATCCAGCCC ATATTTTGGG GAAAAATTAT TAAITATTTT 360
      GAAAAATTATG ATCCCATGGA TTCTGTGGCT TTGAACACAG CGTACGCCTA TGCCACGGTG 420
      CTGACTTTTT GCACGCTCAT TTTGGCTATA CTGCATCACT TATATTTTTA TCACGTTTCAG 480
      TGTGCTGGGA TGAGGTTACG AGTAGCCATG TGCCATATGA TTTATCGGAA GGCACCTCGT 540
      CTTAGTAACA TGGCCATGGG GAAGACAACC ACAGGCCAGA TAGTCAATCT GCTGTCCAAT 600
      GATGTGAACA AGTTTGATCA GGTGACAGTG TTTTACACT TCCTGTGGGC AGGACCACTG 660
      CAGGCGATCG CAGTGACTGC CCTACTCTGG ATGGAGATAG GAATATCGTG CCTTGTCTGG 720
      ATGGCAGTTC TAATCATTTCT CCTGCCCTTG CAAAGCTGTT TTGGGAAGTT GTTCTCATCA 780
      CTGAGGTGGA AACTCTCAAC TTTCAAGGAT GCCAGGATCA GGACCATGAA TGAAGTTATA 840
      ACTGGTATAA GGAATAATAA AATGTAGCCC TGGGAAAAGT CATTTTCAAA TCTTATTACC 900
      AATTTGAGAA AGAAGAGAGT TTCCAAGATT CTGAGAAATT CCTGCGCTAG GGGGATGAAT 960
      TTGGCTTCGT TTTTCAGTGC AAGCAAAATC ATCGTGTTTG TGACCTTCAC CACCTACGTG 1020
      CTCTCTGGCA GTGTGATCAC AGCCAGCCCG GTGTTCGTGG CAGTGACGCT GTATGGGGCT 1080
      GTGGCGCTGA CGGTATACCT CTTCTTCCCC TCAGCCATTG AGAGGGTGTG AGAGGCAATC 1140
      GTGAGCATCC GAAGAAATCA GACCTTTTGG CTACTTGATG AGATATCACA GCGCAACCGT 1200
      CAGCTGCCCT GATAGATGAA AAAGATGGTG CATGTGCAGG ATTTTACTGT TTTTGGGATG 1260
      AAGGCATCAG AGACCCCAAC TCTACAAGGC CTTTCTTTTA CTGTGACACC TGGCGAATTG 1320
      TTAGCTGTGG TCGGCCCGCT GGGAGCAGGG AAGTCATCAC TGTTAAGTGC CGTGTCTGGG 1380
      GAATTGGGCC CAAGTCACGG GCTGGTCAGC GTGCATGAAA GAATTGCCTA TGTGTCTCAG 1440
      CAGCCCTGGG TGTCTCGGG AACTCTGAGG AGTAATATTT TATTGGGAAA GAAATACGAA 1500
      AAGGAACGAT ATGAAAAGT CATAAAGGCT TGTGCTCTGA AAAAGGATTT ACAGCTGTGT 1560
      GAGGATGGTG ATCTGACTGT GATAGGAGAT CGGGGAACCA CGCTGAGTGG AGGGCAGAAA 1620
      GCACGGGTAA ACCTTGCAAG AGCAGTGTAT CAAGATGCTG ACATCTATCT CCTGGACGAT 1680
      CCTCTCAGTG CAGTAGATGC GGAAGTTAGC AGACACTTGT TCGAACTGTG TATTGTCTCA 1740
      ATTTTGCATG AGAAGATCAC AATTTTAGTG ACTCATCAGT TGCAGTACCT CAAAGCTGCA 1800
      AGTCAGATTC TGATATTGAA AGATGGTAAA ATGGTGAGA AGGGGACTTA CACTGAGTTC 1860
      CTAAATCTG GTATAGATTT TGGCTCCCTT TTAAGAAGG ATAATGAGGA AAGTGAACAA 1920
      CCTCCAGTTT CAGGAATCTC CACACTAAGG AATCGTACCT TCTCAGAGTC TTGGGTTTGG 1980
      TCTCAACATC CTCTAGAGC CTCCTTGAAA GATGGTGCTC TGGAGAGCCA AGATACAGAG 2040
      AATGTCCCAAG TTACACTATC AGAGGAGAAC CGTTCGAAG GAAAGTTTGG TTTTCAGGCC 2100
      TATAAGAATT ACTTCAGAGC TGGTGCTCAC TGGATTGTCT TCATTTTCTT TATTCTCTCA 2160
      AACACTGCAG CTCAGGTTGC CTATGTGCTT CAAGATTGGT GGCTTTCTATA CTGGGCAAAC 2220
      AAACAAGATG TGCTAAATGT CACTGTAAAT GGAGGAGGAA ATGTAAACGA GAAGCTAGAT 2280
      CTTAAGTGTG ACTTAGGAAT TTATTGAGT TTAAGTGTAG CTACCGTTCT TTTTGGCATA 2340
      GCAAGATCTC TATTGGTATT CTAAGTCTCT GTTAAGTCTT CACAACTTTT GCACACAAA 2400
      ATGTTTGAAT GAATTTGAAA AGCTCCGGTA TTATTTCTTT ATAGAAATCC AATAGGAAGA 2460
      ATTTTAAATC GTTTCTCCAA AGACATTGGA CACTTGGATG ATTTGCTGCC GCTGACGTTT 2520
      TTAGATTCCA TCCAGACATT GCTACAAGTG GTTGGTGTGG TCTCTGTGGC TGTGGCCGTG 2580
      ATTCCTTTGA TCGCAATACC CTGTGTTCCC CTTGGAATCA TTTTCATTTT TCTTCGGGGA 2640
      TATTTTGTGG AAACGTCAAG AGATGTGAAG CGCCTGGAAT CTACAACTCG GAGTCCAGTG 2700
      TTTTCCCATC TGTATCTTTC TCTCCAGGGG CTCTGGACCA TCCGGGCATA CAAAGCAGAA 2760
      GAGAGGTGTC AGGAACTGTT TGATGCACAC CAGGATTTAC ATTCAGAGGC TTGGTTCTTG 2820
      TTTTTCACAA CGTCCCGCTG GTTCGCCGTC CGTCTGGATG CCATCTGTGC CATGTTTGTG 2880
      ATCATCGTTG CCTTTGGGTC CCTGATTCTG GCAAAACTC TGGATGCCGG GCAGGTTGGT 2940
      TGGCACTGTG CCTATGCCCT CAGGCTCATG GGGATGTTTC AGTGGTGTGT TCGCAAAAGT 3000
      GCTGAAGTGT AATTAATGAT GATCTCAGTA GAAAGGGTCA TTGAATACAC AGACCTTGAA 3060
      AAAGAAGCAC CTTGGGAATA TCAGAAACGC CCACCAACAG CCTGSCCCCA TGAAGGAGTG 3120
      ATAATCTTTG ACAATGTGAA CTTCTATGAT AGTCCAGGTG GGCCTCTGGT ACTGAAGCAT 3180
      CTGACAGCAC CCAATTAATC ACAAGAAAG GTTGGCATTG TGGGAAGAAC CGGAGCTGGA 3240
      AAAAGTTCCC TCATCTCAGC CCTTTTGA TAAGTCAGAAC CCGAAGGTAA AATTGGATT 3300
      GATAAGATCT TGACAACTGA AATTGGACTT CAGGATTTAA GGAAGAAAT GTCAATCATA 3360
      CCTCAGGAAC CTGTTTTGTT CACTGGAACA ATGAGGAAA ACCTGGATCC CTTAATGAG 3420
      CACACGGATG AGGAAGTGTG GAATGCCTTA CAAGAGGTAC AACTTAAAGA AACCATTGAA 3480
      GATCTTCTCT GTAAATAGGA TACTGAATTA GCAGAACTAG GATCCAAATT TAGTGTGGA 3540
      CAAAGACAACT TGGTGTGCTT TGCCAGGGCA ATTCTCAGGA AAAATCAGAT ATTGATTATT 3600
      GATGAAGGGA CGGCAAAATG GGATCCAAGA ACTGATGAGT TAATACAAAA AAAAATCCGG 3660
      GAGAAATTTG CCCACTGCAC CGTCTAACC ATTGCACACA GATTGAACAC CATTATTGAC 3720
      AGCGACAAGA TAATGGTTTT AGATTGAGGA AGACTGAAAG AATATGATGA GCCGTATGTT 3780
      TTGCTGCAAA ATAAAGAGAG CCTATTTTAC AAGATGGTGC AACAACTGGG CAAGGCAGAA 3840
      GCGCGTCCCC TCACTGAAAC AGCAAAACAG GTATACTTCA AAAGAAATTA TCCACATATT 3900
      GGTCAACTG ACCACATGGT TACAAACACT TCCAATGGAC AGCCCTCGAC CTTAACTATT 3960
      TTGAGACAG CACTGTGA

```

Seq ID NO: 570 Protein sequence

Protein Accession #: XP\_036453.1

```

1      11      21      31      41      51
80     |      |      |      |      |
      MLEPVYQEVKP NPLQDANLCS RVFFWWLNPL FKIGHKRRLE EDDMYSVLPE DRSQHLGEEL 60
      QGFWDKEVLR AENDQAKPSL TRAIKCYNK SYLVLGIFTL IEESAKVIOP IFLGKIINYP 120
      ENYDPMDSVA LNTAYAYATV LTPCTLILAI LHLHYFYHVQ CAGMRLRVAM CHMIYRKALR 180
      LSMAMGKTTT TQIIVNLLSN DVNKFQDVTD FLHFLWAGPL QAIIVTALLW MEIGISCLAG 240
      MAVLIILLPL QSCFGLFSS LRSKTATFTD ARIRTMNEVI TGIRIIMYA WEKSFNSLIT 300
      NLKKKEISKI LRSSCLRGNM LASFFSASKI IVFVTFTTV LLSVITASR VFAVTLYGA 360

```

	VRLTVTLFFP	SAIERVSEAI	VSIRRIQTFL	LLDEISQRNR	QLPSDGKKMV	HVQDFTAFWD	420
	KASETPTLQG	LSFTVRPGEI	LAVVGPVGAG	KSSLSSAVLG	ELAPSHGLVS	VHGRIAYVSQ	480
	QPVWFSGLTR	SNILFGKKYE	KERYEKVIA	CALKKDLQLL	EDGLTLVIGD	RGTTLSGGQK	540
5	ARVNLARAVY	QDADIYLLDD	PLSAVDAEVS	RHLFELCICQ	ILHEKITILV	THQLQYLKAA	600
	SQILILKDGK	MQVQGYTTEF	LKSGIDFGSL	LKKDNEESEQ	PPVPGTPTLR	NRTFSESSVW	660
	SQSSSRPSLK	DGALESQDTE	NVPVTLSEEN	RSEGVGFQA	YKNYFRAGAH	WIVPIFLILL	720
	NTAAQVAYVL	QDWLSYWAN	KQSMNLVTVN	GGGNVTEKLD	LNWYLGIVSG	LTAVTVLFGI	780
	ARSLLVFVYL	VNSSQTLHNK	MPESILKAPV	LFDRNPIGR	ILNRFKIDIG	HLDDLPLTF	840
10	LDPIQTLLQV	VGVVSVAVAV	IPWIAIPLVP	LGIIIFILRR	YFLETSRDVK	RLESTTRSPV	900
	FSLHSSSLQG	LWTIRAYKAE	ERCQELFDAH	QDLHSEAWFL	PLTTSRMFAV	RIDAICAMFV	960
	IIVAFGSLIL	AKTLIDAGQVG	LALSALYALTM	GMFQWCVRS	AEVENMMISV	ERVIEYTDLE	1020
	KEAPWEYQKR	PPPAWPHFEGV	IIFDNVNFMY	SPGGPLVLKH	LTALIKSQEK	VGIVGRTGAG	1080
	KSSLISALFR	LSEPEGKIWI	DKILITEIGL	HDLRKMSII	POEPVLFTGT	MRKNLDPENE	1140
15	HTDEELWNAL	QEVQLKETIE	DLPKMDTEL	AESGSNFSVG	QRQLVCLARA	ILRNKQILII	1200
	DEATANVDR	TDELIQKKIR	EKFAHCTVLT	IAHRLNTIID	SDKIMVLDSG	RLKEYDEPYV	1260
	LLQNKESLFY	KMVQQLGKAE	AAALTETAKQ	VYFKRNYPHI	GHTDHMTNT	SNGQPSTLTI	1320
	PETAL						
20	Seq ID NO: 571 DNA sequence						
	Nucleic Acid Accession #: AF07120						
	Coding sequence: 116..4093						
	1	11	21	31	41	51	
25	GGACAGGCGT	GGCGGCCGGA	GCCCCAGCAT	CCCTGCTTGA	GGTCCAGGAG	CGGAGCCC GC	60
	GGCCACGCGC	GCCGTATCAG	CGCGACCCCG	GCCCGCGCCC	GCCCCGCCCG	GCAAGATGCT	120
	GCCCCGTGAC	CAGGAGGTGA	AGCCCAACCC	GCTGCAGGAC	GCGAACATCT	GCTCACGCGT	180
	GTTCTTCTGG	TGGCTCAATC	CCTTGTTTAA	AATTGGCCAT	AAACGGAGAT	TAGAGGAAGA	240
30	TGATATGTAT	TCAGTGTGTC	CAGAAGACCG	CTCACAGCAC	CTTGAGAGAG	AGTTGCAAGG	300
	GTTCTGGGAT	AAAGAAGTTT	TAAGAGCTGA	GAATGACGCA	CAGAAGCCTT	CTTTAACAAAG	360
	AGCAATCATAT	AGTGTCTACT	GGAAATCTTA	TTTAGTTTGG	GGAATTTTAA	CGTTAATTGA	420
	GGAAAGTGCC	AAAGTAATCC	AGCCCATATT	TTTGGGAAAA	ATTATTAAAT	ATTTTGAAAA	480
	TTATGATCCC	ATGGAATCTG	TGGCTTTGAA	CACAGGTATC	GCCTATGCCA	CGGTGCTGAC	540
35	TTTTTGCAAG	CTCATTTTGG	CTATACTGCA	TCACTTATAT	TTTTATCAGC	TTCAGTGTGC	600
	TGGGATGAGG	TTACAGTAGT	CCATGTGCCA	TATGATTAT	CGGAAGGCAC	TTCGTCTTAG	660
	TAACATGGCC	ATGGGGAAGA	CAACACAGG	CCAGATAGTC	AATCTGCTGT	CCAATGATGT	720
	GAACAAGTTT	GATCAGGTGA	CAGTGTTCTT	ACACTTCTCT	TGGGCAGGAC	CACTGCAGGC	780
	GATCGCAGTG	ACTGCCCTAC	TCTGGATGGA	GATAGGAATA	TGTCGCTTGG	CTGGGATGGC	840
40	AGTTCTAATC	ATTCTCTGTC	CCTTGCAAAG	CTGTTTGGGG	AAGTTGTTCT	CATCACTGAG	900
	GAGTAAACT	GCAACTTTCA	CGGATGCCAG	GATCAGGACC	ATGAATGAAG	TTATAACTGG	960
	TATAAGGATA	ATGGAAGTGT	ACGCCGTGGG	AAAGTCATTT	TCAAATCTTA	TTACCAATTT	1020
	GAGAAAGAAG	GAGATTTCCT	AGATTCTGAG	AAGTTCTCTG	CTCAGGCGGA	TGAATTTGGC	1080
	TTGTTTTTTC	AGTGCAGGCA	AAATCATCGT	GTTTGTGACC	TTACCAACCT	ACGTGCTCCT	1140
45	CGGCAGGTGT	ATCACAGCCA	GCCGCGTGT	CGTGGCAGTG	ACGCTGTATG	GGGCTGTGCG	1200
	GCTGACGGTT	ACCTCTCTCT	TCCCTCTCAG	CATTGAGAGG	GTGTCAGAGG	CAATCGTCAG	1260
	CATCCAGAGA	ATCCAGACCT	TTTTGCTACT	TGATGAGATA	TCACAGCGCA	ACCGTCAGCT	1320
	GCCGTGAGAT	GGTAAAAGAA	TGGTGCAATG	GCAGGATTTT	ACTGCTTTTT	GGGATAAGGC	1380
	ATCAGAGACC	CCAACCTTAC	AAGGCCCTTC	CTTTACTGTC	AGACCTGGCG	AATTGTTAGC	1440
50	TGTGGTGGGC	CCGCTGGGAG	CAGGGAAGTC	ATCACTGTGA	AGTGGCTGTC	TCCGGGAATT	1500
	GGCCCCAAGT	CACGGCTCGG	TCAGCGTGCA	TGGAAGAATT	GCCTATGTGT	CTCAGCAGCC	1560
	CTGGGTGTTT	TGGGGAACCT	TGAGGAGTAA	TAITTTTATT	GGGAAGAAT	ATGAAAAGGA	1620
	ACGATATGAA	AAAGTCATAA	AGGCTGTGTC	TCTGAAAAG	GATTTCACGC	TGTTGGAGGA	1680
	TGGTGATCTG	ACTGTGATAG	GAGATCGGGG	AACCACTGTC	AGTGGAGGGC	AGAAAGCAGC	1740
55	GGTAAACCTT	CGAAGAGCAG	TGTATCAAGA	TGCTGACATC	TATCTCTCGG	ACGATCCTCT	1800
	CAGTGCAAGT	GATCGGGAAG	TTAGCAGACA	CTTGTTGGA	CTGTGATTT	GTCAAATTTT	1860
	GCAATGAGAA	ATCACAATTT	TAGTGACTCA	TCAGTTGACG	TACCTCAATG	CTGCAAGTCA	1920
	GATTCGTGTA	TTGAAAGATG	GTAATAATGGT	GCAGAAGGGG	ACTTACACTG	AGTTCTCTAA	1980
	ATCTGGTATA	GATTTTGGCT	CCCTTTTAAA	GAAGGATAAT	GAGGAAAGTG	AACAACCTCC	2040
60	AGTTCCAGGA	ACTCCACAC	TAAGGAATCG	TACCTTCTCA	GAGTCTCTCG	TTTGGTCTCA	2100
	ACAACTCTCT	AGACCTCTCT	TGAAAGATGG	TGCTCTGGAG	AGCCAAGATA	CAGAGAATGT	2160
	CCCAGTTACA	CTATCAGAGG	AGAACCGTTC	TGAAGGAAAA	GTTGGTTTTT	AGGCCTATAA	2220
	GAATTACTTC	AGAGCTGGTG	CTCACTGGAT	TGTCTTCATT	TTCTTTATTC	TCCTAAACAC	2280
	TGCAGCTCAG	GTTCGCTATG	TGCTTCAAGA	TTGGTGGCTT	TCATCTGGGG	CAACAAACA	2340
65	AAGTATGCTA	AATGTCACCT	TAAATGGAGG	AGGAAATGTA	ACCGAGAAGC	TAGATCTTAA	2400
	CTGGTACTTA	GGAATTTATT	CAGGTTTAAC	TGTAGCTACC	GTTCTTTTTT	GCATAGCAAG	2460
	ATCTCTAATG	GTATTTCTACG	TCCTTGTTAA	CTCTTCACAA	ACTTTGCACA	ACAAAATGTT	2520
	TGAGTCAATT	CTGAAAGCTC	CGGTATTATT	CTTTGATAGA	AATCCAATAG	GAAGAATTTT	2580
	AAATCGTTTC	TCCAAAGACA	TTGGACACTT	GGATGATTTG	CTGCGGCTGA	CGTTTTTAGA	2640
70	TTTCATOCAG	ACATTGCTAC	AAGTGGTTGG	TGTGGTCTCT	GTGGCTGTGG	CGGTGATTC	2700
	TTGGATGCGA	ATACCCCTTG	TTCCCTCTGG	AATCATTTTC	ATTTTCTTTC	GGCGATATTT	2760
	TTGGAAACAT	TCAAGAGATG	TGAAGCGCCT	GGAATCTACA	ACTCGGAGTC	CAGTTGTTTC	2820
	CCACTTGCTA	TCTTCTCTCC	AGGGGCTCTG	GACCATCGGG	GCATACAAAG	CAGAAGAGAG	2880
	GTGTGAGGAA	CTGTTTGATG	CACACCAGGA	TTTACATTCA	GAGGCTTGTT	TCTTGTTTTT	2940
75	GACAACTGCC	CGCTGGTTCG	CCGTCCGTCT	GGATGCCATC	TGTGCCATGT	TTGTCATCAT	3000
	CGTGGCTCTT	GGGTCCCTGA	TTCTGGCAAA	AACTCTGGAT	GCGGGGCGAG	TTGGTTTGGC	3060
	ACTGTGCTAT	GCCTCTACGC	TCAATGGGAT	GTTTCAGTGG	TGTGTTTCAG	AAAGTGTCTGA	3120
	AGTTGAGAAAT	ATGATGATCT	CAGTAGAAGG	GGTCATTGAA	TACACAGACC	TTGAAAAAGA	3180
	AGCACTCTGG	GAATATCAGA	AAAGCCCAAC	ACCAGCCTGG	CCCCATGAAG	GAGTGATAAT	3240
80	CTTTGACAAT	GTGAACCTCA	TGTACAGTCC	AGGTGGGCTC	CTGGTACTGA	AGCATCTGAC	3300
	AGCATCTCAT	AAATCACAAG	AAAAGGTTGG	CATTGTGGGA	AGAACCGGAG	CTGGAAAAAG	3360
	TTCCCTCATC	TCAGCCCTTT	TTAGATTGTC	AGAACCAGAA	GGAATAATTT	GGATTGATAA	3420
	GATCTTGACA	ACTGAAATTTG	GACTTCAACG	TTTAAAGGAG	AAAATGTCAA	TCATACCTCA	3480
	GGAACTGTTT	TGTTTCACTG	GAACAATGAG	GAAAAACCTG	GATCCCTTTA	AGGAGCACAC	3540
	GGATGAGGAA	CTGTGGAATG	CCTTACAAGA	GGTACAACTT	AAAGAAACCA	TTGAAGATCT	3600

TCCTGGTAAA ATGGATACTG AATTAGCAGA ATCAGGATCC AATTTTAGTG TTGGACAAAG 3660  
 ACAACTGGTG TGCCCTGCCA GGGCAATTCT CAGGAAAAAT CAGATATTGA TTATTGATGA 3720  
 AGOGACGGCA AATGTGGATC CAAGAAGCTGA TGAGTTAATA CAAAAAATAA TCCGGGAGAA 3780  
 ATTTGCCCAT TGACACGTGC TAACCATTCG ACACAGATTG AACACCATTA TTGACAGCGA 3840  
 5 CAAGATAATG GTTTTAGATT CAGGAAGACT GAAAGAATAT GATGAGCCGT ATGTTTTGCT 3900  
 GCAAAATAAA GAGAGCCTAT TTTACAAGAT GGTGCAACAA CTGGGCAAGG CAGAAGCCGC 3960  
 TGCCCTCACT GAAACAGCAA AACAGGTATA CTTCAAAGA AATTATCCAC ATATTGGTCA 4020  
 CACTGACCAC ATGGTTACAA ACACCTCCAA TGGACAGCCC TCGACCTTAA CTATTTTCGA 4080  
 GACAGCACTG TGAATCCAAC CAAATGTCA AGTCCGTTCC GAAGGCATTT TCCACTAGTT 4140  
 10 TTTGGACTAT GTAAACCACA TTGTACTTTT TTTTACTTTG GCAACAAATA TTTATACATA 4200  
 CAAGATGCTA GTTCATTGA ATATTCTCC C

Seq ID NO: 572 Protein sequence  
 Protein Accession #: AAC27076.1

15 1 11 21 31 41 51  
 MLPVYQEVKP NPLQDANICS RVFFWNLNPL FKIGHKRRLE EDDMYSVLPE DRSQHLGEEL 60  
 QGFWDKEVLR AEMDAQPSL TRAIKCYWK SYLVLGIFTL IEESAKVIQF IFLGKIINYF 120  
 20 ENYDFMDSVA LNTAYAYATV LTFCTLILAI LHLHYPHYVQ CAGMLRLVAM CHMIYRKALR 180  
 LSNMAMGKTT TQIVNLLSN DVNKFQDQTV FLHFLWAGPL QAIIVTALLW MEIGISCLAG 240  
 MAVLIILLPL QSCFCGLFSS LRSKTATFTD ARIRTMNEVI TGIRIIMKYA WEKSFNSLIT 300  
 NLRKKEISKI LRSSCLRGMN LASFFSASKI IVFVTFTTV LLSGVITASR VFAVTLTYGA 360  
 25 VRLVTILFFP SAIERVSEAI VSIRRIQTFI LLEISQNRN QLPDSDGKQW HVQDFTAFWD 420  
 KASEPTLQGG LSFTVRPGEI LAVVGPGVAG KSSLSSAVLG ELAPSHGLVS VEGRIAYVSQ 480  
 QPWPVSGTLR SNILFGKKYE KERYEKVKA CALKKDLQLL EDGDLTVICD RGTTLGGQK 540  
 ARVNLARAVY QDADIYLLDD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA 600  
 SQILLKIDGK MVQKGTYTEF LKSGIDFGSL LKKNNEESEQ PPVPGTFLR NRTFSESSVW 660  
 30 SQSSSRPSLK DGALESQTE NVPVTLSEEN RSEGVGFOA YKNYFRAGAH WIVFIFLILL 720  
 NTAAGVAYVL QDWLWLYWAN KQSMNLNVTN GGGNVTEKLD LNWYLGIVSG LTVATVLFGI 780  
 ARSLLVFVVL VNSSQTLHNK MFESILKAPV LFFDRNPGR ILNRFSKDIG HLDLLEPLTF 840  
 LDFIQTLQVQ VGVVSVAVAV IPWIAIPLVP LGIIFIPLRR YPLETSRDVK RLESTTRSPV 900  
 FSHLSSSQGG LWTIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRWFAV RLDAICAMFV 960  
 35 IIVAFGSLIL AKTLDAGVQG LALSALYALM GMFQWCVRQS AEVENMMISV ERVIEYTDLE 1020  
 KEAPWEYQKR PPPAWPHEGV IIFDNVNFMY SPGGPLVLKH LTALIKSQEK VGIIVGTGAG 1080  
 KSSLISALFR LSEPEGKIWI DKILTTEIGL HDLRKKMSII PQEPVLTGT MRKNLDPFKE 1140  
 HTDEELWAL QEVQLKETIE DLPGKMDTEL AESGSNFSVG QRQLVCLARA ILRNQILII 1200  
 DEATANVDPR DELIQLKIR EKFAHCTVLT IAHRLNTIID SDKIMVLDGS RLKEYDEPVY 1260  
 40 LLQNKESLFY KMVQQLGKAE AALSTETAKQ VYFKRNYPHI GHTDHMTNT SNGQPSTLTI 1320  
 FETAL

Seq ID NO: 573 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1365

45 1 11 21 31 41 51  
 ATGGAATCAA TCTCTATGAT GGAAGGCCCT AAGAGCCTTA GTGAAACTTG TTTACCTAAT 60  
 GGCATAAATG GTATCAAAGA TGCAAGGAAG GTCACGTAG GTGTGATTGG AAGTGGAGAT 120  
 50 TTTGCCAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180  
 AGAAATCCTA AGTTTGCTTC TGAATTTTTT CCTCATGTGG TAGATGTCAC TCATCATGAA 240  
 GATGCTCTCA CAAAAACAAA TATAATATTT GTTGCTATAC ACAGAGAACA TTATACCTCC 300  
 CTGTGGGACC TGAGACATCT GCTGTGGGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360  
 55 AGGATAAACC AGTACCAGCA ATCCATGCT GAATATTGG CTTCATTATT CCCAGATTCT 420  
 TTGATTGTCA AAGGATTAA TGTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480  
 GCCAGCGGCG AGGTTTATAT ATGCAGCAAC AATATTCAAG CGCGACAACA GGTTATTGAA 540  
 CTTGCCCGCC AGTTGAATTT CATTCCTTACT GACTTGGGAT CCTTATCATC AGCCAGAGAG 600  
 ATTGAATATT TACCCTACG ACTCTTTACT CTCGGAGAG GGCAGTGGT GGTAGCTATA 660  
 60 AGCTTGCCCA CATTTTTTTT CCTTTATTC TTTGTGAGAG ATGTGATTCA TCCATATGCT 720  
 AGAAACCAAC AGAGTGACTT TTACAAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780  
 ATAGTTGCCA TTACTTTGCT CTCCCTAGTA TACCTCGCAG GTCTCTGCG AGCTGCTTAT 840  
 CAACTTTATT ACGGCACCAA GTATAGGAGA TTCCACCTT GGTGGGAAC CTGGTTACAG 900  
 TGTAGAAAAC AGCTTGGAAT ACTAAGTTT TCTCTGCTA TGTCCATGT TGCCTACAG 960  
 65 CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTGTGTT TCAACATGCG TTATCAGCAG 1020  
 GTTCATGCAA ATATTGAAA CTCTTGAAT GAGGAAGAAG TTGGAGAAT TGAATGTAT 1080  
 ATCTCCTTTG GCATAATGAG CCTTGGCTTA CTTTCCCTCC TGGCAGTCACT TTCTATCCCT 1140  
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTA TCCAGTCTAC ACTTGGATAT 1200  
 GTCGCTCTCG TCATAAGTAC TTTCCATGTT TTAATTTATG GATGGAACAG AGCTTTTGAG 1260  
 70 GAAGAGTACT ACAGATTTTA TACACCAACA AACTTTGTT TGTCTCTGT TTTGCCCTCA 1320  
 ATTGTAATTC TGGATCTTTT GCAGCTTTGC AGATACCCAG ACTGA

Seq ID NO: 574 Protein sequence  
 Protein Accession #: Eos sequence

75 1 11 21 31 41 51  
 MESISMMSGP KSLSETCLPN GINGIKDARK VTVGVIGSGD FAKSLTIRLI RCGYHVIVGS 60  
 RNPKFASEFF PHVVDVTHEE DALTKNIIF VAIHREHYTS LWDLRHLVVG KILIDVSNM 120  
 RINQYFESNA EYLASLPDPS LIVKGFNVVS AWALQLGPKD ASRQVYICSN NIQARQVIE 180  
 80 LARQLNFIPI PIEIVNKTLP IVAITLLSLV YLAGLLAAAY QLYGTYKRR FPPWLETWLQ 240  
 RNQSDPFYKI PIEIVNKTLP IVAITLLSLV YLAGLLAAAY QLYGTYKRR FPPWLETWLQ 300  
 CRKQLGLLSP PFAMVHVAYS LCLPMRRSER YLFLNMAVQQ VHANIENSWN EEEVWRIEMY 360  
 ISFGIMSLGL LSLAVTSIP SVSNALNWRP PSFIQSTLGY VALLISTFHV LIYGWKRAPE 420  
 EERYRPTTPP NFVLALVLPs IVILDLLQLC RYFP

Seq ID NO: 575 DNA sequence  
Nucleic Acid Accession #: NM\_001873.1  
Coding sequence: 3..1721

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

```

1      11      21      31      41      51
|      |      |      |      |      |
AAATGGCGTG CCGTCTCTC CGCCGGCCCC CTGCCTGCA GTGGTTTCTC CTGCAGCTCC 60
CTGGGGCTCC GCGGCCAGTA GTGCAGCCCC TGGAGCGCG GCTTTGCCCG TCTCCTCTGG 120
GTGGCCCCAG TGGCGGGGCT GACACTCATT CAGCCGGGGA AGGTGAGGCG AGTAGAGGCT 180
GGTGGCGGAAC TTGCGGCCCC CAGCAGCGCC GCGGGCTAA GCCAGGGGCC GGCAGACAA 240
AAGAGGCGCG CCGCTAGGA AGGCAGCGCC GCGCGGCGG GAGCGCAGCG ATGGCCGGGC 300
GAGGGGGCAG CGCGCTGCTG GCTCTGTGCG GGGCACTGG TGCCTGCGGG TGGCTCCTGG 360
GCGCCGAAGC CCAGGAGCCC GGGCGCCCC CGCGGGCAT GAGGCGGCG CGGCGGCTGC 420
AGCAAGAGGA CGGCATCTCC TTGAGTACC ACCGTACCC CGAGCTGCGC GAGGCGCTCG 480
TGTCCGTGTG GCTGCAGTGC ACCGCCATCA GCAGGATTTA CACGGTGGGG CGCAGCTTCG 540
AGGGCCGGGA GCTCTGGTC ATCGAGCTGT CCGACAAACC TGGCGTCCAT GAGCCTGGTG 600
AGCCTGAATT TAAATACATT GGAATATGC ATGGGAATGA GGCTGTGGA CGAGAACTGC 660
TCATTTTCTT GGCCAGTAC CTATGCAACG AATACAGAA GGGGAACGAG ACAATGTGCA 720
ACCTGATCCA CAGTACCCGC ATTCACATCA TGCTTCCCT GAACCCAGAT GGCTTTGAGA 780
AGGCAGGCTG TCAGCCTGGT GAACTCAAGG ACTGGTTTGT GGGTCGAAGC AATGCCCAGG 840
GAATAGATCT GAACCGGAAC TTCCAGACC TGGATAGGAT AGTGTACGTG AATGAGAAAG 900
AAGGTGTCTC AAATATACAT CTGTTGAAAA ATATGAAGAA AATGTGGAT CAAAACACAA 960
AGCTTGCTCC TGAGACCAAG GCTGTCATTC ATTGATATT GATATTCCT TTTGTGCTT 1020
CTGCCAATCT CCAATGGAGA GACCTGTGTG CCAATTATCC ATATGATGAG ACGCGGAGTG 1080
GTAGTGCTCA CGAATACAGC TCCTCCOCAG ATGACGCCAT TTTCCAAAGC TTGGCCCGGG 1140
CATACTCTTC TTTCACCCCG GCCATGTCTG ACCCCAAATCG GCCACCATGT CGCAAGAATG 1200
ATGATGACAG CAGCTTTGTA GATGGAACCA CCAACGGTGG TGCTGTGATC AGCGTACCTG 1260
GAGGGATGCA AGACTTCAAT TACCTTAGCA CCAACTGTTT TGAGATCACC GTGGAGCTTA 1320
GCTGTGAGAA GTTCCCACTT GAAGAGACTC TGAAGACCTA CTGGGAGGAT AACAAAACT 1380
CCCTCATTAG CTACCTTAG CAGATACACC GAGGAGTTAA AGGATTGTG CGAGACCTTC 1440
AAGGTAACCC AATGTGGAAT GCCACCATCT CCGTGAAGG AATAGACCAC GATGTTACAT 1500
CCGCAAGGA TGGTGATTAC TGGAGATTGC TTATACCTGG AAACATAAA CTTACAGCCT 1560
CAGCTCCAGG CTATCTGSCA ATAACAAGA AAGTGGCAGT TCCTACAGC CCTGCTGCTG 1620
GGGTGATTT TGAATGGAG TCATTTTCTG AAAGGAAGA AGAGGAGAAG GAAGAATTGA 1680
TGGAAATGGT GAAATGATG TCAGAAACTT TAAATTTTAA AAAAGGCTTC TAGTTAGCTG 1740
CTTTAAATCT ATCTATATAA TGTAGTATGA TGTAAATGGG TCTTTTTTTT AGATTTTGTG 1800
CAGTTAATAC TTAACATTGA TTTATTTTTT AATCATTTAA ATATTAATCA ACTTTCCTTA 1860
AAATAAATAG CCTCTTAGGT AAAATATAAA GAACCTGATA TATTTATTC TCTTATATAG 1920
TATTCATTTT CCTACCTATA TTACACAAAA AAGTATAGAA AAGATTAAAG TAATTTTGGC 1980
ATCCTAGGCT TAAATGCAAT ATCTCTGCTA TTATTTACAA TGCAGAAATT TTTGAGTAAT 2040
TCTAGCTTTC AAAAATTAGT GAAGTTCTTT TACTGTAAAT GGTGACAATG TCACATAATG 2100
AATGCTATTG AAAAGGTTAA CAGATACAGC TCGGAGTTGT GAGCACTCTA CTGCAAGACT 2160
TAAATAGTTC AGTATAAAAT GTCGTTTTTT TCTGTGCTG ACTAACTATA AGCATGATCT 2220
TGTTAATGCA TTTTGTATGG GAAGAAAAGG TACATGTTTA CAAAGAGGTT TTATGAAAAG 2280
AATAAAAAAT GACTTCTTGC TTGTACATAT AGGAGCAATA CTATTATATT ATGTAGTCCG 2340
TTAACTACTC TAAAAGTTT AGGGTTTCT CTGTGTTGTA GAGTGGCCCA GAATTGCATT 2400
CTGAATGAAT AAAGGTAA AAATAATCCC CAGTGAAAA AAA

```

Seq ID NO: 576 Protein sequence  
Protein Accession #: NP\_001864.1

55  
60  
65

```

1      11      21      31      41      51
|      |      |      |      |      |
MAGRGGALL ALGALAAACG WLLGAEQEP GAPAGMRRR RRLQEDGIS FEYHRYPELR 60
EALSVVLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEPKYI GNMHGNEAVG 120
RELLIFLAQY LQNEYQKQNE TIVNLHSTR IHIMPSLNPD GFEXAASQPG ELQDWFVGRS 180
NAQGDILMRN FPDRLRIYVV NEKEGGPNNH LKNNMKIVD QNTKLAPETK AVIHWIMDIP 240
FVLSANLEGG DLVANYPYDE TRSGSAEYS SSPDDAIFQS LARAYSSFPN AMSDPNRPFC 300
RKNDSSSPV DGTINGGAWY SVPGMDFN YLSSNCFBIT VELSCCKFPF EETLKYWED 360
NKNSLISYLE QIHRGVKGFV RDLQGNPIAN ATISVEGIDH DVTSKDG DY WRLLIPGNYK 420
LTASAPGYLA ITKVAVPYS PAAGVDFELE SFSEKKEEK EELMENWKM SETLNF

```

Seq ID NO: 577 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..933

70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGTGCAGCA ATGGACGGTG CATCCCGGCG GCCTGGCAGT GTGACGGGCT GCCTGACTGC 60
TTGCACAAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCGACCTTC 120
TTCCCTGTGG CAGCGGCGAT CCAATGCATC ATTGGTGCCT TCGCGTGCAA TGGGTTTGAG 180
GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240
GCCCCGTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300
AATAACTGTG AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT 360
GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTTGTGTATT ACCCCAGCAT CACCTATGCC 420
ATCATCGGCA GCTCCGTCTT TTTTGTGCTG GTGGTGGCCC TGCTGGCACT GGTCTTGAC 480
CACCGCGGGA AGCGGAACAA CCTCATGACG CTGCGCGTGC ACCCGCTGCA GCACCTGTG 540
CTGCTGTCCC GCCTGGTGGT CCTGGACAC CCCCACCACT GCAACGTGAC CTACAACGTC 600
AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTGGGA AGTAGGCTCC 660
CCACCTCTCT ACTCCGAGGC CTTGCTGGAC CAGAGGCGCT CGTGGTATGA CCTTCCTCCA 720
CCGCCCTACT CTTCTGACAG GGAATCTCTG AACCAAGCCG ACCTGCCCCC CTACCGCTCC 780
CGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGAGCCCA GCAGCCTCCT GAGCGTGGAA 840
GACACCAAGC ACAGCCCGGG GCAGCCTGCG CCCCAGGAGG GCATGTGTA GCCCAGGAG 900

```

TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence  
 Protein Accession #: Bos sequence

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40

1	11	21	31	41	51	
MCSNGRCIPG	AWQCDGLPDC	FDKSDKEKECP	RAKSKCGPTF	PPCASGIHCI	IGRFRNGFE	60
DCPDGSDDEEN	CTANPLLCST	ARYHCKNGLC	IDKSFICDQG	MNCQDNDSEE	SCSSSQEPGS	120
GQVFTVSENQ	LVYYPSTIYA	IIGSSVIFVL	VVALLALVLH	HQRKRNNLMT	LPVHRLQHPV	180
LLSLRVLDH	PHRCNVTVNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPWYDLPP	240
PPYSSDTESL	NQADLPPYRS	RSQSANSASS	QAASSLLSVE	DTSHSPQPG	PQEGTAEPDR	300
SEPSQGTTEE						

Seq ID NO: 579 DNA sequence  
 Nucleic Acid Accession #: AF179274.1  
 Coding sequence: 1..1125

20  
 25  
 30  
 35  
 40

1	11	21	31	41	51	
ATGGTGCTGT	GGGAGTCCCC	GCGGCACTGC	AGCAGCTGGA	CACTTTGCGA	GGGCTTTTGC	60
TGGCTGCTGC	TGCTGCCCCG	CATGCTACTC	ATCGTAGCCC	GCCCGGTGAA	GCTCGCTGCT	120
TTCCCTACCT	CCTTAAGTGA	CTGCCAAACG	CCCACCGGCT	GGAATTGCTC	TGGTTATGAT	180
GACAGAGAAA	ATGATCTCTT	CCTCTGTGAC	ACCAACACCT	GTAATTTTGA	TGGGGAATGT	240
TTAAGAATTG	GAGACACTGT	GACTTGCCTC	TGTCAATTCA	AGTGCAACAA	TGACTATGTG	300
CCTGTGTGTG	GCTCCAATGG	GGAGAGCTAC	CAGAATGAGT	GTTACCTGCG	ACAGGCTGCA	360
TGCAACACAG	AGAGTGAGAT	ACTTGTGGTG	TCAGAAGGAT	CATGTGCCAC	AGATGCAGGA	420
TCAGGATCTG	GAGATGGAGT	CCATGAAGGC	TCTGGAGAAA	CTAGTCAAAA	GGAGACATCC	480
ACCTGTGATA	TTTGCCAGTT	TGGTGCAGAA	TGTGACGAAG	ATGCCGAGGA	TGTCTGGTGT	540
GTGTGTAATA	TTGACTGTTC	TCAAACCAAC	TTCAATCCCC	TCTGCGCTTC	TGATGGGAAA	600
TCTTATGATA	ATGCATGCCA	AATCAAAGAA	GCATCGTGTC	AGAAACAGGA	GAAAATTGAA	660
GTCATGTCTT	TGGTGTGATG	TCAAGATAAC	ACAACACTCA	CTACTAAGTC	TGAAGATGGG	720
CATTATGCAA	GAACAGATTA	TGCAGAGAAT	GCTAACAAAT	TAGAAGAAAG	TGCCAGAGAA	780
CACCACATAC	CTTGTCCGGA	ACATTACAAT	GGCTTCTGCA	TGCATGGGAA	GTGTGAGCAT	840
TCTATCAATA	TGCAGGAGCC	ATCTTGCAGG	TGTGATGCTG	GTTATACITG	ACAACACTGT	900
GAAAAAAAGG	ACTACAGTGT	TCTATACGTT	GTTCGCCGTC	CTGTACGATT	TCAGTATGTC	960
TTAATGCGAG	CTGTGATTGG	AACAAATCAG	ATTGCTGTCA	TCTGTGTGGT	GGTCTCTCTG	1020
ATCACAAAGG	AATGCCCCAG	AAGCAACAGA	ATTACAGAC	AGAAGCAAAA	TACAGGGCAC	1080
TACAGTTCAG	ACAATACAAC	AAGAGCGTCC	ACGAGGTAA	TCTGA		

Seq ID NO: 580 Protein sequence  
 Protein Accession #: NP\_057276.2

45  
 50

1	11	21	31	41	51	
MVLWESPRQC	SSWTLCEGFC	WLLLLFVMLL	IVARFVKLAA	FPTSLSDQQT	PTGWNCSTGYD	60
DRENDLFLCD	TNTCKFDGEC	LRIGDVTVCV	CQFKCNNDYV	PVCGSNGESY	QNECYLRQAA	120
CKQQSEILV	SEGSCATDAG	SGSGDVHEG	SGETSQKETS	TCDIQCFGAE	CDEADVDWC	180
VCNIDCSQTN	FNPLCASDGK	SYDNACQIKE	ASCQKQEKIE	VMSLGRQDN	TTTTTKSEDE	240
HYARTDYAEN	ANKLEESARE	HHIPCEPHYN	GFCMHGKCEH	SINMQEPSCR	CDAGYTGQHC	300
EKKDYSVLVY	VPGPVRFPYV	LIAAVIGTIQ	IAVICVVVLC	ITRKCFRPNR	IHRQKQNTGH	360
YSSDNTTRAS	TRLI					

Seq ID NO: 581 DNA sequence  
 Nucleic Acid Accession #: S78203.1  
 Coding sequence: 1..2190

60  
 65  
 70  
 75  
 80

1	11	21	31	41	51	
ATGAATCCTT	TCCAGAAAAA	TGAGTCCAAG	GAAACTCTTT	TTTCACTGT	CTCCATTGAA	60
GAGGTACCAC	CTGACCAACC	TAGCCCTCCA	AAGAAGCCAT	CTCOGACAAT	CTGTGGCTCC	120
AACATACCA	TGAGCATGCG	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTCTCTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCTGTATT	TCTGCACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCTTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCCTGGGA	300
GCAGCCATTG	CTGACTGTGT	GTGGGAAAAA	TTCAAGACAA	TATCTATCT	CTCCTTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAAGTCCTTG	GGTGCCCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCCTATCATT	GATCGGCCTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCCCTGT	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTTGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGGAGTTC	CAGGACTGCT	CATGGTAATT	GCATTTGTTG	TGTTTGCAAT	GGGAAGCAAA	720
ATATACAATA	AACCAACCCC	TGAAGGAAAC	ATAGTGGCTC	AAGTTTTCAA	ATGTATCTGG	780
TTTGCTATT	CCAATGTTT	CAAGAACCGT	TCTGGAGACA	TTCCAAAGCG	ACAGCACTGG	840
CTAGACTGGG	CAGCTGAGAA	ATATCCAAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTAT	TCCTTTATAT	CCCATTGCCC	ATGTTCTGGG	CTCTTTTGA	TCAGCAGGGT	960
TCAGATGGA	CTTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGGTTTTT	TGTGCTTCAG	1020
CGGACACAGA	TGCAAGTTCT	AAATCCCTTT	CTGGTTCTTA	TCTTCATCCC	GTGTTTGAC	1080
TTTGCTATT	ATGCTCTGTT	CTCCAAGTGT	GGAATTAAT	TCTCATCACT	TAGGAAATG	1140
GCTGTTGGTA	TGATCTTAGC	GTGCTTGCCA	TTTGCACTTG	CGGCAGCTGT	AGAGATAAAA	1200
ATAAATGAAA	TGGCCCCAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCTTACA	AGTCTTGAAT	1260
CTGGCAGATG	ATGAGGTGAA	GGTGACAGTG	GTGGGAATG	AAAACAATTC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAACACCCA	CACTATTCCA	AACTGCACCT	GAAACAAAAA	1380
AGCCAGGATT	TCTCACTCCA	CCTGAAATAT	CACAATTGT	CTCTCTACAC	TGAGCACTCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTGTGC	ATTCGTGAAG	ATGGGAACAG	TATCTCCAGC	1500

5 ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGTT 1560  
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620  
 GAAGACTATG GTGTGTCTGC TTATAGAACT GTGCAAGAG GAGAAATACCC TGCAGTGCAC 1680  
 TGTAAGACAG AAGATAAGAA CTTTTCTCTG AATTGGGCTC TTCTAGACTT TGGTGCAGCA 1740  
 10 TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCTTGGAA GATTGAAGAC 1800  
 ATTCACGCCA ACAAAATGTC CATTGCGTGG CAGTACCAC AATATGCCCT GGTACAGCT 1860  
 GGGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTTCTT ATTCTCAGGC TCCTCTAGC 1920  
 ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG 1980  
 CTGTGTGTGG CACAGTTCAG TGGCCTGGTA CAGTGGGCGG AATTCATTTT GTTTTCTCTG 2040  
 CTCTGCTGCG TGATCTGCTT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG 2100  
 ACAGAGGATA TCGGGGTCC AGCAGATAAG CACATTCCTC ACATCCAGGG GAACATGATC 2160  
 AAACAGAGA CCAAGAAGAC AAAACTCTGA

Seq ID NO: 582 Protein sequence  
 Protein Accession #: AAB34388.1

15  
 20  
 25  
 30  
 1 11 21 31 41 51  
 MNPFQKNESK ETLFSPVSIE EVPPRPSPSP KKPSPITCGS NYPLSIAFIV VNEFCERFSY 60  
 YGMAVLILY FLYFLHWNED TSTSIYHAFS SLCYFTPLIG AAIADSWLKG FKTIYLSLV 120  
 YVLGHVILSL GALPILGQV VHTVLSLIGL SLIALGTGGI KPCVAAFVGD QFEKHAER 180  
 TRYFSVFLYS INAGSLISTF ITPMLRGDVQ CFGEDCYALA FGVFGLLMVI ALVVFAWGSK 240  
 IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKQHW LDWAAEKYPK QLIMDVKALT 300  
 25 RVLFILYILP MFALLDQOG SRWTLQAIRN NRNLGFFVLQ PDQMVLNPF LVLFIPLFD 360  
 FVIYRLVSKC GINFFSLRKM AVGMILACLA FAVAAVEIK INEMAPAQSG POEVFLQVLN 420  
 LADDEVKVTV VGNNNSLLI ESIKSFQKTP HYSKLHLKTK SQDFHFLKY HNLSLYTEHS 480  
 VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540  
 EDYGSAYRT VQRGEPYAVH CRTEDKNFSL NLGLDFGAA YLFVITNNTN QGLQANKIED 600  
 IPANKMSIAW QLPQYALVTA GEVMFSVTGL EFSYSQAPSS MKSVLQAAWL LTIAGVNIIV 660  
 30 LVVAQFSLGV QWAEFLFSC LLLVICLIFS IMGYIVPVK TEDMRGPADK HIPHIQNMNI 720  
 KLETKTKTL

Seq ID NO: 583 DNA sequence  
 Nucleic Acid Accession #: NM\_032642.1  
 Coding sequence: 184..1263

35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80  
 1 11 21 31 41 51  
 GACCATTAGC AGGCACCCAG GCCTGTCTTT GGCTCGGAAA CGGTGGCCCC CAATGTAGCC 60  
 TAGTTTGAAC CTAGGAACCTG CAGGACCAGA GAGATTCCAC TGGAGCCTGA TGGACGGGTG 120  
 ACAGAGGGAA CCCTACTCTG GAAACTGTCA GTCCAGGGGC ACTGGGAGG GCTGAGGCCG 180  
 ACCATGCCCA GCCTGCTGCT GCTGTTACAG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT 240  
 CTGACAGAGC CGAACTCCTG GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300  
 45 TTTATCATCG GTGCCACGCC CGTGTGCAGT CAGCTTCCCG GGCTCTCCCC TGGCCAGAGG 360  
 AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC 420  
 ATCAAGGAAT GCCAGCACCA GTTCCGGCAG CGGCGGTGGA ATTGCAGCAC AGCGGACAA 480  
 GCATCTGTCT TTGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGCCTT CACCCACGG 540  
 GTGAGCGCCG CGGCGTGGT CAACGCCATC AGCCGGGCTT GCGCGAGGG CGAGTCTCTC 600  
 50 ACCTGCGGCT GCAGCCGAGC GCGCGGCCCC AAGGACCTGC CCGCGGACTG GCTGTGGGGC 660  
 GGCTGTGGGG ACAACGTGGA GTACGGCTAC CGCTTCGCCA AGGAGTTTGT GGATGCCCGG 720  
 GAGCGAGAGA AGAACTTTGC CAAAGGATCA GAGGAGCAGG GCGGGTGTCT CATGAACCTG 780  
 CAAAACAACG AGGCGGCTCG CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAAAATG 840  
 CAGGCGCTCT CGGCGTCTG CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTCTCGC 900  
 55 AAGTTCGGGG ACCGGCTGAA GGAGAAATAC GACAGCGCGG CCGCCATCGC CGTCAACCCG 960  
 AAGGCGCGGC TGGAGCTGGT CAACAGCCGC TTCAACCCAGC CCACCCCGGA GGACCTGGTC 1020  
 TATGTGGACC CCAGCCCGGA CTACTGCCTG CGCAACGAGA GCAACGGCTC CTTGGGACG 1080  
 CAGGGCCCGC TCTGCAACAA GACCTCGGAG GGCATGGATG GCTGTGAGCT CATGTCTGTC 1140  
 GGGCGTGGT ACAACAGTGT CAAGAGCGTG CAGGTGGAGC GCTGCCACTG CAAGTTCCAC 1200  
 60 TGGTGTGCTT TCGTCAAGTG TAAGAAATGC ACGGAGATCG TGGACCACTA CATCTGTAAA 1260  
 TAGCCCGGAG GGCTGTCTCC CGGCCCCCCC TGCACTCTGC CTCACAAAGG TCTATATTAT 1320  
 ATAAATCTAT ATAAATCTAT TTTATATTG TATAAGTAAA TGGGTGGGTG CTATACAAAT 1380  
 GAAAGATGAA AATGGAAAGG AAGAGCTTAT TTAAGAGACG CTGGAGATCT CTGAGGAGTG 1440  
 GACTTTGTGT GTTCTCTCTT CTGTGTGGT GGGAGACAGG GCTTTTCTCT TCCTCTGGC 1500  
 65 GAGGACTCTC AGGATGTAGG GACTTGGAAA TATTTACTGT CTGTCCACCA CGGCTTGGAG 1560  
 GAGGGAGGTT GTGGTTGGAT GGAGGAGATG ATCTGTCTGT GAAGTCTAGA GTCTTTGTTG 1620  
 GTTAGAGGAC TGCTGTGAT CTGGGCACT AGGCCAAGAG GCCCTATGAA GGTGGGGGGA 1680  
 ACTCAGCTTC AACCTCGATG TCTTCAGGCT CTTGTCCAGA ATGTAGATGG GTTCGGTAAG 1740  
 AGGCCTGGTG CTCTCTTACT CTTTCATCCA GTTGCACCTG TGGCGCATCT GCAGTTTACA 1800  
 70 GGAACGCGCT CTTCCTTAAA ATGAGAAATC CAAGGTCAAT TCTGGCCAG TGACCAACAG 1860  
 GAGATCTGCA CCTCCCGGAC TTCAGGCGTG CCTTCCAGC GAGAATTCIT CATCCTCCAC 1920  
 GGTTCACTAG CTCTACCTG AAGAGGAAAG GGGGCCATTT GACCTGACAT GTCAGGAAAG 1980  
 CCCTAAACTG AATGTTTGGC CTTGGGCTGC AGAAGCCAGG GTGCAATGAC AGGCTCGGTG 2040  
 GACGTTATAT TGTCTTCTCC CACCCCGGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100  
 75 CTCCACCGAG GGAGGCTTCA CAAACACAG GACGCTGCAA CGGCTCAGGC TGGCGGGGCC 2160  
 GCGGTGCTCA TCATCTCTGC CCCAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA 2220  
 TGGAAAAAAA AAAAGAAAAA AAAAAAAA AA

Seq ID NO: 584 Protein sequence  
 Protein Accession #: NP\_116031.1

80  
 1 11 21 31 41 51  
 MPSLLLLFTA ALLSSNAQLL TDANSWWSLA LNPVQRPEMF IIGAQPVCQSQ LPGLSPGQRK 60  
 LCQLYQEHMA YIGEGAKTGI KECQHQRQR RNWNCSTADNA SVFGRVMQIG SRETAFTHAV 120

SAAGVVNAIS RACREGELST CGCSRTARPK DLPRDNLWGG CGDNVEYGYR FAKEFVDARE 180  
 REKNFAKGEY EQGRVLMNIQ NNEAGRRAVY KMADVACKCH GVSQCSLKT CWLQLAEPK 240  
 VGDRLEKEDY SAAAMRVTRK GRLELVNSRF TQPTPEDLVY VDSPDYCLR NESTGSLGTQ 300  
 GRLCNKTSSE MDGCELMCCG RGYNQFKSVQ VERCHCKFWH CCFVRCKCT EIVDQYICK

Seq ID NO: 585 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1479

1 11 21 31 41 51  
 | | | | |  
 ATGGCTTTGA ACTCAGGGTC ACCACCAGCT ATTGGACCTT ACTATGAAAA CCATGGATAC 60  
 CAACCGGAAA ACCCTATCC CGCACAGCCC ACTGTGGTCC CCACTGTCTA CGAGGTGCAT 120  
 CGGGCTCAGT ACTACCCGTC CCCCGTGCCC CAGTAGCCCC CGAGGGTCTT GAOCGAGGCT 180  
 TCCAAACCCG TCGTCTGCAC GCAGCCCAA TCCCATCCG GGACAGTGTG CACCTCAAAG 240  
 ACTAAGAAAG CACTGTGCAT CACCTTGACC CTGGGGACCT TCCTCGTGGG AGCTGCGCTG 300  
 GCCGTGGGCC TACTCTGGAA GTTCATGGGC AGCAAGTGCT CCACTCTGCG GATAGAGTGC 360  
 GACTCTCAG GTACTCTGAT CAACCCCTCT AACTGGTGTG ATGGCGTGTG ACACCTGCCC 420  
 GGCGGGGAGG AGGAGAATCG GTGTGTTCCG CTCTACGGAC CAAACTTCAT CCTTCAGGTG 480  
 TACTCATCTC AGAGGAAGTC CTGGCACCTT GTGTGCCAAG ACGACTGGAA CGAGAACTAC 540  
 GGCGGGGCGG CTGACAGGGA CATGGGCTAT AAGAATAATT TTTACTCTAG CCAAGGAATA 600  
 GTGGATGACA GCGGATCCAC CAGCTTTATG AAAGTGAACA CAAGTGCCGG CAATGTCGAT 660  
 ATCTATAAAA AACTGTATCCA CAGTGATGCC TGTTCCTCAA AAGCAGTGGT TTCTTTACCG 720  
 TGTATAGCCT GCGGGGTCAA CTGAACTCA AGCCGCCAGA GCAGGATCGT GGGCGGGCGAG 780  
 AGCGCGCTCC CGGGGGCTCG GCCCTGGCAG GTGAGCTGCG ACGTCCAGAA CGTCCACGTG 840  
 TGCGGAGGCT CCATCATCAC CCCCGAGTGG ATCGTGACAG CCGCCCACTG CGTGGAAAAA 900  
 CCTCTTAAAC ATCCATGGCA TTGGACGGCA TTTGCGGGGA TTTTGAGACA ATCTTTTCATG 960  
 TTCTATGAGG CGGGATACCA AGTAGAAAAA GTGATTTCTC ATCCAAATTA TGACTCCAAG 1020  
 ACCAAGAAAC ATGACATTGC GCTGATGAAG CTGCAGAAC CTCTGACTTT CAACGACCTA 1080  
 GTGAACACAG TGTGTCTGCG CAACCCAGGC ATGATGCTGC AGCCAGAACA GCTCTGCTGG 1140  
 ATTTCCGGGT GGGGGGCCAC CGAGGAGAAA GGAAGACCT CAGAAGTGTG GAACGCTGCC 1200  
 AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGTCTATGA CAACCTGATC 1260  
 ACACAGACCA TGATCTGTGC CGGCTTCCTG CAGGGGAACG TCGATTCTTG CCAGGGTGAC 1320  
 AGTGGAGGGC CTCTGCTCAC TTCGAAGAAC AATATCTGGT GGCTGATAGG GGATACAAGC 1380  
 TGGGGTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGGTATTC 1440  
 ACGGACTGGA TTTATCGACA AATGAGGGCA GACGGCTAA

Seq ID NO: 586 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTA 60  
 SNPVVCTQPK SPFGTCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMS SKCSNSGIEC 120  
 DSSGTACNPS NWCDGVSHCP GGEDENRCVR LYGNPFIQV YSSQRKSWHP VQDDWNENY 180  
 GRAACRDMGY KNFYSSQGI VDSGGSFEM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240  
 CIACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGSIIITPEW IVTAAHCVEK 300  
 PLNNPFWHAT FAGLLRQSFY FYGAGYQVEK VISHPNYDSK TKNNDIALMK LQKPLTFNDL 360  
 VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNL 420  
 TPAMICAGFL CGNVDSQCGD SGGPLVTSKN NIWWLIGDTS WSGCAKAYR PGVYGNVMVF 480  
 TDWIYRQMBR DG

Seq ID NO: 587 DNA sequence  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57..1535

1 11 21 31 41 51  
 | | | | |  
 GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGTATAAC AGCAAGATGG 60  
 CTTTGAATC AGGGTACCA CCAGCTATTG GAOCCTACTA TGAAGAACAT GGATACCAAC 120  
 CGGAAACCC CTATCCGCCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180  
 CTCAGTACTA CCGTCCCCC GTGCCCACT AGCCCCGAGG GGTCTGAGC CAGGCTTCCA 240  
 ACCCCGTCGT CTGCACGCG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300  
 AGAAAGCATT GTGCATCACC TTGACCTGCG GGAACCTTCT CGTGGGAGCT GCGCTGGCCG 360  
 CTGGCCTACT CTGGGAAGTT ATGGGCGAGCA AGTGTCTCAA CTCTGGGATA GAGTGCAGCT 420  
 CCTCAGGTAC CTGCATCAAC CCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGCGG 480  
 GGGAGGACGA GAATCGGTGT GTTCGCTCTT ACGGACCAA CTTCCTCTT CAGATGTACT 540  
 CATCTCAGAG GAAGTCTGTG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 GGGCGGCTGT CAGGGACATG GGCCTATAAGA ATAATTTTCT CTCTAGCCAA GGAATAGTGG 660  
 ATGACAGCGG ATCCACACAG TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720  
 ATAAAAAAT GTACCAAGT GATGCTGTGT CTTCAAAAGC AGTGGTTTCT TTAACGCTGT 780  
 TAGCTCCGGG GGTCACTGT AACTCAAGCC GCCAGAGCAG GATCGTGGGC GTGAGAGCG 840  
 CGCTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CACGTGTGCG 900  
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960  
 TTAACAATCT ATGGCATTGG ACGGCATTTC CGGGGATTTT GAGACAATCT TTCATGTTCT 1020  
 ATGGAGCCGG ATACCAAGTA CAAAAGTGA TTTCTCATCC AAATATGAC TCCAAGACCA 1080  
 AGAACAAATG CATTGCGCTG ATGAAGCTGC AGAAGCTCT GACTTTCAC GACCTAGTGA 1140  
 AACCAGTGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200  
 CGGGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGTCTGAC GCTGCCAAGG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAA CTGATCACAC 1320  
 CAGCCATGAT CTGTGCCCGC TTCCTGCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG 1380  
 GAGGCGCTCT GGTCACTTCG AACAAACAATA TCTGTGGGCT GATAGGGGAT ACAAGCTGGG 1440  
 GTTCTGCGTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTACGG 1500  
 ACTGGATTAT TCGACAAATG AAGGCAAACG GCTAATCCAC ATGGTCTTCT TCCTTGACGT 1560

CGTTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCG TGCAATGATT ACTCTTAGAG 1620  
 ATGATTCAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGCTGGCTT TGGCACTCTC 1680  
 TGCCATACATG TGCAGGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTTGT 1740  
 CCGCAAGGGG TGAATGCCCG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800  
 GTTGGAGGCT GCCCCCATTG AGATCTTCCT GCTGAGTCTT TCCAGGGGC CAATTTTGA 1860  
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GATGACTTG AGATGAAAA GGAGAGACAT 1920  
 GGAAGGGAGG ACAGCCAGGT GGCACCTGCA GCGGCTGCC TCTGGGSCCA CTGGTAGTGT 1980  
 TCCCCAGCCT ACTTCAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040  
 GATGGTGGCC AGAAATAAG GACACAGCCC TCCATGGGTG GTGACGTGGT AGTCACTTGT 2100  
 AAGGGGAACA GAACATTTT TGTCTTATG GGGTGAGAAT ATAGACAGTG CCTTGGTGC 2160  
 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCTT GGTGCAGGTC TCCACCTGCA 2220  
 CATTGGGTGG GGCTCTGGG AGGGAGACTC AGCCTCTCTC CTCATCTCTC CTGACCCCTG 2280  
 TCCTAGCACC CTGAGAGTGT AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340  
 ATGTCCGCTT CTTCAGGCTT GATAGTCATT GGAATTTAG GTCCATGGGG GAAATCAAGG 2400  
 ATGCTCAGTT TAAGGTACAC TGTTCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460  
 CTGAGTTCAA AGCCATCTT

Seq ID NO: 588 Protein sequence  
 Protein Accession #: NP\_005647.1

1 11 21 31 41 51  
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTOA 60  
 SNFVVCTQPK SPSGTVCSTK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120  
 DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VQDDWNENY 180  
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240  
 CLACGVNLNS SRQSRIVGGE SALPGANFPWQ VSLHVQNVHV CGSSIITPEW IVTAAHCVKE 300  
 PLNNPWHWTF FAGILRQSFY FYGAGYQVOK VISHENYDSK TKNDIALMK LQKPLTFNDL 360  
 VKFVCLNPNP MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLETQRC NSRYVYDNL 420  
 TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIWMLIGDTS WSGGCAKAYR PGVYGNVMVF 480  
 TDWIYRQMKK NG

Seq ID NO: 589 DNA sequence  
 Nucleic Acid Accession #: NM\_001935.1  
 Coding sequence: 1..2301

1 11 21 31 41 51  
 ATGAAGACAC CGTGAAGATG TCTTCTGGGA CTGCTGGGTG CTGCTGCGCT TGTCAACATC 60  
 ATCACCCTGC CGTGGTCTCT GCTGAACAAA GGCACAGATG ATGCTACAGC TGACAGTCGC 120  
 AAAAATTACA CTCTAACTGA TTACTTAAAA AATACTTATA GACTGAAGTT ATACTCCTTA 180  
 AGATGGATTT CAGATCATGA ATATCTCTAC AAACAAGAAA ATAATATCTT GGTATTCAAT 240  
 GCTGAATATG GAACAGCTC AGTTTCTTGG GAGAACAGTA CATTGTATGA GTTTGGACAT 300  
 TCTATCAATG ATTATTCAT ATCTCTGAT GGGCAGTTTA TTCTCTAGA ATACAACATC 360  
 GTGAAGCAAT GGAGGCATTC CTACACAGCT TCATATGACA TTTATGATT AAATAAAGG 420  
 CAGCTGATTA CAGAAGAGAG GATTCCAAAC AACACACAGT GGGTCACATG GTCACCACTG 480  
 GGTCATAAAT TGGCATATGT TTGGAACAA GACATTATG TTAATAATGA ACCAAATTTA 540  
 CCAAGTTACA GAATCACATG GACGGGGAAG GAAGATATAA TATATAATGG AATAACTGAC 600  
 TGGGTTTATG AAGAGGAAGT CTTCAGTGCC TACTCTGCTC TGTGGTGGTC TCCAAACGGC 660  
 ACTTTTITAG CATATGCCCA ATTTAACGAC ACAGAAGTCC CACTTATTGA ATACTCTTC 720  
 TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAGGCAGGA 780  
 GCTGTGAATC CAACTGTAAA GTTCTTGTGT GTAAATACAG ACTCTCTCAG CTCAGTCACC 840  
 AATGCAACTT CCATACAAAT CACTGCTCCT GCTTCTATGT TGATAGGGGA TCACTACTTG 900  
 TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTTCTTTCG AGTGGCTCAG GAGGATTCTG 960  
 AACTATTCCG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACTGCTTA 1020  
 GTGGCAGCGC AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCTTCA 1080  
 GAACCTCATT TTACCTTGA TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT 1140  
 TACAGACACA TTTGCTATTT CCRAATAGAT AAAAAGACT GCACATTAT TACAAAAGGC 1200  
 ACCTGGGAAG TCATCGGAT AGAAGCTCTA ACCAGTGATT ATCTATACTA CATTAGTAAT 1260  
 GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCACTTAG TGACTATACA 1320  
 AAAGTGACAT GCCTCAGTTG TGAGCTGAAT CCGGAAAGGT GTCAGTACTA TTCTGTGTCA 1380  
 TTCAGTAAAG AGGCGAAGTA TTATCAGCTG AGATGTTCCG GTCCCTGGTCT GCCCCTCTAT 1440  
 ACTCTACACA GCAGCGTGAA TGATAAAGGG CTGAGAGTCC TGGAGACAA TTCAGCTTGT 1500  
 GATAAAATGC TGCAGATGT CCAGATGCCC TCCAAAAAAC TGGACTTCAT TATTTTGAAT 1560  
 GAAACAAAT TTTGGTATCA GATGATCTTG CCTCTCAT TTTGATAATC CAAGAAATAT 1620  
 CCTCTACTAT TAGATGTGTA TGCAGGCCCA TGTAGTCAAA AAGCAGACAC TGTCTTCAGA 1680  
 CTGAACCTGG CCACCTACCT TGCAAGCACA GAAACATTA TAGTAGCTAG CTTTGATGGC 1740  
 AGAGGAAGTG GTTACCAAGG AGATAAGATC ATGCATGCAA TCAACAGAAG ACTGGGAACA 1800  
 TTTGAAGTTG AAGATCAAT TGAAGCAGCC AGACAATTTT CAAAAATGGG ATTTGTGGAC 1860  
 AACAAACGAA TTGCAATTTG GGGCTGGTCA TATGGAGGT ACGTAACTC AATGGTCTCTG 1920  
 GGATCGGGAA GTGGCGTGT CAAGTGTGGA ATAGCGGTGG CGCTGTATC CCGTGGGAG 1980  
 TACTATGACT CAGGTACAC AGAAGCTTAC ATGGGTCTCC CAATCCAGA AGACAACCTT 2040  
 GACCATTACA GAATTTCAAC AGTCATGAGC AGAGCTGAAA ATTTTAAACA AGTTGAGTAC 2100  
 CTCCTTATTC ATGGAACAGC AGATGATAAC GTTCACTTTC AGCAGTCAGC TCAGATCTCC 2160  
 AAAGCCCTGG TCGATGTTGG AGTGGATTTC CAGGCAATGT GGTATACTGA TGAAGACCAT 2220  
 GGAATAGCTA GCAGCAGC ACACCAACAT ATATATACCC ACATGAGCCA CTTCAATAAA 2280  
 CAATGTTTCT CTTTACCTTA G

Seq ID NO: 590 Protein sequence  
 Protein Accession #: NP\_001926.1

1 11 21 31 41 51  
 MKTPWKILLG LIGAAALVTI ITVPVLLNK GTDDATADSR KTYTLIDYLK NTYRLKLYSL 60



5 RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQFILLEYN 120  
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVWNN DIYVKIEPNL 180  
 PSYRITWTGK EDIYNGITD WYEEVFSA YSALMWSPNG TFLAYAQFND TEVPLIEYSF 240  
 YSDESLQYPK TVRVPYPKAG AVNPTVKPFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300  
 10 CDVTNATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGVVGRFRPS 360  
 EPHFTLDGNS FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYIYN 420  
 EYKMPGGGRN LYKIQLSDYT KVTCLSCSELN PERCQYYSVS FSKEAKYQYL RCGSGPLPLY 480  
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDIFIILN ETKFWYQMKI PPHFDKSKKY 540  
 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RGSQYQDKI MHAINRRLGT 600  
 FEVEDQIEAA RQFSKMGFVD NKRIAIWNS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660  
 YDVSVYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720  
 KALVDVGVDG QAMWYDDEH GIASSTAHOH IYTHMSHFIF QCFSLP

15 Seq ID NO: 591 DNA sequence  
 Nucleic Acid Accession #: NM\_016077.1  
 Coding sequence: 128..667

20 1 11 21 31 41 51  
 TCGCTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60  
 CGCGATAGAA ACGTGTTCGC TTGCCAGAA GAAGGGAAG CGCGAGTGAG GAAAGGAGGT 120  
 ACTGTAGATG CCTTCCAAAT CCTTGGTTAT GGAATATTTG GCTCATCCCA GTACACTCGG 180  
 CTGGCTGTT GAGATTGCTT GTGGCATGTG CCTGGGCTGG AGCCTTGGAG TATGCTTTGG 240  
 25 GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300  
 CTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGTTT CGAAATGACT TAAGATGGG 360  
 AAAAGGGAAG GTGGCTGCCC AGTGCTCTCA TGCTGCTGTT TCAGCTTACA AGCAGATTCA 420  
 AAGAAGAAAT CCTGAAATGC TCAAAACATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT 480  
 CAAAGCTCCT GATGAAGAAA CCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT 540  
 30 GACTGTAAGT TTAATTCAGG ATGCTGGACG TACTCAGATT GCACCAGGCT CTCAAACTGT 600  
 CCTAGGAGAT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCAGTGGTC ACCTAAACT 660  
 TTAAGTGGT GACTTTGATA TGACAACAAC CCTCCATCA CAAGTGTITG AAGCCTGTCA 720  
 GATTCTAACA ACAAAAGCTG AATTCTTCA CCAACTTAA ATGTTCTTGA GATGAAAAATA 780  
 AAACCTATTC CCATGTTCTA AAAAA

35 Seq ID NO: 592 Protein sequence  
 Protein Accession #: NP\_057161.1

40 1 11 21 31 41 51  
 MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHI DTESEASILG 60  
 DSSEYKMLLV VRNDLKMKGK KVAAQCSHAA VSAYXQIQRR NPEMLKQWEY CGQPKVVVKA 120  
 PDEETLIALL AHAKMLGLTV SLIQDAGRQ IAPGSQTVLG IGPSPADLID KVTGHLKLY

45 Seq ID NO: 593 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1896

50 1 11 21 31 41 51  
 ATGCGCGCGC TGCGCGTGC CGCCCCGCTC CTGCGCGTGC TGCTGCTCGC GCTCCTGGCC 60  
 GCTCCGCGCG CCGCGGCCAG CAGAGCCGAG TCCGTCTCCG CGCGTGGCC CGAACCAGAG 120  
 CGCGAGTGGC GGCACCGGCC CGGCCCGGGG CCCGGGAACA CCACCGCGTT TGGGTCTGGG 180  
 GCGCGCGGGG CGAGCGGCAG CTCAGCTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240  
 55 ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CCGTGTGCTT GCGGTTCGCC 300  
 TTTACCAACC TCCTCATGCG CTGCGTCTGT CTGCGGCTCT TCAGGTGGG AAGAGGTTA 360  
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGA AATGGCGCCA 420  
 CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480  
 TCCTGCGCG CTGCATGATG ACGTCAGCTG CCAGGGTGGC AGACGCTACT GACAGTTCCT 540  
 60 GTGCCCCCACC CCTTCATCCT CGACATGAC CTTCAGCAA GATGCACTGG AAGGCCTGAT 600  
 GGTGGAATCA GACCTGGTAA AACCTGTTT CCAGCCTGGT GGCATCCTGT GGAAGTTGG 660  
 TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGGT CGGAGTGT 720  
 GAAACCAAAA CGAAGCTTAT GTATAAAACC CCAGCTCCAT CGTGGGTGTC AGGCATCTGC 780  
 TCAGACTGAC ACTGGCAAGC TGTGTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840  
 65 TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900  
 CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCGG GGCTCCATCT 960  
 GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020  
 CCTTGGTGGC ACTTCAGGCG CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAAACATG 1080  
 70 AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TTGTGAAGAC 1140  
 AGAGCAGTGA CTAAGGTTCT CCAGGTTAGC TCTTTCTCCA AACAGTGGC CTGGAAGCCA 1200  
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCGCTGAGC 1260  
 ACCCATCTGT TCAGGTGGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGAGG 1320  
 AGGGTGTTCG GCGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGGGG TACCGCAACT 1380  
 TGCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440  
 75 ATCTGTCTCC CCGTGTGTGC CGTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500  
 GTCTTGTGGT CATTTGAGCA GAGCCACAA AAGGCAGCTG CTGCCACGG GGAGCCTGTC 1560  
 AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620  
 GCGAACCTGC AGACAATCC AGATACCCAA GGCACAGGAG GCCCAGTGA GGATGTCACT 1680  
 80 CACCTTGGAG GAGACTTGA TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTCCAG 1740  
 GATGGCAGAT GCCAGAAGAT GGTCTGTATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800  
 TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTCTCTT 1860  
 TCCCCCGAC AGCCCTGTT TCTGTCCAG CCCTGA

Seq ID NO: 594 Protein sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
| | | | |  
5 MRVPLPAPL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60  
AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTLILLIACLL LRVFRSGKRL 120  
KKTRKYDIIT TPAERVEMAP LNEEDEDDED STVFDIKYRV SLPAALRRQL PGQTLTLLVP 180  
VPPPFILID LPARCSGRPD GGIRPGKTCF PAWHPVESH SAATWGVKDW TWKPSCVGGV 240  
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHFPKVPPT STPHGFRQLQ 300  
10 LNLMEKLDSS ALRRNRTRAPS ARCLPLVLAE MAAAESDLNP PWHFSAATGS PIKTLTYQTM 360  
STLGLDVFQ AGQRTFCED RAVTKVLQGS SFSKQLRWKP ALES GFPHHL RLLRECPPLS 420  
THFVRLARSD ARGQASITGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480  
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAA AHGEPV KRGPSSQLTR HTPCPWGITH 540  
ANLQTIPTDQ GQEGPREDDT HPGGDLQGA NFYLEEEGFQ DGRCCQKMLM SEEGPPSLTG 600  
15 CERLTGSHHF SSKSKSWFL SPRQPLFLSR P

Seq ID NO: 595 DNA sequence  
Nucleic Acid Accession #: NM\_021614.1  
Coding sequence: 1..1740

20 1 11 21 31 41 51  
| | | | |  
25 ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGGCGGC TCAGCAACTT GAGCGCGTCC 60  
CGCGGGAACC TGCAGAGAT GGAATCAGAG GCGCAGCCCC TGACGCCCCC CGCGTCTGTC 120  
GGAGGAGGTG GCGGCGCGTC CTCCCCTCTC GCAGCCGCTG CGCGCGCGCC CGCTGTTTCG 180  
TCCTCAGCCC CCGAGATGCT GGTGTCTAAG CCGAGACACA ACACTCCAA CAACCTGGCG 240  
CTCTATGAA CGGCGCGCGG AGGCAGCACT GGAGGAGCGG CGCGCGGTGG CGGAGCGGG 300  
CACGCGACGA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360  
CTGGGCCACC GCGCGCGCCT GTTCGAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC 420  
TTCCGCGATG TCGGCATGCT GGTATGCTC ATCGAGACCG AGCTGCTCGT GGGCGCCTAC 480  
30 GACAAGGCT CGCTCTATTCT CTTAGCTCTG AATGCTCTA TCAGTCTCTC CAGATCATC 540  
CTGCTCGGTC TGATCATCTG GTACCAGCC AGGGAATATC AGTGTCTCAT GGTGGACAAT 600  
GGAGCAGATG ACTGAGAAAT AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTTGGAA 660  
ATATCTGGTG GTGCTATTCA TCCCATACCT GGAATATATA CATTCACATG GACGCGCCGG 720  
CTTGCTCTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGATATATTAT TTTATCTATA 780  
35 CCAATGTCTT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAACTTTTC 840  
ACTGATGCTT CCTCTAGAAG CATTTGAGCA CTTAATAAGA TAACTTCAA TACACGTTT 900  
GTTATGAAGA CTTTAAATGAC TATATGCCA GGAATCTGAT TCTTGTGTTT TAGTATCTCA 960  
TTATGGATAA TTGCGCATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT 1020  
40 GTTACTAGCA ACTTCTCTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATGGT 1080  
TATGTGACA TGGTACTTAA CACATACTGT GGAAGAGGAG TCTGCTTACT TACTGGAAT 1140  
ATGGGTGCTG GTTGACAGC CCTGTGTGTA GCTGTAGTGG CAGGAAGCT AGAATTAACC 1200  
AAAGCAGAAA AACACGTGCA CAATTTCTAT ATGGATACTC AGCTGACTAA AAGAGTAAA 1260  
AATGCACTG CCAATGTACT CAGGGAACA TGGCTAATT ACAAAATATC AAGCTAGTG 1320  
45 AAAAAGATAG ATCATGCAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTCTAT 1380  
CAATTAAGAA GTGTAAAAAT GGAGCAGAGG AAATCTGAAT ACCAAGCAAA CACTTGGTG 1440  
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATT CTGACTTAAA CGAAGAGGAT 1500  
GAAGACTTCG AGAAGAGGAT TGTATCCCTG GAACAAAAAC TAGAGACTTT GATTGGTAGC 1560  
ATCCAGCCCT TCCCTGGGCT CATAAGCCAG ACCATCAGCG AGCAGCAGAG AGATTTCTAT 1620  
50 GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACTTACA ATGCTGAGCG GTCCCGGTCC 1680  
TCGTCCAGGA GCGGCGGTC CTCTCCACA GCACCACCA CTTATCAGA GAGTAGCTAG

Seq ID NO: 596 Protein sequence  
Protein Accession #: NP\_067627.1

55 1 11 21 31 41 51  
| | | | |  
60 MSSCRYNGGV MRPLSNLSAS RRNLHENDSE AQPLQPPASV GGGGGASSPS AAAAAAAVS 60  
SSAPEIVVVK PEHNNNNLA LYGTGGGGST GGGGGGGSGS HGSSSGTKSS KKNQNIYK 120  
LGHRRALFEK RKRLSDYALI FGMPGIVVMV IETELSWAY DKASLYSLAL KCLISLSTII 180  
65 LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIP GNYFTWTAR 240  
LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300  
VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQD VTSNPLGAMW LISITFLSIG 360  
YGDVMPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAERHVNFM MDQLTKRVK 420  
70 NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVIOMEQR KLNDQANTLV 480  
DLAKTNIMY DMISDLNERS EDFEKRIVTL ETKLETIGS IHALPLGISQ TIRQQQRDFI 540  
EAQMESYDKH VTYNAERSRS SSRRRSSST APPTSSESS

Seq ID NO: 597 DNA sequence  
Nucleic Acid Accession #: NM\_016029.1  
Coding sequence: 228..1097

75 1 11 21 31 41 51  
| | | | |  
80 CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGC GGCG CGTCTTCTTC CCCCCGAGCT 60  
GGCGGTGCGC GCGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC 120  
TGCTCCTGCT CTGGTGCGAG CTGCTGCGCT TCCTGAGGGC TGACGCGGAC CTGACGCTAC 180  
TATGGGCGGA GTGGCAGGGA CGACGCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG 240  
TGACTGGAGC CTGAGTGGA ATTGGTGAGG AGCTGGCTTA CCACTGTGCT AAAGTAGGAG 300  
TTTCTCTGTG GCTGTGAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360  
TAGAAGATG CAATTTAAAG GAAAAAGATA TACTTGTGTT GCCCTTGAC CTGACGACA 420  
CTGTTTCCCA TGAAGCGGCT ACCAAGCTG TTCTCCAGGA GTTGTGTAGA ATGACATTC 480  
TGGTCAACAA TGGTGAATG TCCAGCGCTT CTCTGTGCTG GATACACAG TTGGATGTCT 540  
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTG CTTGACAAA TGTGTTCTGC 600  
CTCAGATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660

5 TATCTGTACC TCTTTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA 720  
 ATGGCCTTGG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCG 780  
 GACCTGTGCA ATCAAAATATT GTGGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840  
 GCAATAATGG AGACAGTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900  
 TCAGCATGGC CAATGATTTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960  
 CATATTTTGG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020  
 AAAGGATTGA GAATCTTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080  
 AGACAAAACA TGACTGAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140  
 10 AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200  
 ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260  
 AGATTGCCAT GAATCTTGCA AA

Seq ID NO: 598 Protein sequence  
 Protein Accession #: NP\_057113.1

15 1 11 21 31 41 51  
 MNWELLMLL VLCALLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS 60  
 GIGEEAYQL SKLVSVLVL ARRVEHLERV KRRCLNENL KEKDILVLP DLTDTGSHEA 120  
 20 ATKAVLQEFQ RIDILVNNGG MSQRSLOMDT SLDVYRKLE LNYLGTVSLT KCVLPHMIER 180  
 KQKIVTVNS ILGISVPLS IGYCASKHAL RGFFNGLRTE LATYPGIIVS NICPGPVQSN 240  
 IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISQEP FLLVTYLMQY 300  
 MPTNWWITN KMGKRIENF KSGVDADSSY FKIFKTKHD

25 Seq ID NO: 599 DNA sequence  
 Nucleic Acid Accession #: NM\_000793.2  
 Coding sequence: 401..1222

30 1 11 21 31 41 51  
 GCCTGCAGAG AGAGGCACCT TGCAACCACG ACAGATAGCA AGAAGGGAAA GACAGAGAGT 60  
 GAGAAAAAAG AGGAGTCAGT CGCTCCTGGG GAAGGGAGAG AGTGAGACTG GGAGAAAGAG 120  
 AAGCACAGAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAAAC TACCCTTAAA 180  
 GCACATTAA AAAAAAATA CTCTGGCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG 240  
 35 CATAGAGACA ATGAAGGCT AAAGAAAATT TAAATCTC TGCCACAGTC TCATAGTGCC 300  
 TTGAAATGA AAGTAGAAT GCCTGTCTTT AACGGACTCT GACAGAGAGG GTGAAGGGGA 360  
 ACCAGAGCGC ACAAGGGAAC TGACTCAGGA GGCAGAGAAG ATGGGCATCC TCACGTTAGA 420  
 CTTGCTGATC ACACCTGCAA TTCTGCCAGT TTTTCTCC AACTGCCTCT TCCTGGCTCT 480  
 40 CTATGACTCG GTCAATTGCG TCAAGCAGCT GGTGCTGCTG TTGAGCGCT CCAAGTCCAC 540  
 TCGCGGAGAG TGGCGGCGCA TGCTGACCTC AGAGGGAAGT CGCTGCTCTC GGAAGAGCTT 600  
 CCTCCTCGAT GCCTACAAAC AGGTGAAATT GGTGAGGAT GCCCCAATT CCAAGTGTGT 660  
 GCATGTCTCC AGTACAGAA GAGGTGACAA CAGTGGCAAT GGTACCCAGG AGAAGATAGC 720  
 TGAGGGAGCG ACATGCCACC TTCTTGACTT TGCCAGCCCT GAGCGCCAC TAGTGTGCAA 780  
 45 CTTGGCTCA GCCATGTGAC CTCTTTTAC GAGCCAGCTG CAGCCTTCC GCAACTGGT 840  
 GGAAGAGTTC TCCTCAGTGG CTGACTTCCT GCTGGTCTAC ATTGATGAGG CTCATCCATC 900  
 AGATGGCTGG GCGATACCGG GGGACTCCTC TTTGTCTTT GAGGTGAAGA AGCACCAGAA 960  
 CCAGGAGAT CGATGTGAC CAGCCGACGA GCTTCTGGAG CGTTTCTCT TGCCGCCCA 1020  
 GTGCGAGATT TGGGCTGACC GCATGGACAA TAAOGCCAA ATAGCTTACG GGTAGCCCTT 1080  
 50 TGAACGTGTG TGCAATTGTC AGAGACAGAA AATTGCTTAT CTGGGAGGAA AGGGCCCTT 1140  
 CTCCTCAAC CTTCAAGAA TCCGCAATG GCTGGAGAAG AATTTCAGCA AGAGATGAAA 1200  
 GAAACTAGA TTAGCTGGTT AAAGGTATGA TTATAAGAGA GCTTATTGTT TTAAGAGTT 1260  
 ATATAAGGC AAGGAAATTA AGAATGAAT CCATATTCA ACAGAGCCCT ATTGGCTTAC 1320  
 TGAAGACAG GAGTTTATCT ATCGGAAGAA CATGAATCTC TAACAGCTCC ATACTTCTT 1380  
 55 CACTACTCA ATGGCAATTG GCTGAGTAA TAACCATATC ACCTCTCTT TTAGTAAAAA 1440  
 GCCCTATGT AAGAGATCCC AAGATGAGGA GGAAGAAACG CTAATTACG ATGTGTTTCA 1500  
 TCTGCATTGA GAAGGAAGT ATACATCTGA TGCAATGCTT GAGACCAGAA GAAAGACTT 1560  
 ACCTGAATTA TTACTACATT AGGGAAGCTA CTGTCTACGT TAAGATAAAG GGTATTGCTT 1620  
 TGGCTCTATT TGGCATGGAT GGAGCCCACT TGGAAAATTC CCAATATTA CAACAGTCC 1680  
 60 TTGAACCCAG GCCATGTGCT TAGAAGTTGG TGTAAAGTT AGACCTTATG TTAGATCAT 1740  
 TTCTGATGTT CCAGCTTCTA GCCATGTAGT GCTCTCAGTC TTCATACCCC AGAATTAAT 1800  
 GGTATATTG TAGATACGA GAATGATCCC TCAGTCTGAG AGGTTAGAAT GATCATCTGT 1860  
 AATCTGAGGG TTAATTTCTA GGCAGGTGGA GAGAGTGGTA AAAAGAAAT GAAATTGACA 1920  
 AGCTAGGAAA GAGGAGGCAG AAAGATTGG AAAATTCACA GAGTTTACC CTTAAGCTGT 1980  
 65 AGAGAGTGG TCACATTTGT TAGCCACGGA AACATAGAAA CATACACAAG GCCAGAAAAA 2040  
 AAGAAGGAG CTCACTAAA AGTGGCATAG AGAATACACA TATAAAAAA ATATATTGT 2100  
 CATATGCTCC TAGAGAGGAG AAAGGGGTGA TTGAAGAAA AAAAAATACT TAAATATTG 2160  
 TAATTGTGAG GGGTTTCTTT TGGAAATAAT TACTTTTGAA CCATGTATGT GGTATGTATA 2220  
 TTTTCAGTGG GTTAATTATA CCCCATGATA CCTATTAAAG GAAAACCACT GGGTCTGGTG 2280  
 70 GTGCTGCTCT TTTCTCTCCC ATTCTACAA TTCTATGTG GCCCAAGTCA TTCCTAATCT 2340  
 TGGTCTCTAT AGCAGTGTTC TCTCTGAATG CTGAGCTGAA GAAATTATAC GTACATACAC 2400  
 ACATACATAC ATACATACAA ATATATGTAT ATATATTCTC AGCTGCTGCG GGAGGTAGGT 2460  
 ACCATGGCCA TTCAGCACAG CCTTGATTTT CTCCCAAAGT AGGTGAGTGA TAGTGAAGAA 2520  
 TAGGTGCAAA AGAACAAGCT TACTTCCATT GCAAAATAGA AGAAGAGGAA GTTAGAGATA 2580  
 75 ATTCTGATCA ATCATTTTGG AGGCTTTGTT ATAAGGCAAC CCCCGGTATA TCATGGAATT 2640  
 TCCATTGACA TTTGAATTGG GACTTGGATC TTCCCTTGGT CCATTAGCT GAGGTTTAGT 2700  
 AATCTAAAGT CCCTATAGTA TATGATTATA ATGCTATTTT AAAAAATATA TATATAAAT 2760  
 ATTTTCTCT TTTTAAATA GACACTATAG TTTTACCCTAT AAGTAATATT TAAAGATTAT 2820  
 AGCTCCCAAA AGAATGGACC AACCACTTC GTATCATAAT TTCTTTTGG TAAATATGAG 2880  
 80 ACTATTATGA AATCATAGTA TATGATTGTA TTTAAAGGTA CAATCAAGG ATCTTTTGT 2940  
 CATTCCATTA TAACTGAAT AAAAAATAA TAAATGGAT AGAAAAAAC TAAAGTTGAA 3000  
 AATACATTCT TAACTAGTT GTCGAAATG AGAAAAGAGT GAGAACTAGG TGTGCAAGAA 3060  
 CCAACGATAT TTTATTTTAT TTTTAAATG GGAGCAACAT ATCAGTGTGT TCACCAGCTG 3120  
 GTATATTGTG TAAATATTA AGCTCCATG GGACTGATT TTCAATGGCA CATCAGCTT 3180  
 CTAATGTTCT AAATCTATA AAAACCAACC ACAAGAAAC AAAGCAAAAT TCATTATCTA 3240

5 ATGAGTTGCT GGAAATCAT ATTGAGAATA ATTATTTTCAG ATTCCTCAGT TGTTAACTTC 3300  
 TACATTCAAG GGCCTATCTC TGCCCCCATT GATTTTAAAC CTCAAAATGG TGTGAGATT 3360  
 ACTGTGGAAC CCTAAAGCAG TAAATAAATA AACCTGGTTG CAGCACATTC ACACGTGTGT 3420  
 CCTTAAAT CCCTTTTTT CTCTATGTAC GATAAGTAA CAGTATGTCA GATAAGCCGG 3480  
 TGGGGGATG AGATTAGGCT GAGGCACTGC TAGTCACTG GGGGAAAGG ATGATGGAAA 3540  
 AATCACCCAG TTGTGCTATA TTTTAAAGA AGGAGGTGCT TTATGTGTGC AGACAATTCT 3600  
 CCCTGAGGTT AGCCCAATGG AGAAATGAAG CAGAGGAAGG AAACATAGAA AGACATGGGC 3660  
 TATCAGGGAG GAAGATGTTC AATAGAACAT GCAAGAATT CTGGAAGAAA GGCTGTGGAA 3720  
 GGGCCAATGG AGAAATGAA TGGCAAAAGC TCAGGAATCC CTACGCTATG TAGAATGTTC 3780  
 10 TTGGTGTAT CAGGGTTAAG CCCTGTAATT ATGTAACCTA TTTATCGCAA CATGAATTTT 3840  
 TATGATTCT TGTGATGTAT TCTTTTATGA AATTAACAG AACCTATTAT TTTGAGGTAG 3900  
 AGGAAATCA ATGCTTTATC TGATATGCTG AGAAATATT AGATTGCCAA TACTCATGTG 3960  
 CGTTTCATGT GTTTTATAAG GTTTGTCTCT TTGAAGAATT GTAGTTCTTA GTCCACAGG 4020  
 15 GAAATGTGTA TCTATTATA TATCATAGTA TAAATCATG ATATATTTAT ATCATATATA 4080  
 AAAGTCTGAG TTCTCTTTCT TAGTCCCTAA TCATGTTTCT CCCATAGGCT GTGTTTACAT 4140  
 GGAGCTATCG GTTAGCCTT TTAAGCTTCA TTAGCTGTG TATTATTGAA ATAGTTTCCA 4200  
 AGAAATTTTA GATATTATCA TAACATCTGG GTCTACTCAA ACCTTATTG TTTGAAAGAC 4260  
 TTATGTCTTG GACCTATCAA AAACCTGACT TATTATTGC TTAGTGAAA TACTAGTGGG 4320  
 20 ATCAACAATG ATTTTCTGTA ATGGGCATGA ATGGAGATGC CGGCACAGTA ATGTAGAAAT 4380  
 GTTTCATACA GCTATTAAAA TGTAACGTAC CTCCTTAGAG GCAGATTAGT AACTGTTCTT 4440  
 ACTTTGTATA GCTAAGTGAC AGTCACCTAA CTTACATGAC TTTCTTTTT CACATTGGGT 4500  
 CTCGTGCTCT GTGTCTTAC CTCAATTATA GCAAGTCTCC TTGATTTTG GTAGTATCAA 4560  
 CTCCCATGAT GTTTTATAAG TTAAGTCTCT CTCCGTTAA CCAGGAAGTG CTTATTCTCT 4620  
 25 CATCACAGTG GGAAGAATAG CCTATTGCT TTTCTTTGCT CTGAGTGTAT TTTACTATT 4680  
 GGGCTCTGAA ATAAAAATTA TGAATATGG TGAGGTACA TGTGTGTGCT GCCTGTGCTG 4740  
 ATAAATTTCT AGGAGGCGAG GTTAGGAGAC AGTTATGTAT GSCCTTTCCG GAAATTTCAA 4800  
 AGGGTGGAT TACAAGGGTG TTCTCAGGC ATGCCCTAT GGGCCCTATG TGAAGCAAG 4860  
 AAGAATTGAC TGATTACAG GACTTCTCT TATGTCAAT TTAAGAGGAT GGATGAATCT 4920  
 30 GGACATTTGT TCCACCCGAC CTCTGACTGA TGGTTTGGAA AATACTTTA ATTAGGATCA 4980  
 TATGACCATT GAAAAAGGAA AAATGTAGAC TCTGACTTCC GTCCCACTGA AGGATTAAATG 5040  
 AAAACCTTTA CTAGCATTTA GAGCTTTTCA GAACATCCCC ACTGTCTATG GTCTCAGCAG 5100  
 TGGAGACTGC AAGTAAGGCT TTTAATTTTA GGAGGTTTT TTTTTCCTCC 5160  
 TAAATGGTAT GGCCTAAAGT CAGAGTTAAA ATATATATAG TTAGATTCCA ACTTCTCTCT 5220  
 35 TCACTCTAAA AATAGAATCC AAACCACTC TTCAATATG CTTCAGAAAT GGGGCTTAAG 5280  
 TACCAATCTC TGCTTTGCAA TGGGCACAAT CTGTGTCATG TCCTGAGGCT CTCTAAGAAA 5340  
 AGAGAGGATC TAGGATGGGA GAGCTAGAAA GTTGCTAACT GGGGAAGACA AGGCCCTGAG 5400  
 GGGTGTGCT ACCAATCTGG GAAGATTGA AAACAACTT CTCGCACTG AAGGAAGGCT 5460  
 GAAGGCTGAT GCAAGTCAAT GAGTGACTT AGGATGAGCA AAACATTGGG CCACTTCTTA 5520  
 40 ATGCCCTATG TGTATAGTAC CAGAAGCAAG GTCTCAGACT TAACAGACCC AGCTCTGTTC 5580  
 CAAGGTGAGT CTGAACCAAT AGAAAGCAAA CATGTGCAGA TATCCAACA AGACTGTCTCA 5640  
 TGCAAGTCGG GGCCTGCTAC CCGTCTTAGG CAGCAACAGC AGAGCTCCAG GGAGCTTATT 5700  
 CAATATTAC TGAGACTTCG AAGACCCAGC AGATGTTTAA TGAAGTCACT ATTTGGCTC 5760  
 AAACCTTCCA CTTCTCCCTC TCCCTCAA AAGCCAACAG GTAAACACAT AAATGAAAGA 5820  
 45 AACCACAGA AGGGATGGG AATAAGAA AATTCTCTCA AGACTTCTCC AGGCCATGT 5880  
 CACTGTCATG CGTGGTTTT ATGTGATTA GGATTGGGG ATGTGAAGAA ATAAGTATCC 5940  
 AGTACTTTAT AACCAAGCA ATTAATGAT ATTGGGAGT GGAATGTTG CCAGTTTTGT 6000  
 TTAGTTTGC CATCACTTG TCACCCAGAC CTCACCTAGC CCAAGTAAAT CGGGCGCCCC 6060  
 50 GAAGAGGAG CATCAGATGT GCCAGAGTTG ACCAGTGTG CGGATGATA CTACTGACGA 6120  
 AAGAGTATC GACCTCAGT AGTGGTTGGA TGTAGTCACA TTAGTTTGC TCTCCCATC 6180  
 TTTGTCTCCC TGGCAAGGAG AATATGCGGG ACATGATGCT AAGAGCCCTG GSTAAATGTG 6240  
 GTGAGAAATG ACOCGTGAT ATGCTACACA TATGTGCTTC TCAAGTGCAG AAAATGAAT 6300  
 GCTTTGGGAG ATTATCAGTA GAAAGAGTGT TATCATATTG GTGCTGAGTG CTATGTGTG 6360  
 55 TTATACAATT TGTTCTGTGA TTTAATAAAA CTTGAATAA AAGAATAAAA AAAAAA 6420  
 AAAAAA

Seq ID NO: 600 Protein sequence  
 Protein Accession #: NP\_000784.2

60 1 11 21 31 41 51  
 | | | | |  
 MGILSVLLI TLQILPVFFS NCLFLALYDS VILLKHVLL LSRKSTRGE WRRMLTSEGL 60  
 RCVWKSFLLD AYKQVKGLED APNSSVVHVS STEGGDNNGN GTQEKIAEGA TCHLLDFASP 120  
 ERPLVNFVGS ATUPPPTSQ PAFKLVVEEF SSVADFLVY IDEAHPDGV AIPGSSLSF 180  
 65 EVKHKQNEQD RCAAQQLLE RFLPQCRV VADRMNNAN IAYGVAFERV CIVQRQKIAY 240  
 LGGKGPFSYN LQEVHWELEK NPSKRUKTR LAG

Seq ID NO: 601 DNA sequence  
 Nucleic Acid Accession #: NM\_005233.1  
 Coding sequence: 101..3052

70 1 11 21 31 41 51  
 | | | | |  
 CCATGGATGG TAACTTCTCC AGCAATCAGA GOGCTCCCC TCACATCAGT GGCATGCTTC 60  
 ATGGAGATAT GCTCTCTCA CTGCCCTCTG CACCAGCAAC ATGGATTGTC AGCTCTCCAT 120  
 75 CCTCTCTCT CTACGTGCT CTGTTCTCGA CAGCTTCGGG GAACGTATTC CGCAGCCTTC 180  
 CAATGAAGTC AATCTACTGG ATTCAAAAC AATTCAAGGG GAGCTGGGCT GGATCTCTTA 240  
 TCCATCAGT GGGTGGGAAG AGATCAGTGG TGTGATGAA CATTACACAC CCATCAGGAC 300  
 TTACCAAGTG TGCAATGTCA TGGACCAAG TCAAAACAAT TGGTGGAGAA CAACTGGGT 360  
 80 CCCCAGGAAC TCAGCTCAGA AGATTATGT GGAGCTCAAG TCACTCTAC GAGACTGCAA 420  
 TAGCATTCCTA TTGGTTTATG GAACCTGCAA GGAGACATTC AACCTGTACT ACATGGAGTC 480  
 TGATGATGAT CATGGGGTGA AATTTGAGA GCATCAGTTT ACAGAGATTG ACACCATTCG 540  
 AGCTGATGAA AGTTTCACTC AAATGGATCT TGGGGACCGT ATTCTGAAGC TCAACACTGA 600  
 GATTAGAGA GTAGGTCTCTG TCAACAAGAA GGGATTTTAT TTGGCATTTT AAGATGTTGG 660  
 TGCTTGTGTT GCCTTGGTGT CTGTGAGAGT ATACTTCAAA AAGTGCCCAT TTACAGTGAA 720

5  
10  
15  
20  
25  
30  
35  
40

GAATCTGGCT ATGTTTCCAG ACACGGTACC CATGGACTCC CAGTCCCTGG TGGAGGTTAG 780  
AGGGTCTTGT GTCAACAATT CTAAGGAGGA AGATCCTCCA AGGATGTACT GCAGTACAGA 840  
AGGGGAATGG CTGTACCCCA TTGGCAAGTG TTCCTGCAAT GCTGGCTATG AAGAAAGAGG 900  
TTTTATGTGC CAAGCTTGTC GACCAGGTTT CTACAAGGCA TTGGATGGTA ATATGAAGTG 960  
TGCTAAGTGC CCGCCTCACA GTTCTACTCA GGAAGATGGT TCAATGAACT GCAGGTGTGA 1020  
GAATAATTAC TTCGGGCGAG ACAAAGACCC TCCATCCATG GCTTGTACCC GACCTCCATC 1080  
TTCACCAAGA AATGTTATCT CTAATATAAA CGAGACCTCA GTTATCCTGG ACTGGAGTTG 1140  
GCCCTCGGAC ACAGGAGGCC GGAAAGATGT TACCTTCAAC ATCATATGTA AAAAAATGTG 1200  
GTGGAATATA AAACAGTGTG AGCCATGCAG CCCAATATGC CGCTTCTCC CTGCACAGTT 1260  
TGGACTCACC AACACCACGG TGACAGTGAC AGACCTTCTG GCACATACTA ACTACACCTT 1320  
TGAGATTGAT GCGGTTAATG GGGTGTGAGA GCTGAGCTCC CCACCAAGAC AGTTTGTCTG 1380  
GGTCAGCATC ACACTAATC AGGCTGTCTC ATCAGCTGTC CTGACGATTA AGAAAGATCG 1440  
GACCTCCAGA AATAGCATCT CTTTGTCTG GCAAGAACCT GAACATCCTA ATGGGATCAT 1500  
ATTGGACTAC GAGGTCAAAT ACTATGAAA GCAGGAACAA GAAACAAGTT ATACCATCTT 1560  
GAGGGCAAGA GGCACAAATG TTACCATCAG TAGCCTCAAG CCTGACACTA TATACGTAIT 1620  
CCAAATCCGA GCCCGAACAG CCGCTGGATA TGGGACGAAC AGCCGCAAGT TTGAGTTTGA 1680  
AACTAGTCCA GACTCTTCT CCATCTCTGG TGAAGTAGC CAAGTGGTCA TGATCGCCAT 1740  
TTCAGCGGAC GTACCAATTA TTCTCCTCAC TGTGTCTATC TATGTTTTGA TTGGGAGGTT 1800  
CTGTGGCTAT AAGTCAAAC ATGGGGCAGA TGA AAAAAGA CTTCAITTTG GCAATGGGCA 1860  
TTTAAACTT CCAGGTCTCA GGACTTATGT TGACCCACAT ACATATGAAG ACCCTACCCA 1920  
AGCTGTTTAT GAGTTTGGCA AGGAATTGGA TGCCACCAAC ATATCCATTG ATAAAGTTGT 1980  
TGGAGCAGGT GAATTTGGAG AGGTGTGCAG TGGTCTGTTA AAACCTTCTT CAAAAAAGA 2040  
GATTTTCAGT GCCATTAAAC CCTGAAAGT TGGCTACACA GAAAGCAGA GGAGAGACTT 2100  
CCTGGGAGAA GCAGCATTA TGGGACAGTT TGACCAACCC AATATCATTC GACTGGAAGG 2160  
AGTTGTTACC AAAAGTAAGC CAGTTATGAT TGTACAGAA TACATGGAGA ATGTTTCTT 2220  
GGATAGTTTC CTACGTAAC ACAGTGCCCA GTTACTGTTC ATTCAGCTAG TGGGGATGCT 2280  
TGGAGGGAAT GCATCTGGCA TGAAGTACCT GTCAGACATG GGCTATGTTC ACCGAGACCT 2340  
CGCTGCTCGG AACATCTTGA TCAACAGTAA CTTGGTGTGT AAGGTTTCTG ATTTGGGACT 2400  
TTGCGGTGTC CTGGAGGATG ACCCAGAAGC TGCTTATACA ACAGAGGAG GGAAGATCCC 2460  
AATCAGGTGG ACATCACCAG AAGCTATAGC CTACCGCAAG TTCAOGTCAG CCAGCGATGT 2520  
ATGGAGTTAT GGGATTGTTT TCTGGGAGGT GATGTCTTAT GGAGAGAGAC CATACTGGGA 2580  
GATGTCCAAAT CAGGATGTAA TTAAGCTGT AGATGAGGGC TATGACTGTC CACCCCCCAT 2640  
GGAAGTCCCA GCTGCCCTGT ATCAGCTGAT GCTGGACTGC TGGCAGAAAG ACAGGAACAA 2700  
CAGACCCCAAG TTGTAGCAGA TTGTTAGTAT TCTGGACAAG CTTATCCGGA ATCCCGGAG 2760  
CCTGAAGATC ATCACCAGTG CAGCCGCAAG GCCATCAAC CTTCTTCTG ACCAAAGCAA 2820  
TGTGGATATC TCTACCTTCC GCACAACAGG TGACTGGCTT AATGGTGTCC GGACAGCACA 2880  
CTGCAAGGAA ATCTTCAAGG CGGTGGAGTA CAGTTCTTGT GACACAATAG CCAAGATTTC 2940  
CAGACATGAC ATGAAAAAGG TTGGTGTGAC CGTGGTTGGG CCACAGAAGA AGATCATCAG 3000  
TAGCATTAAA GCTCTAGAAA CGCAATCAA GAATGGCCCA GTTCCCGTGT AAAGCAAGAC 3060  
GGAAGTGCTT CTGACCGGAA GTGGTGGCTG TGGAGGCGT CAAGTCATCC TGCAGACAGA 3120  
CAATAATTCT GGAGATACCT GTGGAAGTT

Seq ID NO: 602 Protein sequence  
Protein Accession #: NP\_005224.1

45  
50  
55  
60  
65

1 11 21 31 41 51  
MDCQLSILL LSCSVLDSFG ELIPQPSNEV NLLDSKTIQG ELGWISYPSP GWEEISGVDE 60  
HYTPRTYQV CNVMDHSQNN WLRTNWNVPRN SAQKIYVELK FTLRDCNSIP LVLGTCKETF 120  
NLYYMESDDD HGKVFREHQF TKIDTIAADE SFTQMDLGR ILKLNTEIRE VGPVNNKGFY 180  
LAFQDVGACV ALVSVRVYFK KCPFTVKNLA MFPDTPVMD SLSLEVRGSC VNNSKEEDPP 240  
RMYCSTEGEW LVPIGKCSN AGYEERGFMC QACRPGPYKA LDGNMKCAK PPHSSTQEDG 300  
SMNRCENNY FRADKPPSM ACTREPSSPR NVISININETS VILDNSWPLD TGRKDVTFN 360  
IICKKCGWNI KQCEPCSPNV RFLPRQFGLT NTTVTVIDLL AHTNYTFEID AVNGVSELSS 420  
PFRQFAAVSI TINQAAPSPV LTIKIDRTSR NSISLSWQEP EHPNGIILDY EVKYKQEQ 480  
ETSYTLRAR GINVTISSLK PDTIYVQFIR ARTAAGYGTN SRKFEPETSP DSPSISGESS 540  
QVVMIAISAA VAILLLTVVI YVLIGRFGY KSKHGADEKR LHPGNGLHLK PGLRTYVDFH 600  
TYEDPTQAVH EFAKELDATN ISIDKVVAG EPGEVCSGR LKPSKKEISV AIKTLKVGYT 660  
EKQRDLFGE ASIMQFDPHP NIIRLEGVVT KSKPVMIVTE YMENGSLDSF LKHKDAQPTV 720  
IQLVGMRLGI ASGMKYLSDM GYVHRDLAAR NILINSNLVC KVSDFGLSRV LEDDPEAAVT 780  
TRGGKPIRWR TSPEAIAYRK FTSASDVWSY GIVLNEVMSY GERPYWEMSN QDVIKAVDEG 840  
YRLPPMDCP AALYQLMLDC WQKDRNNRPK FEQIVSILDK LIRNPGSLKI ITSAAARPSN 900  
LLLDQSNVDI STFRFTGDLW NGVRTAHCKE IFTGVEYSSC DTTAKISTDD MKRVGVTTVG 960  
PQKIISSIK ALETQSKNGP VFV

Seq ID NO: 603 DNA sequence  
Nucleic Acid Accession #: NM\_005727.1  
Coding sequence: 122..847

70  
75  
80

1 11 21 31 41 51  
GCCAGGCGTC CCTCTGCTG CCCACTCAGT GGCAACACCC GGGAGCTGTT TTGTCTTTG 60  
TGGAGCCTCA GCAGTTTCCCT CTTTCAAGAC TCACTGCCAA GAGCCCTGAA CAGGAGCCAC 120  
CATGCAGTGC TTCACTTCA TTAAGACCAT GATGATCCTC TCAATTTGC TCATCTTTCT 180  
GTGTGGTGA GCCTGTGTTG CAGTGGGCAT CTGGGTGTC ATCGATGGGG CATCTTTCT 240  
GAAGATCTTC GGGCCACTGT CGTCCAGTGC CATGCAGTTT GTCAACGTGG GCTACTTCT 300  
CATCGCAGCC GCGTGTGTG TCTTTGCTCT TGGTTTCTG GGCTGCTATG GTGCTAAGAC 360  
TGAGAGCAAG TGTGCCCTCG TGACGTTCTT CTTCACTCTC CTCTCATCT TCATTGCTGA 420  
GGTTGCACTG CGTGTGCTG CCTTGGTGT CACCACAATG GCTGAGCACT TCCTGACGTT 480  
CCTGTGATGT CCTGCCATCA AGAAAGATTA TGGTTCACG GAAGACTTCA CTCAGTGTG 540  
GAACACCAAC ATGAAAGGCG TCAAGTGTG TGGCTTCACC AACTATACCG ATTTTGAGGA 600  
CTCACCTTAC TTCAAAGAGA ACAGTGCTCT TCCCTCATTC TGTGCAATG ACAACGTGAC 660  
CAACACAGCC AATGAAACCT GCACCAAGCA AAGGCTCAC GACCAAAAAG TAGAGGGTTG 720  
CTTCAATCAG CTTTGTATG ACATCCGAAC TAATGCACTC ACCCTGGGTG GTGTGGCAGC 780

5 TGGAAATTGGG GGCCTCGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT 840  
ACAATAAGTC CACTTCTGCC TCTGCCACTA CTGCTGCCAC ATGGGAACCTG TGAAGAGGCA 900  
CCCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACAAATGTCA CTTGGGCCAG 960  
AATGGACCTG CCGTTTCTGC TCCAGACTTG GGGCTAGATA GGGACCACCTC CTTTATAGGCG 1020  
ATGCCTGACT TTCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080  
GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAACC CTTGATATGC CCCTAGGCC 1140  
TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200  
AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC 1260  
10 TGTACAATG TTAATAAA

Seq ID NO: 604 Protein sequence  
Protein Accession #: NP\_005748.1

15 1 11 21 31 41 51  
MQCFSPFKTM MIFNLILFL CGAALLAVGI WVSIDGASPL KIFGPLSSSA MQFVNVGYPFL 60  
IAAGVVVFAL GFLGCTGAKT ESKCALVTFE FILLIFIAE VAAAVVALVY TMAEHFRTL 120  
LVVPAIKDXY GSGEDFTQVW NTKMGLKCC GFNTYTDPED SPYFKENSAF PPFCCNDNV 180  
20 NTANETCTEQ KAHDQKVEGC FNQLLYDIRT NAVTVGGVAA GIGGLELAAM IVSMYLYCNL 240  
Q

Seq ID NO: 605 DNA sequence  
Nucleic Acid Accession #: NM\_000729.2  
Coding sequence:

25 1 11 21 31 41 51  
GGCTCAGCTG CCGGGCTGCT CCGGTTGGAA ACGCCAAGCC AGCTGCCGTC CTAATCCAAA 60  
AGCCATGAAC AGCGGGGTGT GCCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120  
30 GAGCAGCCGG GTGCTCTCCG CAGATCCCGG GGGCTCCGGG CTGCAGCGGG CAGAGGAGGC 180  
GCCCCGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240  
CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300  
CGTTAAGAAC CTGCAGAAC TGGACCCGAG CCACAGGATA AGTGACCGGG ACTACATGGG 360  
CTGGATGGAT TTTGGCGTGC GCGATGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420  
35 GCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA 480  
TCACACTCAT AACTCATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540  
TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACAGCCT CACCAGAAGT 600  
40 TGTCAAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTGTG 660  
TATGCTATTA AAGTGATTTC ATTCTGCC

Seq ID NO: 606 Protein sequence  
Protein Accession #: NP\_000720.1

45 1 11 21 31 41 51  
MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRQLRVSRQT DGESEHLGA 60  
LLARYIQQAR KAPSGRMSIV KNLQNLDPFH RISDRDYMGW MDFGRRSAP EYEYPS

50 Seq ID NO: 607 DNA sequence  
Nucleic Acid Accession #: NM\_001423.1  
Coding sequence: 219..692

55 1 11 21 31 41 51  
AGCACTCTCC AGCCTCTCAC CGAAAAATTA CACACCCAG TACACGACGA GAGGAACTT 60  
ATAACCTCGG GAGGCGGGTC CTCTCCCTCA GTGCGGTGAC ATACTTCGAG AAGAGCGGAC 120  
CAGGGCTGCT GCCAGCACCT GCCACTCAGA GCGCCTCTGT CGCTGGGACC CTTGAGAAT 180  
CTCTTTGCTC ACAAGTTACC AAAAAAATAA GAGCCAACAT GTTGGTATTG CTGGCTGGTA 240  
60 TCTTTGTGGT CCACATCGCT ACTGTTATTA TGCTATTGTT TAGCACCATT GCCAATGTCT 300  
GGTTGGTTTC CAATACGGTA GATGCATCAG TAGGTCTTTG GAAAAACTGT ACCAATATTA 360  
GCTCGAGTGA CAGCCTGTCA TATGCCAGTG AAGATGCCCT CAGACAGTGT CAGGCCTTCA 420  
TGATTCTCTC TATCATCTTC TGTGTCTTTC CCCTCCTGGT CTTCTGTGTC CAGCTCTTCA 480  
CCATGGAGAA GGGAAACCGG TTCTTCTCT CAGGGGCCAC CACACTGGTG TGCTGGCTGT 540  
GCATTCTTGT GGGGGTGTCC ATCTACACTA GTCATATGCG GAATCGTGAT GGAACGCTAG 600  
65 ATCACCACGG CTATCTCTAC ATCTTGGGCT GGATCTGCTT CTGCTTCAGC TTCTATCATG 660  
GGTTCTCTTA TCTGTCTCTG AGAAAGAAAT AAGGCGGAGC GAGTTCATGG GGATCTGGGG 720  
GGTGGGGAGG AGGAAGCGGT TGAATCTGGG AGGGAAGTGG AGGTTCTGTT ACAGGAAAAA 780  
COGAGATAGG GGAGGGGGGA GGGGGAAGCA AAGGGGGGAG GTCAATATCC AAACCATTAC 840  
TGAGGGGATT CTCTACTGCC AAGCCCTGCT CCTGGGGAGA AAGTAGTTGG CTAGTACTTT 900  
70 GATGCTCCCT TGATGGGGTC CAGAGAGCCT CCCTGCAGCC ACCAGACTTG GCCTCCAGCT 960  
GTTCTTAGTG ACACACACTG TCTGGGGCCC CATCAGCTGC CACAACACCA GCCCACTTCT 1020  
TGGGTATGTC ACTGAGGTCC ACAGACCTAC TGCACTGAGT TAAATAGCG GTACAAGTTC 1080  
TGGCAAGAGC AGATACTGTC TTTGTGCTGA ATACGCTAAG CCTGGAAGCC ATCCTGCCCT 1140  
TCTGACCCAA AGCAAAACAT CACATTCCAG TCTGAAGTGC CTACTGGGGG GCTTTGGCCT 1200  
75 GTGAGCCATT TCCCTCTTTT GGAAACAGATA TTTAGCTCTG TGGAAATCAG TGACAAAATG 1260  
GGAGAGAGAA AGAGAGTTTG TAAGGTATAG CTGGTGGGTT AGCTAAACCA AGAAGGAGAC 1320  
CTTTTACAAA TGGAAAACCT GGGGGATGGT CAGAGCCGAG TCGAGACCTC ACACAGGGCT 1380  
GTCCCTCATG GAGACCTCAT GCCATGGTCT TTGCTAGGCC TCTTGCTGAA AGCCAAGGCA 1440  
GCTCTTCTGG AGTTTCTCTA AAGTCACTAG TGAACAATTC GGTGGTAAAA GTACCAACA 1500  
80 AACTATGGGA TCCAGGGGGC AGTCTTGCAA CAGTGCCATG TTAGGGTTAT GTTTTATAGGA 1560  
TTCCCTCTCA TGCATCAGT GTTTCTTTTA AGTATACAAC AGGAGAGAGA TGGACATGGC 1620  
TCATTGTAGC ACAATCTTAT TACTCTTCTT CTAACATTTT TGAGGAAGTT TTGTCTAATT 1680  
ATCAATATTG AGGATCAGGG CTCTAGGCT CAGTGTAGC TCTGGCTTAG ACACCACTGT 1740  
GAGTGATCAC CTCTGGGGA CCCTGCCTAT CCCACTTCA AGGTGAGGCA TGGCAATTCT 1800

5 GGAAGCTGAT TAAACACAC ATAAACCAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860  
 CTATATAATT GTGAAGTATT AAGCCCTACCG TATTTCAGCC ATGATAAGAA CAGAGTGCCT 1920  
 GCATTCCAG GAAATACGA AATCCCATG AGATAAATAA AATATAGGT GATGGGCAGA 1980  
 TCTTTTCTTT AAAATAAAAA AGCAAAACT CTGTGGTAC CTAGTCAGAT GGTAGACGAG 2040  
 CTGTCTGCTG CCGCAGGAGC ACCTCTATAC AGGACTTAGA AGTAGTATGT TATTCTCGGT 2100  
 TAAGCAGGCA TTGCTTTGCC CTGGAGCAGC TATTTTAAGC CATCTCAGAT TCTGTCTAAA 2160  
 GGGGTTTTTT GGGAGAGCGT TTCTTTTATC GCCCTGAGAA GATCTACCCC AGGGAGAATC 2220  
 TGAGACATCT TGCCTACTTT TCTTTATTAG CTTTCTCCTC ATCCATTCT TTTATACCTT 2280  
 TCCTTTTTGG GAGATTGTTA TGCCATGATT TTTGGTATTT ATGTAAAAGG ATTATTAATA 2340  
 ATTCTATTTC TCTATTGTTA TTCTAGTTAA GGAATGTGT AGGGCAAGCC ACCAAATTAC 2400  
 CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAAACTGTGG GAAGATGAAC TTTGTCTATA 2460  
 TGATTTCTAT ATCAGATGAT TATAGAAGGC TGTCTTAGTG CAAAAACAT ACTTACATTT 2520  
 CAGACATATC CAAAGGGAAT ACTCACATT TGTTAAGAAG TTGAACTATG ACTGGAGTAA 2580  
 ACCATGTATT CCCTTATCTT TTAATTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTGC 2640  
 ATTACTCTGG TGGATTGTTT TAGTACTGTA TTGGGCTTCT TCGTTAATAG ATTATTTCAT 2700  
 ATACTATAAT TGTAATATT TTGATACAAA TGTTTATAAC TTAGGGGATA TAAAAACAGA 2760  
 TTCTGATCC CTTCAAAAA AAAAAA

20 Seq ID NO: 608 Protein sequence  
 Protein Accession #: NP\_001414.1

25 1 11 21 31 41 51  
 MLVLLAGIFV VHIATVIMLF VSTIANVWLV SNTVDASVGL WKNCTINISCS DLSLYASEDA 60  
 LKTVQAFMIL SIIFCVIALV VFVFQLFME KGNRPFLSGA TTLVWCIL VGVSIYTSY 120  
 ANRDGTQYH GYSYILGWIC FCFSPFIIGVL YLVLRKK

30 Seq ID NO: 609 DNA sequence  
 Nucleic Acid Accession #: NM\_004961.2  
 Coding sequence: 55..1575

35 1 11 21 31 41 51  
 GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCGCGC CGGTCTCCGC GGAATGTTG 60  
 TCCAAAGTTC TTCCAGTCTT CCTAGGCATC TTATTGATCC TCCAGTCGAG GGTCCAGGGA 120  
 CCTCAGACTG AATCAAAGAA TGAAGCCTCT TCCCGTGATG TTGTCTATGG CCCCCAGCCC 180  
 CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTGAGAC TGAGACTGGG 240  
 AGCAGAGTTG GCAAACTGCC AGAAGCCTCT CGCATCTGA ACACATCTCT GAGTAATTAT 300  
 GACCACAAAC TGCCGCCCTG CATTGGAGAG AAGCCCACTG TGGTCACTGT TGAGATCGCC 360  
 GTCAACAGCC TTGGTCTCTT CTCTATCCTA GACATGGAAT ACACCATGTA CATCATCTTC 420  
 TCCGAGACCT GGTACGAGCA ACGCCTCTGT TACAACGACA CCTTTGAGTC TCTGTCTCTG 480  
 AATGGCAATG TGGTGGGCA GCTATGGATC CCGGACACCT TTTTATAGAA TTCTAAGAGG 540  
 ACCCAGAGC ATGAGATCAC CATGCCCAAC CAGATGGTCC GCATCTACAA GGATGGCAAG 600  
 GTGTTGTACA CAATTAGGAT GACCATTGAT GCCGGATGCT CACTCCACAT GCTCAGATT 660  
 CCAATGGATT CTCATCTCTG CCTCTATCTT TTCTCTAGCT TTTCTCTATC TGAGAAATGAG 720  
 ATGATCTACA CTGAGGAAAT TTCAAGCTT GAAATCAATG AGAAGAACTC CTGGAAGCTC 780  
 TTCCAGTTTG ATTTTACAGG AGTGAGCAAC AAAACTGAAA TAATCAACAC CCCAGTTGGT 840  
 GACTTCAGTC TCAATACGAT TTTCTTCAAT GTGAGCAGGC GGTTTGGCTA TGTGTCTTT 900  
 CAAACTATG TCCCTCTCTC CGTGACCAGC ATGCTCTCTT GGGTTTCCIT TTGGATCAAG 960  
 ACAGAGTCTG CTCCAGCCCG GACCTCTCTA GGGATCACCT CTGTTCTGAC CATGACCAGC 1020  
 TTGGGCACCT TTCTCTGTAA GAATTTCCCG CGTGTCTCTT ATATCACAGC CTGGATTTC 1080  
 TATATGCCCA TCTGCTTGT CTCTGCTCTC TGCGCTCTGT TGGAGTTTGC TGTGCTCAAC 1140  
 TTCTCTGATC ATAGACAGAC AAAAGCCCAT GCTTCTCTTA AACTCCGCCA TCCTCGTATC 1200  
 AATAGCCGTG CCCATGCCCG TACCCTGTCA CGTTCGCCAG CCTGTGCCCG CCAACATCAG 1260  
 GAAGCTTTTG TGTGCCAGAT TGTCAACACT GAGGGAAGTG ATGGAGAGGA GCGCCCGTCT 1320  
 TGTCTAGCCC AGCAGACCCC TAGCCAGGT AGCCCTGAGG GTCCCCGCGC CCTCTGCTCC 1380  
 AAGCTGGCCT GCTGTGAGTG GTGCAAGCGT TTTAAGAAGT ACTTCTGCAT GGTCCCGAT 1440  
 TGTGAGGGCA GTACCTGGCA GCAGGGCCGC CTCTGCATCC ATGTCTACCG CTGGATAAC 1500  
 TACTCGAGAG TTGTTTTCCT AGTGACTTTC TTCTTCTTCA ATGTCTCTA CTGGCTTGT 1560  
 TGCTTAACCT TGTAGGTACC AGCTGTGACC CTGTGGGSCA ACCTCTCCAG TTCCCAAGGA 1620  
 GGTCCAAGCC CTTGCCAAG GAGTTGGGG GAAAGCAGCA GCAGCAGCAG GAGCGACTAG 1680  
 AGTTTTCTCT GCCCATTTCC CAAACAGAA GCTTGCAGAG GGTGTGTCTT TGCTGCCCT 1740  
 CTCCTCTACC TGGCCCATTC ACTGAGTCTT CTCAGCAGAC CATTTCAAAT TATTAATAAA 1800  
 TGGGCCACCT CCCTCTCTCT CAAGGAGCAT CCGTGATGCT CAGTGTCAA AACCAAGCC 1860  
 ACTTAGTGAT CAGCTCCCTA AAACCATGCC TAAGTACAGG GGAATTAGCT ATCTTCCAAC 1920  
 AATGCTGACC ACCAGACAAT TACTGCATTT TTCCAGAAGC CCATATTGCT CTTTGTAGTG 1980  
 CTTTGGCCCC AGTTCTGGCC TCAGCCCTCA AGTGACCCGA CTAGTTGCTT GCCTATACCT 2040  
 GGCACCTCAT TAAGATGCTG GGCAGCAGTA TAACAGGAGG AAGAGATCCC TCTCCTTTGG 2100  
 TCAGATTATT ATGTTCTCAG TTCTCTCTCC CTGCTACCCC TTTCTCTGCA GATAGATAGA 2160  
 CACTGGCATT ATCCCTTTAG GAAGAGGGGG GGGCAGCAAG AGAGCCTATT TGGGACAGCA 2220  
 TTCTCTCTCT TCTGCTCTG TGACATCTCC CTCTCCTTGC TGGCTCCATC TTTGCTCTGC 2280  
 ACTACCAATT CAATGCCCTT CATCAATGG GTATCTATTT TTGTGTGTGA TTATAGTAAC 2340  
 TACTCCCTGC TTTTATATGC ACCCTCTTCC TTCTCTTTGA CCGCTGTGAC TCTTTCTGTA 2400  
 ACTTTCCAG TGACTTCCCC TAGCCCTGAC CCAGGCACTA GGCCTTGGTG ACTTCTCTGG 2460  
 GCCAGAAAC TAAGAAACT CGGCTTTGCA ACAGGCATTA CTGCCATTG ATTGGTGCCC 2520  
 ACCCAGGGCA CACTGTGCGA GTTCTATCAC TTGCTTGACC CTGGAGCCCA TAAACCATG 2580  
 CACTGTATATA CCGGGGGCAC TCTAACCATC ACAATCAATC AATCAAATTC CCTTAAATTT 2640  
 GTATGGCAT GGAACCTTTGG CAAAGCACTT TTGACAAGTT GTGTCTGATT GGAGCTTCAT 2700  
 GATAGCCTTG TGACATCTTT AGGGCAGGAT TCTATCCCC ATTTGTCAGA TGAACCCCT 2760  
 GAGTCACAGA TTTCTGTGGG ACTGTGGATC TCACTGGAG CTATCCAAGA GCCACTGTG 2820  
 ACCTTCTAGA CCACATGATA GGGCTAGACA GCTCAGTTCA CCATGATTCT CTCTGTCTAC 2880  
 CTCTGCTGGC ACACAGTGG CAAGGCCAGC AATGGGAGCC TCTCTTAGC TCAATTTCTG 2940  
 GGCCTGAGGT GCTCAGACTG CCCCCAAGAT CAAATCTCTC CTGGCTGTAG TAACCCAGTG 3000  
 GAATGAATTT GGACATGCCC CAATGCTCTT ATATGCTAAG TGAATCTGT GTCTGTAAT 3060

TGTTGGGGGG TGGATAGGGT GGGGTCTCCA TCTACTTTTT GTCCACATCA TCTGAAATGG 3120  
GGAAATATGT AAATAAATAT ATCAGCAAAG CAAAAGAAA AAAAAAAA

Seq ID NO: 610 Protein sequence  
Protein Accession #: NP\_004952.1

1 11 21 31 41 51  
10 MLKVLPLVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60  
TGSRVGKLPE ASRIILNTLS NYDHKLRLPGI GEKPTVVIVE IAVNSLGPLS ILDMEYITDI 120  
IFSQTWYDER LCSYNDTFESL VLNGNVVSQQL WIPDTFFRNS KRTHHEHEITM PNQMVRIYKD 180  
GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIYKWNF KLEINEKNSW 240  
KLFQDFDTGV SNKTEIITTP VGDFMVMITF FNVSRFRGYV AFQNVVPSSV TMLSNWSEFV 300  
15 IKTESAPART SLGITSVLTM TLGTFSRKN FPRVSITAL DFYIAICFVF CFCALLEPAV 360  
LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TTEGSDGEER 420  
PSCSAQQPPS PGSPEGPRSL CSKLACCEWC KRFIKYFCMV PDCEGSTWQQ GRLCIHVYRL 480  
DNYSRVVPV TFFFNVLVYV LVCLNL

Seq ID NO: 611 DNA sequence  
Nucleic Acid Accession #: NM\_021984.1  
Coding sequence: 572..1753

1 11 21 31 41 51  
25 GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCTCCG CGGTCTCCGC GGAAATGTTG 60  
TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120  
CAGAGAAGTG CTCAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180  
CGTAAAGAA AGCCAAATCA AGGACCGGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTTGT 240  
CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300  
30 TCAGACTGAA TCAAGAATG AAGCCTCTTC CGTGATGTT GTCTATGGCC CCCAGCCCA 360  
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420  
CAGAGTTGGC AAAGTCCGAC AAGCCTCTCG CATCCTGAAC ACTATCTCTGA GTAATTATGA 480  
CCACAAACTG CGCCTTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTTG AGATCTCCGT 540  
CAACAGCCTT GGTCTCTCT CTATCTTAGA CATGGAATAC ACCATTGACA TCATCTTCTC 600  
35 CCAGACCTGG TACGACGAC GCCTCTGTTA CAACGACACC TTTGAGTCTC TTGTTCTGAA 660  
TGGCAATGTG GTGAGCCAGC TATGGATCCC GGACACCTTT TTTAGGAATT CTAAGAGGAC 720  
CCAGGAGCAT GAGATCACC TGCCCAACCA GATGGTCCGC ATCTACAAGG ATGGCAAGGT 780  
GTGTACACA ATTAGGATGC CCATTGATGC OGGATGCTCA CTCACATGTC TCAGATTCTC 840  
AATGGATTCT CACTCTTGGC CTCTATCTTT CTCTAGCTTT TCCTATCTCT AGAATGAGAT 900  
40 GATCTACAAG TGGGAAAATT TCAAGCTTGA AATCAATGAG AAGAACTCTT GGAAGCTCTT 960  
CCAGTTGGAT TTACAGGAG TGAGCAACAA AACTGAAATA ATCAACACCC CAGTTGGTGA 1020  
CTTCTAGTTC ATGACGATT TCTTCAATGT GAGCAGCGGG TTTGGCTATG TTGCTTTTCA 1080  
AAACTATGTC CCTTCTCTCG TGACCAAGAT GCTCTCTGCG GTTTCCTTTT GGATCAAGAC 1140  
AGAGTCTGCT CAGCCCGGGA CCTCTCTAGG GATCACTCT GTTCTGACCA TGACCAAGTT 1200  
45 GGGCACCTTT TCTCTGAAGA ATTTCCCGCG TGTCTCTAT ATCACAGCCT TGGATTCTTA 1260  
TATCGCCATC TGCTTGTGCT TCTGCTTCTG CGTCTCTGTT GAGTTTGCTG TGCTCAACTT 1320  
CCTGATCTAC AACCAGACAA AAGCCCATGC TTCTCTCTAA CTCGCCATC CTCGTATCAA 1380  
TAGCCGTGCC CTTTCTCTCA CCGGTGACG TTCCCGAGCC TGTGCCCGCC AACATCAGGA 1440  
AGCTTTTGTG TGGCAGATTG TCACCACTGA GGAAGTGAT GGAGAGGAGC GCCCGTCTG 1500  
50 CTCAGCCCGC CAGCCCTTA GCCCAGGTAG CCTGAGGGT CCCCAGAGC CTCGTCTCAA 1560  
GCTGGCCTGC TGTGAGTGGT GCAAGCGTTT TAAGAAGTAC TTCTGCTTGG TCCCGGATTG 1620  
TGAGGGCAGT ACCTGGCAGC AGGCCCGCCT CTGCATCCAT GTCTACCGCC TGGATACTA 1680  
CTCGAGATTG GTTTTCCGAG TGACTTTCTT CTCTCTCAAT GTGCTCTACT GGTCTGTTTG 1740  
CCTTAATCTG TAGTACCAG CTGGTACCCT GTGGGGCAAC CTCTCCAGTT CCCCAGGAGG 1800  
55 TCCAGCCCGC TTGCAAGGG AGTTGGGGGA AAGCAGCAGC AGCAGCAGGA GCGACTAGAG 1860  
TTTTTCTGTC CCCATTCCCC AAACAGAAAGC TTGCAGAGGG TTTGCTTTTG CTGCCCTCT 1920  
CCCTTACCTG GCCCATCTAC TGAGTTTCTT CAGCAGACCA TTTCAAAATTA TTAATAAATG 1980  
GGCCACCTCC CTCTTCTTCA AGGAGCATCC GTGATGCTCA GTGTTCAAAA CCACAGCCAC 2040  
60 TTAGTGATCA GCTCCCTAAA ACCATGCCTA AGTACAGCGG GATTAGCTAT CTTCACAA 2100  
TGCTGACCA CAGACAATTA CTGCATTTT CCAGAAGCCC ACTATTGCC TTTGAGTGCT 2160  
TTCGGCCCG TCTGCGCTC AGCCTCAAAG TGCACCGACT AGTTGCTTGC CTATACCTGG 2220  
CACCTCATT AAGTGTGGG CAGCAGTATA ACAGGAGGAA GAGATCCCTC TCCTTTGGTC 2280  
AGATTATTG GTTCTCAGT CTCTCTCCCT GCTACCCCTT TCTCTGAGA TAGATAGACA 2340  
CTGGCATTAT CCCTTTAGGA AGAGGGGGGG GCAGCAAGAG AGCCTATTGG GGACAGCATT 2400  
65 CCTCTCTCTC TGCTGCTGTG ACATCTCCCT CTCTTGTCTG GCTCCATCTT TGTCTGCAC 2460  
TACCAATTCA ATGCCCTTCA TCCAATGGGT ATCTATTTTT GTGTGTGATT ATAGTAACCTA 2520  
CTCCCTGCTT TATATGCCAC CCTCTCTCTT CTCTTGACC CCTGTGACTC TTTCTGTAAC 2580  
TTTCCAGTG ACTTCCCTTA GCCCTGACCC AGGCACTAGG CCTTGGTGAC TTCCTGGGGC 2640  
70 CAAGAACTA AGGAACTCG GCTTTGCAAC AGGCATTACT CGCCTATTGAT TGGTGCCAC 2700  
CCAGGGCACA CTGTGGAGT TCTATCACTT GCTTGACCCC TGGACCCATA AACCACTCCA 2760  
CTGTATACC CGGGGCACTC TAACCATCAC AATCAATCAA TCAAAATCCC TTAATTTTGT 2820  
ATGGCATCG AACTTTGGCA AAGCACTTTT GACAAGTTGT GTCTGATTGG AGCTTCATGA 2880  
TAGCCTTTGT ACATCTTAG GGCAGGATTCT TTATCCCAT TTTGCAGATG AAAACCTGGA 2940  
75 GTCACAGATT TCTGTGGGAC TGTGGATCTC ACTGGAAGCT ATCCAGAGC CCACTGTAC 3000  
CTTCTGACC ACATGATAGG GCTAGACAGC TCAGTTTACC ATGATTCTCT TCTGTACCT 3060  
CTGTGCGAC ACCAGTGGCA AGGCCAGAA TGGGACCTC TCTTTAGCTC AATTTCTGGG 3120  
CCTGAGGTGC TCAGACTGCC CCCAAGATCA AATCTCTCTT GGTGTAGTA ACCCAGTGG 3180  
ATGAATTGG ACATGCCCA ATGCTTCTAT ATGCTAAGTG AAATCTGTGT CTGTAATTGG 3240  
80 TTGGGGGGTG GATAGGGTGG GGTCTCCATC TACTTTTGT CACCATCATC TGAATGGGG 3300  
AAATATGTAA ATAAATATAT CAGCAAAGC

Seq ID NO: 612 Protein sequence  
Protein Accession #: NP\_068819.1



1 11 21 31 41 51  
MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFPRNSKRT HEHEITMPNQ 60  
5 MVRKYDKGV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSPYENEM IYKWFNFLE 120  
INEKNSWKLQ QLDFTGVSNK TEIITTPVGD FMVTIIFNV SRREGVYVAFQ NYVPSSVTIM 180  
LSWVSWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IAIQFVFCPC 240  
ALLEFAVLNF LIYNQTKAHA SPKLRRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300  
GSDGEERPSC SAQPPSPGSG PEGPRSLCSK LACCEWCKRF KKYFCMVDFC BGSTWQQARL 360  
10 CHIVYRLDNY SRVVPVTFP FFNVLVWLC LNL

Seq ID NO: 613 DNA sequence  
Nucleic Acid Accession #: NM\_021987.1  
Coding sequence: 572..1657

15 1 11 21 31 41 51  
GCCAGAGCGT GAGCCGCGAC CTCGCGCAG GTGGTCGCGC CGGTCTCCGC GGAAATGTTG 60  
TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120  
20 CAGAGAAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGOG 180  
GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTGT 240  
CACTGCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300  
TCAGACTGAA TCAAGAAATG AAGCCTCTTC CGTGATGTT GTCTATGGCC CCCAGCCCCA 360  
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420  
CAGAGTTGGC AAATGCTCCAG AAGCCTCTCG CATCTGAAC ACTATCTCGA GTAATTATGA 480  
25 CCACAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTTG AGATCTCCGT 540  
CAACAGCCTT GGTCTCTCT CTATCTAGA CATGGAATAC ACCATTGACA TCATCTCTC 600  
CCAGACTGG AATCTAAGA GGACCCACGA GCATGAGATC ACCATGCCCC ACCAGATGGT 660  
CCGCATCTAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATG ATGCCGGAGT 720  
30 CTCACTCCAC ATGCTCAGAT TTCCAATGGA TTCTCACTCT TGCCCTCTAT CTTTCTCTAG 780  
CTTTCTGAT CCTGAGAAAT AGATGATCTA CAAGTGGGAA AATTTCAGC TTGAAATCAA 840  
TGAGAAGAAC TCCTGGAAGC TCTTCCAGTT TGATTTTACA GGAGTGAGCA ACAAAGTGA 900  
AATAATCACA ACCCCAGTTG GTGACTTCAT GGTGATGAGC ATTTTCTTCA ATGTGAGCAG 960  
GCGGTTGGC TATGTTGCC TTCAAAACTA TGTCCCTTCT TCCGTGACCA CGATGCTCTC 1020  
35 CTGGGTTTC TTTTGGATCA AGACAGAGTC TGCTCCAGCC CGGACCTCTC TAGGGATCAC 1080  
CTCTGTTCTG ACCATGACCA CGTTGGGCAC CTTTCTCGT AAGAAATTC CGCGTGCTCT 1140  
CTATATCACA GCCTTGGATT TCTATATCGC CATCTGCTTC GTCTCTGCT TCTGCGCTCT 1200  
GTTGAGGTTT GCTGTGCTCA ACTTCTGAT CTACAACCAG ACAAAGCCC ATGCTTCTCC 1260  
TAAACTCCGC GCCTGTCGTA TCAATAGCCG TGCCCATGCC CGTACCCGTG CACGTTCCCG 1320  
40 AGCCTGTGCC GGCACACATC AGGAAGCTTT TGTGTGCCAG ATTGTACCCA CTGAGGGGAG 1380  
TGATGGAGAG GAGCGCCCGT TTGCTCAGC CCAGCAGCCC CTAGGCCAG GTAGCCCTGA 1440  
GGTCCCCGC AGCCTCTGCT CCAAGCTGSC CTGCTGTGAG TGGTGCAAGC GTTTTAAAG 1500  
GTACTTCTGC ATGCTCCCCG ATTGTGAGGG CAGTACCTGG CAGCAGGGCC GCCTCTGCAT 1560  
CCATGCTAC GCCTGTGATA ACTACTCGAG AGTTGTTTTC CCAGTGACTT TCTTCTCTT 1620  
45 CAATGTGCTC TACTGGCTTG TTTGCCCTTA CTGTAGGTA CCAGCTGGTA CCTGTGGGG 1680  
CAACCTCTCA CTTTCCCCAG GAGGTCCAAG CCCCTTGCCA AGGGAGTTGG GGGAAAGCAG 1740  
CAGCAGCAGC AGGAGCGACT AGAGTTTTC CTGCCCATC CCCCACACG AAGCTTGCAG 1800  
AGGGTTTGTC TTTGCTGCCC CTCTCCCTTA CCTGGCCCAT TCACTGAGTT TTCTCAGCAG 1860  
50 ACCATTTCAA ATTATTAAAT AATGGGCCAC CTCCTCTTTC TTCAAGGAGC ATCCGTGATG 1920  
CTCAGTGTTC AAAACACAGC CCACTTAGTG ATCAGCTCCC TAAACCATG CCTAAGTACA 1980  
GGCGGATTAG CTATCTTCCA ACAATGCTGA CCACAGACA ATTACTGCAT TTTTCCAGAA 2040  
GCCCACTATT GCCTTTCAG TGTCTTCCG CAGTTTCTGG CCTCAGCCTC AAAGTGCACC 2100  
GACTAGTTC TTGCTTATAC CTGGCACCTC ATTAAGATGC TGGGCAGCAG TATAACAGGA 2160  
GGAAGAGTC CCTCTCTCTT GGTGAGATTA TTATGTTCTC AGTTCTCTCT CCCTGCTACC 2220  
55 CCTTCTCTG CAGATAGATA GACACTGSCA TTATCCCTTT AGGAAGAGGG GGGGGCAGCA 2280  
AGAGAGCCTA TTGGGACAG CATTCCTCTC TCTCTGCTGC TGTGACATC CCTCTCTCT 2340  
GCTGGCTCCA TCTTGTGCT GCACTACCAA TTCAATGCCC TTCACTCAAT GGGTATCTAT 2400  
TTTTGTGTGT GATTATAGTA ACTACTCCCT GCTTATATG CCACCTCTT CCTTCTCTT 2460  
GACCCCTGTG ACTCTTCTG TAACCTTCCC AGTGACTTCC CCTAGCCCTG ACCAGGCAT 2520  
60 AGGCCTTGGT GACTTCTGCG GGCCAGAGAA CTAAGGAAAC TCGGCTTGG AACAGGCATT 2580  
ACTGCGCAT GATTGTGCGC CACCCAGGGC AACTGTGCG AGTTCTATCA CTGTCTGAC 2640  
CCCTGGACCC ATAAACCACT CCACTGTAT ACCCGGGCCA CTCTAACCAT CACAATCAAT 2700  
CAATCAAAAT CCTTAAAT TGTATGGCAC TGAACCTTG GCAAGCACT TTTGACAAAT 2760  
TGTGTCTGAT TGGAGCTTCA TGATAGCCTT GTGACATCT TAGGGCAGGA TTCTTATCCC 2820  
65 CATTTTCAG ATGAAACCC TGAGTCACAG ATTTCTGTGG GACTGTGGAT CTCACTGGAA 2880  
GCTATCCAAG AGCCCACTGT CACCTTCTAG ACCACATGAT AGGGCTAGAC AGCTCAGTTC 2940  
ACCATGATTC TCTTCTGCA CCTCTGCTGG CACACCAGTG GCAAGGCCCA GAATGGCGAC 3000  
CTCTCTTAT CTCAATTCT GGGCTGAGG TGCTCAGACT GCCCCCAAGA TCAAACTCT 3060  
CCTGGCTGTA GTAACCCAGT GGAATGAATT TGGACATGCC CCAATGCTTC TATATGCTAA 3120  
70 GTGAAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGGTCTCC ATCTACTTTT 3180  
TGTCACATC ATCTGAAAT GGGAAATATG TAAATAARTA TATCAGCAA GC

Seq ID NO: 614 Protein sequence  
Protein Accession #: NP\_068822.1

75 1 11 21 31 41 51  
MEYTIIDIFS QTWNSKRTHE HEITMPNQMV RIYKDGKVLV TIRMTIDAGC SLHMLRFPMD 60  
SHSCPLSFSS FSYPENEMIY KWENFKLEIN EKNSWKLQF DFTGVSNKTE IITTPVGDFM 120  
80 VMTIIFNVSR RFGYVAFQNY VPSSVTIMLS WVSFWIKTES APARTSLGIT SVLTMITLGT 180  
FSRKNFPRVS YITALDFYIA ICFVFCFAL LEFAVLNFI YNQTKAHSP KLRHPRINSR 240  
AHARTRARSR ACARQHQEAF VQIVITTEGS DGEERPSCSA QPPSPGSGPE GPRSLCSKLA 300  
CEWCKRPFK YFCMVDFCEG STWQQRGLCI HVYRLDNYSR VVPVTFPFF NVLYVWLVCIN 360  
L

Seq ID NO: 615 DNA sequence  
Nucleic Acid Accession #: NM\_021990.1  
Coding sequence: 1309..2490

5 1 11 21 31 41 51  
GCCAGAGCGT GAGCCGCGAC CTCGCGCGAG GTGGTCGCGC CGGTCTCCGC GGAAATGTTG 60  
TCCAAAGTTC TTCCAGTCTT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120  
CAGAGAAGTG CTCAATCAT AAGTGACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180  
10 GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCCTTTGT 240  
CACTGCCCTCC CAGCAAGGCG AGCACTATCC GGACTTCTAA CACCATCGGT GAGTTTCATA 300  
CCTTGGCAGA TGGCCTTTAA CATTTTGTG TAATTCAATT ATCTTACTA ATCTTCTCT 360  
TTTTCTTGGC TGTGTGTCAT GGCTGTGGAG CTCAGGCTGG ACTCCTGTTG GGCAGCCAGT 420  
15 TCCTGGATGG CTGTCTGTGG GTGGAGGACT CCTGCCTTTC CTGTTAGAC ACCCAAAAG 480  
GCTGCTCTTT AGCCTCTCTC CCTTCATCCC CTTCCTCTGC CCCCAGTGCA ACGAGTATTA 540  
CACAACCAAC AAAACCGCAA AATATTCCCA CAATTTTCTG TGCTCTCTCG GGAGAGGCCG 600  
CTCTGGCTTT TCCTCTCAGC CCTGGCCCTC TGCTGCTCC TCACTCCTGG TTGGTGCTGG 660  
TCAGGCTGAC TAGAGGCCAA GCGACCAAC ACTAGGCAAA CGCGCCAGC GCTCAGACAT 720  
20 AAATGCCCTC TTCATTTTCA GTGTAACATT CTTTAAAAAT CTAGGTCTTG GTTTTGTGA 780  
TTTTTTCTTA AATAAAGAG TGATCATAAA AGAGGAGCAG CATAGAAAGT CCCCAGAGAG 840  
CAGCAAGGTT TTAAGAGAAAT TCACAAGCCT AATCTGTAC TGCTTTATAA TTTGCTATTA 900  
CAAGTCAAAA TTTAACTAGG TTTTGTGTG AAAACTTGTG TTGGTTTGTG TCTGTCCCAA 960  
GAGGCTGAC TAGGGGCCAA TACAGAGTGC AGGGCAGAGC TTCAATTTTC GTTTGAATGT 1020  
25 TCTAGGGTGG AGGGACCTCA GACTGAATCA AAGAATGAAG CCTCTCCCG TGATGTTGTC 1080  
TATGGCCCCC AGCCCCAGCC TCTGGAAAAT CAGCTCCTCT CTGAGGAAAC AAAGTCAACT 1140  
GAGACTGAGA CTGGGAGCAG AGTTGGCAAA CTGCAGAAAG CCTCTCGCAT CCTGAACACT 1200  
ATCCTGAGTA ATTATGACCA CAAACTGCGC CCTGGCATTG GAGAGAAGCC CACTGTGGTC 1260  
ACTGTTGAGA TCTCCGTCAA CAGCCTTGGT CCTCTCTCTA TCCTAGACAT GGAATACACC 1320  
30 ATTGACATCA TCTTCTCCCA GACCTGGTAC GACGAAGCC TCTGTTACAA CGACACCTTT 1380  
GAGTCTCTTG TTTCTGAATGG CAATGTGGTG AGCCAGCTAT GGATCCCGGA CACCTTTTTT 1440  
AGGAATTCTA AGAGGACCCA CGAGCATGAG ATCACCATGC CCAACCAGAT GGTCCGCATC 1500  
TACAAGGATG GCAAGGTGTT GTACACAATT AGGATGACCA TTGATGCCGG ATGCTCACTC 1560  
CACATGCTCA TCTTCCCAAT GGATTCTCAC TCTTGCCCTC TATCTTTCTC TAGCTTTTCC 1620  
35 TATCCTGAGA ATGAGATGAT CTACAAGTGG GAAAATTTCA AGCTTGAAT CAATGAGAAG 1680  
AACTCTGGA AGCTCTTCCA GTTTGATTTT ACAGGAGTGA GCAACAAAC TGAATAATC 1740  
ACAAACCCAG TTGGTGACTT CATGGTCATG ACGATTTTCT TCAATGTGAG CAGGCGGTTT 1800  
GGCTATGTTG CCTTCAAAA CTATGTCCCT TCTTCCGTGA CCACGATGCT CTCCTGGGTT 1860  
TCCTTTTGA TCAAGACAGA GTCTGTCCA GCCCGGACCT CTCTAGGGAT CACCTCTGTT 1920  
40 CTGACCATGA CCACGTTGGG CACCTTTTCT CGTAAGAATT TCCGCGGTGT CTCCTATATC 1980  
ACAGCCTTGG ATTTCTATAT CGCCATCTGC TTCGTCTTCT GCTTCTGCGC TCTGTTGGAG 2040  
TTTGCTGTGC TCAACTTCCG GATCTACAAC CAGACAAAAG CCAATGCTTC TCCTAAACTC 2100  
CGCCATCTCT GTATCAATAG CCGTGCCCAT GCCCGTACCC GTGCACGTT CCGAGCCTGT 2160  
GCCGCGTCA ATCAGGAAGC TTTTGTGTGC CAGATTGTCA CCACTGAGGG AAGTGATGGA 2220  
45 GAGGAGCGCC CGTCTGTCTC AGCCACAGCAG CCCCCTAGCC CAGGTAGCCC TGAGGGTCCC 2280  
CGCAGCCTCT GCTCCAGCTT GGCCTGCTGT GAGTGGTGCA AGCGTTTTAA GAAGTACTTC 2340  
TGCATGTGTC CGATTTGTGA GGGCAGTACC TGGCAGCAGG GCGCCTCTG CATCCATGTC 2400  
TACCGCTCGG ATAACACTC GAGAGTTGTT TTCCCACTGA CTTTCTTCTT CTTCAATGTG 2460  
CTCTACTGGC TTGTTTGGCT TAACCTGTAG GTACCACTGT GTACCTGTG GGGCAACCTC 2520  
50 TCCAGTTCCT CAGGAGGTCC AAGCCCTTGG CCAAGGGAGT TGGGGGAAAG CAGCAGCAGC 2580  
AGCAGGAGCG ACTAGAGTTT TTCTGCCCC ATTCCCCAA CAGAAGCTTG CAGAGGGTTT 2640  
GTCTTGTGTC CCCCCTCTCC CTACCTGCCC CATTCACTGA GTTTTCTCAG CAGACCAATT 2700  
CAAAATATTA AATAATGGG CACCTCCCTC TTCTTCAAGG AGCATCCGTG ATGCTCAGTG 2760  
TTCAAAACCA CAGCCACTTA GTGATCAGCT CCCTAAACC ATGCCTAAGT ACAGGCGGAT 2820  
55 TAGCTATCTT CCAACAATGC TGACCAACAG ACAATTACTG CATTTTCCA GAAGCCCACT 2880  
ATTGCTTTG CAGTGCTTTC GGCCTAGTTC TGGCCTCAGC CTCAAAGTGC ACCGACTAGT 2940  
TGCTTGCTTA TGCTGGCAG CTTAATAAGA TGCTGGCAG CAGTATAACA GGAGGAAGAG 3000  
ATCCCTCTCC TTGGTGCAGA TTAATATGTT CTCAGTTCTC TCTCCCTGCT ACCCTTTCT 3060  
CTGCAGATG ATAGACTGCT GCATTATCCC TTAGGAAGA GGGGGGGGCA GCAAGAGAGC 3120  
60 CTAATTGGGA CAGCACTTCT CTCTCTCTGC TGCTGTGACA TCTCCTCTC CTGTCTGGCT 3180  
CCATCTTTG TCTGCATAC CAATTCAATG CCCTTCAATC AATGGGTATC TATTTTGTG 3240  
TGTGATTATA GTAACACTC CTGCTTTAT ATGCCACCTT CTTCTTCTC TTTGACCCCT 3300  
GTGACTCTTT CTGTAACCTT CCCAGTGACT TCCCCTAGCC CTGACCAGGC ACTAGGCCCT 3360  
GGTGACTTCC TGGGGCCAAG AAACCTAAGA AACTCGGCTT TGCAACAGGC ATTACTCGCC 3420  
65 ATTGATTGGT GCCCACCAG GGCACACTGT CGGAGTTCTA TCACTTGCTT GACCCCTGGA 3480  
CCCATAAACC AGTCCACTGT TATACCGGG GCACTCTAAC CATCAATC AATCAATCAA 3540  
ATTCCTTTAA ATTTGTATGG CACTGGAAC TGGCAAAAG ACTTTTGACA AGTTGTGTCT 3600  
GATTGGAGCT TCATGATAGC CTTGTGACAT CTTAGGGCA GGATCTTAT CCCCATTGTT 3660  
CAGATGAAAA CCTGAGTCA CAGATTCTG TGGGACTGTG GATCTCACTG GAAGCTATCC 3720  
70 AAGAGCCAC TGTCACCTTC TAGACCACAT GATAGGGCTA GACAGCTCAG TTCACCATGA 3780  
TTCTCTCTG TCACCTCTGC TGGCACCA CA GTGGCAAGG CCAGAATGGC GACCTCTCTT 3840  
TAGCTCAATT TCTGGGCTG AGGTGCTCAG ACTGCCCCA AGATCAAAAT TCTCTGGCT 3900  
GTAGTAACCC AGTGAATGA ATTTGGACAT GCCCAATGC TTCTATATGC TAAGTGAAAT 3960  
75 CTGTGTCTGT AATTGTGTTG GGGGTGGATA GGGTGGGTG TCCATCTACT TTTGTCAACC 4020  
ATCATCTGAA ATGGGGAAT ATGTAATAA ATATATCAGC AAAGC

Seq ID NO: 616 Protein sequence  
Protein Accession #: NP\_068830.1

80 1 11 21 31 41 51  
MEYTIIDIFS QTYWYDERLCY NDTFESLVLN GNVVSQWLIP DTPFRNSKRT HEHEITMPNQ 60  
MVRIVKDGKV LYTIKMTIDA GCSLHMLRFP MDHSCPLSF SSFSPYENEM IYKWFNFKLE 120  
INEKNSWKLFP QFDFTGVSNK TELIITPVGD FMVMTIFENV SRRFGYVAFQ NYVPSVVTIM 180  
LSNVSWFIKT ESAPARTSLG ITSVLMTITL GTPSRKNPFR VSYITALDFY IAI CFVFCFC 240

ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVQCQIVTTE 300  
GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPCD EGSTWQGGRL 360  
CHVYRLDNY SRVFPVTFV FNVLYWLVC LNL

5

Seq ID NO: 617 DNA sequence  
Nucleic Acid Accession #: NM\_004864.1  
Coding sequence: 26..952

10

1	11	21	31	41	51	
CGGAACGAGG	GCAACCTGCA	CAGCCATGCC	CGGGCAAGAA	CTCAGGACGG	TGAATGGCTC	60
TCAGATGCTC	CTGGTGTTCG	TGGTGTCTCT	GTGGCTGCCG	CATGGGGGGG	CCCTGTCTCT	120
GGCCGAGGCG	AGCCGCGCAA	GTTCCTCCGG	ACCTCAGAG	TTGCACTCCG	AAGACTCCAG	180
ATTCCGAGAG	TTGCGGAAC	GCTACGAGGA	CCTGCTAACC	AGGCTGCGGG	CCAACGAGAG	240
CTGGGAAGAT	TCCGAACCCG	ACCTCGTCCC	GGCCCTGCA	GTCGCGATAC	TCACGCCAGA	300
AGTGGGCTG	GGATCCGCG	GCCACCTGCA	CCTGCGTATC	TCTCGGGCGG	CCCTTCCCGA	360
GGGGTCTCCC	GAGGCTCTCC	GCCTTCACGG	GGCTCTGTTC	CGGCTGTCCC	CGACGGCGTC	420
AAGGTCGTGG	GACGTGACAC	GACCGCTGCG	CGCTCAGCTC	AGCCTTGCAA	GACCCCAAGC	480
CGCCGCGCTG	CACCTCGCAC	TGTGGCGGCC	GCGTGCAGC	TCGGACCAAC	TGCTGGCAGA	540
ATCTTGTGCC	GACCGGCCCC	AGCTGGAGTT	GCATTGCGG	CCGCAAGCCG	CCAGGGGGCG	600
CCGCAGAGCG	CGTGGCGGCA	ACGGGGACGA	CTGTCCGCTC	GGGCGGGGGC	GTTGCTGCGG	660
TCTGCACACG	GTCCGCGCGT	CGCTGGAAGA	CCTGGGCTGG	GCCGATTGGG	TGCTGTGCGC	720
ACGGGAGGTG	CAAGTGACCA	TGTGCATGCG	CGGCTGCCCG	AGCCAGTTCC	GGGCGGCAAA	780
CATGCACGCG	CAGATCAAGA	CGAGCCTGCA	CCGCTGAAG	CCCGACACGG	AGCCAGGCGC	840
CTGCTGAGTG	CCCGCCAGCT	ACAATCCCAT	GGTCTCATT	CAAAAGACCG	ACACCGGGGT	900
GTCGCTCCAG	ACCTATGATG	ACTTGTAGC	CAAAGACTGC	CACTGCATAT	GAGCAGTCCT	960
GGTCTCTCCA	CTGCGCAGCT	GCGCGGGGGA	GGCGACCTCA	GTTGTCTCTG	CCTGTGGAAT	1020
GGGCTCAAGG	TTCTGTGAGC	ACCCGATTCC	TGCCAAACA	GCTGTATTTA	TATAAGTCTG	1080
TTATTATTAT	TTAATTATT	GGGGTGACCT	TCTTGGGGAC	TCGGGGGCTG	GTCTGATGGA	1140
ACTGTGTATT	TATTTAAAC	TCTGTGATA	AAAATAAAGC	TGTCTGAAC	GTTAAAAAA	1200
AAAA						

Seq ID NO: 618 Protein sequence  
Protein Accession #: NP\_004855.1

35

1	11	21	31	41	51	
MPGQELRTVN	GSQMLLVLLV	LSWLPHGGAL	SLAEASRAS	PGPSELHSED	SRFRELRKRY	60
EDLLTRLRAN	QSNEDSNTDL	VPAPAVRILT	PEVRLGSGGH	LHLRISRRAA	PEGLPEASRL	120
HRALFRLSPT	ASRSWDVTRP	LRRQLSLARP	QAPALHLRLS	PPPSQSDQLL	AESSSARFQL	180
ELHLRQAAR	RRRRARARNG	DDCPLGPRC	CRLHTVRASL	EDLGWADWVL	SPREVQVTMC	240
IGACPSQFRA	ANMHAQIKTS	LHRLKPDTEP	APCCVPASYN	PMVLIQKTD	GVSLQTYDDL	300
LAKDCHCI						

45

Seq ID NO: 619 DNA sequence  
Nucleic Acid Accession #: NM\_003979.2  
Coding sequence: 254..1357

50

1	11	21	31	41	51	
ATAACAGCAT	GAAGTGCCGT	GGAACGTGAA	TAGGCGTGTC	CTCTCCCTCG	ACCCCTCCCC	60
TCCTTGTCCT	CTGTCTCACC	CCTCGCTCGT	TCCCTCCCTC	CGGCGAGGGC	GCCTTTATA	120
ACAACTGCTC	AGAGTGCGAG	GGCGGGATAG	CTGTCCAAGG	TCTCCCCCAG	CACTGAGGAG	180
CTCGCTGCTC	GCCTCTTGTC	GCGCGGGAAG	CAGCACCAAG	TTACGCGCCA	ACGCGCTGGC	240
ACTAGGGTCC	AGAAATGGCTA	CAACAGTCCC	TGATGGTTGC	CGCAATGGCC	TGAATCCAA	300
GTAATACAGA	CTTTGTGATA	AGGCTGAAGC	TTGGGGCATC	GTCCTAGAAA	CGGTGGCCAC	360
AGCCGGGGTT	GTGACCTCGG	TGGCTTTCAT	GCTCACTCTC	CGATCTCTCG	TCTGCAAGGT	420
CGAGGACTCC	AACAGGCGAA	AAATGCTGCC	TACTCAGTTT	CTCTTCTCTC	TGGGTGTGTT	480
GGGCATCTTT	GGCTCACTCT	TGCGCTTTCAT	CATCGGACTG	GACGGGAGCA	CAGGGCCAC	540
ACGCTTCTTC	CTCTTTGGGA	TCCTCTTTTC	CATCTGCTTC	TCTGCTGCTC	TGGCTCATGC	600
TGTCAGTCTG	ACCAAGCTCG	TCCGGGGGAG	GAAGCCCTTT	TCCCTGTGGG	TGATCTGGG	660
TCTGGCGGTG	GGCTTCAGCC	TAGTCCAGGA	TGTTATGCTC	ATTGAATATA	TTGTCTGAC	720
CATGAATAGG	ACCAAGCTCA	ATGTCTTTTC	TGAGCTTTCC	GCTCCTCGTC	GCAATGAAGA	780
CTTTGTCTCT	CTGCTCACTC	ACGTCTCTCT	CTTGATGGCG	CTGACCTTCC	TCAATGCTTC	840
CTTCACTTTC	TGTGGTTCCCT	TCACGGGCTG	GAAGAGACAT	GGGGCCCACT	TCTACCTCAC	900
GATGCTCTCT	TCCATTGCCA	TCTGGGTGGC	CTGGATCACC	CTGCTCATGC	TTCTGACTTC	960
TGACCGCAGG	TGGGATGACA	CCATCCTCAG	CTCCGCTTGG	GCTGCCAATG	GCTGGGTGTT	1020
CCTGTTGGCT	TATGTTAGTC	CCGAGTTTGT	GCTGCTCACA	AAGCAACGAA	ACCCCATGGA	1080
TTATCTGTGT	GAGGATGCTT	TCTGTAAACC	TCAACTCGTG	AAGAAGAGCT	ATGGTGTGGA	1140
GAACAGAGCC	TACTCTCAAG	AGGAAATCAC	TCAAGGTTTT	GAAGAGACAG	GGGACACGCT	1200
CTATGCCCCC	TATTCCACAC	ATTTCAGCT	GCAGAACCAG	CCTCCCAAAA	AGGAATCTCT	1260
CATCCACCGG	GCCCAAGCTT	GGCCGAGCCC	TTACAAAGAC	TATGAAGTAA	AGAAAGAGGG	1320
CAGCTAACTC	TGTCCTGAAG	AGTGGGACAA	ATGCAGCCGG	GCGGCAGATC	TAGCGGGAGC	1380
TCAAAGGGAT	GTGGGGGAAA	TCTTGAGTCT	TCTGAGAAAA	CTGTACAGAA	CACTACGGGA	1440
ACAGTTTGCC	TCCCTCCGAC	CCTCAACCAC	AATTCTTCCA	TGCTGGGGCT	GATGTGGGCT	1500
AGTAAGACTC	CAGTCTTAG	AGGCGCTGTA	GTATTTTTTT	TTTTTGTCT	CATCCTTTGG	1560
ATACTTCTTT	TAAGTGGGAG	TCTCAGGCAA	CTCAGTTTAA	GACCCCTTACT	CTTTTGTGTT	1620
GTTTTTTGAA	ACAGGATCTT	GCTCTGTAC	CCAGGCTTGA	GTGCACTGGT	GCGATCACAG	1680
CCAGTGTCAG	CCTCGACAC	CTGTGCTCAA	GCAATCTCTC	CATCTCCATC	TCCCAAGATG	1740
CTGGGATGAC	AGGCGTGAGC	CACAGCTCCC	AGCCTAGGCC	CTTAATCTTG	CTGTTATTTT	1800
CCATGGAATA	AAGGCTGGT	CATCTGAGCT	CACGCTGGCT	CACACAGCTC	TAGGGGCGCTG	1860
CTCCTCTAAC	TCACAGTGGG	TTTTGTGAGG	CTCTGTGGCC	CAGAGCAGAC	CTGCATATCT	1920
GAGCAAAAT	AGCAAAAGCC	TCTCTCAGCC	CACCTGGCTG	AATCTACACT	GGAAGCCAACT	1980
TGCTGGGCAC	CCCCGCTCCC	CAACCTCTCT	TGCCTGGGTA	GGAGAGGCTA	AAGATCAACC	2040

TAAATTACT CATCTCTCTA GTGCTGCCTC ACATTGGGCC TCAGCAGCTC CCCAGCACCA 2100  
 ATTCACAGGT CACCCCTCTC TTCTTGCACT GTCGCCAAAC TTGCTGTCAA TTCGAGATC 2160  
 TAATCTCCCC CTACGCTCTG CCAGGAATTC TTTCAGACCT CACTAGCACA AGCCCGGTG 2220  
 CTCCTTGCTA GGAGAATTTG TAGATCATTG TCACCTCAA TTTCTGGGGC TGATACTTCT 2280  
 CTCATCTTGC ACCCAACCT CTGTAAATAG ATTTACCGCA TTTACGGCTG CATTCTGTAA 2340  
 GTGGGCATGG TCTCCTAATG GAGGAGTGT CATTGTATAA TAAGTTATTC ACCTGAGTAT 2400  
 GCAATAAAGA TGTGGTGGCC ACTCTTTCAT GGTGGTGGCA GCAAAAAAAA AAAAAA

Seq ID NO: 620 Protein sequence  
 Protein Accession #: NP\_003970.1

1 11 21 31 41 51  
 MATTVPDCCR NGLKSKYYRL CDKAEANGIV LETVATAGVV TSVAFMLTLP ILVCKVQDSN 60  
 RRKMLPTQFL FLLGVLGIFG LTFAPFIIGLD GSTGPTRFPL FGILFSCIFS CLLAHAVSLT 120  
 KLVGRKRPFL LLVLGLLAVG FSLVQDVIAI EYIVLTMRNT NVNVFSELSA PRNEDFVLL 180  
 LTVVLFLMAL TFLMSSFTFC GSFTGWKRHG AHYLTMLLS IAIWVWITL LMLPDFDRRW 240  
 DDTILSSALA ANGVFLLAY VSPEFWLLTK QRNPMDFPVE DAFCKPQLVK KSYGVENRAY 300  
 SQEITQGFGE GTDTLYAPY STHFQLQNP PQKEFSIPRA HAWPSPYKDY EVKKEGS

Seq ID NO: 621 DNA sequence  
 Nucleic Acid Accession #: NM\_002423.2  
 Coding sequence: 48..851

1 11 21 31 41 51  
 ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG 60  
 TGCTGTGTGC TGTGTGCTCG CTGCCTGGCA GCCTGGCCCT GCGCTGCCT CAGGAGGCGG 120  
 GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180  
 ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT 240  
 TCTTTGCGCT ACCATAAAT GGAATGTTAA ACTCCCGCGT CATAGAAATA ATGCAGAAAGC 300  
 CCAGATGTGG AGTGCCAGAT GTTGCAAGAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360  
 TCTCAAAGT GGTCACTTAC AGGATCGTAT CATATACTCG AGACITACCG CATATTACAG 420  
 TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTC 480  
 GGAAAGTTGT ATGGGGAACT GCTGACATCA TGATTGGCTT TGCGCGAGGA GCTCATGGGG 540  
 ACTCTACCCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCTTTGCG CCTGGGACAG 600  
 GTCTCGGAGG AGATGCTCAC TCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660  
 GGATTAACCT CTGCTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT 720  
 CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGAAA TGGAGATCCC CAAAATTTTA 780  
 AACTTTCCCA GGATGATATT AAAGGCATTG AGAAACTATA TGGAAAGAGA AGTAATTCAA 840  
 GAAAGAAATA GAAACTTCAG GCAGAACATC CATTATTCA TTCAATGGAT TGTATATCAT 900  
 TGTGACAA TCAGATTTGA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCACC 960  
 CTTTTTATT CAGTPTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACCTCCTT 1020  
 ATGGTGTGAC TGTGCTTAT TCCATCTATG AGCTTTGTCA GTGCGGCTAG ATGTCAATAA 1080  
 ATGTTACATA CACAAATAAA TAAATGTTT ATTCATGGT AATTTA

Seq ID NO: 622 Protein sequence  
 Protein Accession #: NP\_002414.1

1 11 21 31 41 51  
 MRLTVLCAVC LLPGSLALPL PQEAGGMSEL QWEQAQDYLK RFYLYDSEK NANSLEAKLK 60  
 EMQKFGLEPI TGLMNSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120  
 PHITVDRLVS KALNMWKEI PLHFRKVVWG TADIMIGFAR GAHGDSYPFD GPGNTLAHAF 180  
 APGTGLGDDA HFDIEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND 240  
 PQNFKLSQDD IKGIQKLYGK RSNRKK

Seq ID NO: 623 DNA sequence  
 Nucleic Acid Accession #: NM\_031457.1  
 Coding sequence: 204..956

1 11 21 31 41 51  
 AAACAGGAAA TAAATACGAA TGAAGCTGAG CTCTAAGCAG CATGTAACCT GGCCTGCATC 60  
 CAGGAAATAG AGGACTTGG ATCCTTCTAA CCTACCACC CACTGGCCC CAGTACATTC 120  
 ATTCTCTCAG GAAAAAACA AAGGTCCCCA CAGCAAGAA AAGGAATAGG ATCAAGAGAT 180  
 ACGTGGCTGC TGGCAGAGCA AGCATGAATT CGATGACTTC AGCAGTTCCG GTGGCCAATT 240  
 CTGTGTTGGT GGTGGCAGCC CACAATGGTT ATCCTGTGAC CCCAGGAATT ATGTCTCAGC 300  
 TGCCCTGTGA TCCAAACAGC CAGCCGCAAG TCCACCTAGT TCTTGGGAAC CCACCTAGTT 360  
 TGGTGTGCAA TGTGAATGGG CAGCCTGTGC AGAAAGCTCT GAAAGAAGGC AAAACCTTGG 420  
 GGGCCATCCA GATCATCATT GGCCTGGCTC ACATCGCCT CGGCTCCATC ATGGGGAOAG 480  
 TTCTCGTAGG GGAATACCTG TCTATTTCAT TCTACGGAGG CTTTCCCTTC TGGGGAGGCT 540  
 TGTGTTTAT CATTTACGGA TCTCTCTCCG TGGCAGCAGA AAATCAGCCA TATTCTTATT 600  
 GCCTGCTGTC TGGCAGTTTG GGCCTGAACA TGGTCACTGC AATCTGCTCT GCAGTTGGAG 660  
 TCATACTCTT CATCACAGAT CTAAGTATTC CCCACCCATA TGCTTACCCC GACTATTATC 720  
 CTACCGCTCA GATCATCATT CCTGGAATGG CGATTCTGG CGTCTGCTG GTCTTCTGCC 780  
 TCTTGGAGTT TGGCATCGCA TGGCATCTT CCCACTTTGG CTGCCAGTTG GTCTGCTGTC 840  
 AATCAAGCAA TGTGAGTGTG ATCTATCCAA ACATCTATGC AGCAAAACCA GTGATCACCC 900  
 CAGAACCGGT GACCTCACCA CCAAGTTATT CCAAGTATG CCAAGCAAT AAGTAAGGCT 960  
 ACAGATTCTG GAAGCATCTT TCACTGGGAG CAAAAGAAGT CCTCTCCCTT TTCTGGGCTT 1020  
 CCATAACCCA GTGCTTCTCT GTTCTGACAG CTGAGGAAAC GTCTCTCCCA CTGTTTGTAC 1080  
 TCTCACCTTC ATTCTTCAAT TCAGTCTAGG AAACCATGCT GTTCTCTAT CAAGAAGAAG 1140  
 ACAGAGATT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGCACATG CATCAGACA 1200  
 TATGTGGGCA TCCAGCTCT GGGCCCTTGG CACACACACA TTGCTGTGCT CTGCTGCATG 1260

TGAGCTTGTG GGTAGAGGA ACAAATATCT AGACATTCAA TCTTCACTCT TTCAATTGTG 1320  
CATTCATTTA ATAAATAGAT ACTGAGCATT CAAAAA AAAA

5 Seq ID NO: 624 Protein sequence  
Protein Accession #: NP\_113645.1

1 11 21 31 41 51  
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPNSQ PQVHLVPGNP PSLVSNVNGQ 60  
10 PVQKALKEGK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFPFW GGLWFIISGS 120  
LSVAAENQPY SYCLLSGSLG LNIIVSAICSA VGVILFITDL SIPHPYAYPD YYPYAWGVNP 180  
GMAISGVLLV FCLLEFGIAC ASSHFGCQLV CQSSNVSVI YPNIIAANPV ITPEVTSPP 240  
SYSSEIQANK

15 Seq ID NO: 625 DNA sequence  
Nucleic Acid Accession #: NM\_005221.3  
Coding sequence: 1..870

1 11 21 31 41 51  
20 ATGACAGGAG TGTITGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60  
TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACATT GCCCGAGTCT 120  
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCGSCAGCG CTACTGCTCT 180  
25 CCTACTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG 240  
AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300  
TACCACAGT ACGGGGGGCG CTACACCGCG GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360  
GAAGTAGCCG AGCCCGAGGT GAGAAATGGT AATGGCAAA CAAAGAAAGT TCGTAAACCC 420  
AGGACTATTT ATCTCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480  
TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCTCGC TGGGATTGAC ACAACACAG 540  
30 GTGAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AACCGGGGAG 600  
ATGCCCCCGG AGCAGAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC CCGCAGTCT 660  
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCAACC TCATGCCAC 720  
CCTCGACCT CCAACCACTT CCGAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780  
35 ACAAGTGACG CAGCTCAAT CAATTCCAC CTGCCGCCG CCGGCTCCTT ACAGCACCCG 840  
CTGGCGCTGG CCTCCGGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence  
Protein Accession #: NP\_005212.1

40 1 11 21 31 41 51  
MTGVFDRVP SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSYYSF TGGAPHGYCS 60  
PTSASYGKAL NPYQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120  
45 EVTEPEVRMV NGPKPKVRKP RTIYSSPOLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180  
VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHHPAH 240  
PPTSNSQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLV

50 Seq ID NO: 627 DNA sequence  
Nucleic Acid Accession #: NM\_014420  
Coding sequence: 118..792

1 11 21 31 41 51  
55 GCACGAGAGA CGACGTGCTG AGCTGCCAGC TTAGTGGAAG CTCTGCTCTG GGTGGAGAGC 60  
AGCCTCGCTT TGGTGACGCA CAGTGCTGGG ACCCTCCAGG AGCCCGGGA TTGAAGGATG 120  
GTGGCGGCGG TCCTGCTGGG GCTGAGCTGG CTCTGCTCTC CCTGCGGAGC TCTGGTCTG 180  
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCAATGGG CCGGAAGGG CTCACAGTGC 240  
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCTCTC AGCCCGGGA TGAGAAGCGC 300  
60 TTCTGTGCTA CATGCTGTGG GTTGGGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360  
GGGACACTCT GTGTGAACGA TGTTTGTACT ACGATGGAAG ATGCAACCCC AATATTAGAA 420  
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA CCCAGTCCAG 480  
GAAACCAAC CCAAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540  
GGAGAAAGTT GTCTGAGAAC TTTTGAAGT GTGCTGTGCT TTTGCTGTGC TCGTCAITTT 600  
65 TGGACGAAAA TTTGTAAGCC AGTCTTTT GAGGGACAGG TCTGCTCCAG AAGAGGGCAT 660  
AAAGACACTG CTCAGAGTCC AGAAATCTTC CAGCGTTGCG ACTGTGGCCC TGGACTACTG 720  
TGTGAAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780  
GAAAGCTAT AAATATTTC AATAAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840  
A

70 Seq ID NO: 628 Protein sequence  
Protein Accession #: NP\_055235

1 11 21 31 41 51  
75 MVAALLGLS WLCSPILGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCLQPRDEK 60  
PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TIMEDATPIL ERQLDEQDGT HAEGTIGHPV 120  
QENQPKRKPS IKKSQGRKGQ EGESCLRTFD CGPGLCCARH FWTKICKPVL LEGQVCSRRG 180  
HKDTAQAPEI FQRCDGGL LCRSGLTSNR QHARLRVCQK IEKL

80 Seq ID NO: 629 DNA sequence  
Nucleic Acid Accession #: NM\_002448.1  
Coding sequence: 241..1134

1 11 21 31 41 51

5  
10  
15  
20  
25  
30

```

GGGCGAGTGC TCCCGGGAAC TCTGCCTGCG CGGCGGCAGC GACCGGAGGC CAGGCCAGGC 60
ACGCCCGGAGC TGGCCTGCTG GGGAGGGGCG GGAGGCGGCG GCGGAGGGT CCGCCCGGCC 120
AGGCCCGGGG CCTTCGCGAGA GGGCGGCGCG GCTCCAGACC CGCCCGGAGC CCATGCCCGG 180
CGGCTGGCCA GTGCTGCGGC AGAAGGGGGG GCGCGGCTCT GCATGGCCCC GGCTGCTGAC 240
ATGACTTCTT TGGCACTCGG TGTCAAAGTG GAGGACTCCG CCTTCGGCAA GCCGCGGGGG 300
GGAGCGCGGG GCCAGGCCCG CAGCGCCGCG GCGGCCACGG CAGCCGCCAT GGGCGCGGAC 360
GAGGAGGGGG CCAAGCCCAA AGTGTCCCTC TCGCTCCTGC CCTTCAGCGT GGAGGCGCTC 420
ATGGCCGACC ACAGGAAGCC GGGGGCCAA GAGAGCGCCC TGGCGCCCTC CGAGGCGCTG 480
CAGGCGCGGG GTGGCTCGGC GCAGCCACTG GCGTCCCGC CGGGGTGCTG GGGAGCCCCG 540
GACGCGCCCT CTTCGCGCGG GCGGCTCGGC CATTCTCGG TGGGGGGACT CCTCAAGCTG 600
CCAGAAGATG CGCTCGTCAA AGCCGAGAGC CCGAGAGAGC CCGAGAGGAC CCGTGGATG 660
CAGAGCCCCC GCTTCTCCCC GCGCGCGGCC AGGCGGCTGA GCCCCCAGC CTGCACCTTC 720
CGCAAAACAC AGACGAACCG TAAGCGCGGG ACGCCCTTCA CCACCGCGCA GCTGCTGGCG 780
CTGGAGCGCA AGTTCGCGCA GAAGCAGTAC CTGTCCATCG CCGAGCGCGC GGAGTTCTCC 840
AGCTCGCCCT TCTCGCTGAG GACGAGGTG AAGATATGGT TCCAGAACCG CCGCGCCAAG 900
GCAAGAGAC TACAAGAGGC AGAGCTGGAG AAGCTGAAGA TGGCCGCCAA GCCCATGCTG 960
CCACCGCGTG CCTTCGCGCT CTCTTCCCTC CTCGGCGGCC CGCAGCTGT AGCGCGCGCG 1020
GGGGGTGCTT CGCTCTAGGG TGCTCTGGC CCTTCCAGC GCGCGCGCT CCTGTGGCG 1080
CCCGTGGGAC TCTACAGGCG CCATGTGGGC TACAGCATGT ACCACCTGAC ATAGAGGGTC 1140
CAGGTGCCCC ACCTGTGGGC CAGCGGATTC CTCCAGCCCT GGTGCTGTAC CCGGACGCTG 1200
CTCCCTGCTC CGGCACGCGC AGCCGCTTC CCTTTAACCC TCACATGCTC CCGATTTCAC 1260
CTCTTGTGCT CCTGAGTTCA CTCTCGAAG TCTGATCCCT GCCAAAAGT GGCTGGAAGA 1320
GTCCCTTAGT ACTCTTTAGC CATTAGATC TACACTCTCG AGTTAAAGAT GGGGAAACTG 1380
AGGGCAGAGA GGTAAACAGA TTTATCTAGG GTCCCCAGCA GAATTGACAG TTGAACAGAG 1440
CTAGAGGCCA TGTCTCTGCG ATAGCTTTTC CCGTCTCTGA CACCAGGCAA GAAAAGCGCA 1500
GAGAAATCGG TGTCTGACGA TTTTGAAAT GAGAACAAAT TCAAAAAAAA AAAAAAAGCA 1560
AAAAAAGAAA GAAAAGAGAA AAAAAAGACT AGCCAGCCAG GAAGATGAAT CCTAGCTTCT 1620
TCCATTGGAA AATTTAAGAC AAGTTCAACA ACAAACATT TGCTCTGGGG GGCAGGGAAA 1680
ACACAGATGT GTTGCAAAGG TAGGTTGAAG GGA

```

Seq ID NO: 630 Protein sequence  
Protein Accession #: NP\_002439.1

35  
40

```

1 11 21 31 41 51
MTSLPLGVKV EDSAFGKPGK GGAGQAPSAA AATAAMGAD EBGAKPKVSP SLLPFSVEAL 60
MADHRKPGAK ESALAPSEGV QAAGGSAQPL GVPPGSLGAP DAPSSPRPLG HFSVGLLKL 120
PEDALVKAES PEKPERTPMW QSPRFPSPPA RRLSPACTL RKHKTNRKPR TPTTTAQLLA 180
LERKFRQKQY LSIATERAFS SLSLSTETQV KIWPQNRRK AKRLQEAELE KLMMAAKPML 240
PPAAFGLSFP LGGPAAVAAA AGASLYGASG PFQRAALEVA PVGLYTAHVY YSMYHLT

```

Seq ID NO: 631 DNA sequence  
Nucleic Acid Accession #: NM\_002557.1  
Coding sequence: 13..2049

45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
CAGACCATTG AGATGTGGAA GCTGTTGCTG TGGGTGGGGC TGGTCTTGT GCTGAAACAC 60
CAGCATGGTG CTGCCCATAA ACTCGTGTGT TATTTCACCA ACTGGGCACA CAGTCGGCCA 120
GGCCCTGCGT CGATCTTGCC CCATGACCTG GACCCCTTTC TCTGCACCCA CCTGATATT 180
GCCCTTGCTT CAATGAACAA CAATCAGATT GTTGCTAAGG ATCTCCAGGA TGAGAAAAAT 240
CTCTACCCAG AGTTCAACAA ACTAAGGAG AGGAACAGAG AGCTGAAAC ACTACTGTCC 300
ATCGGCGGGT GGAACCTTGG CACCTCAAGA TTCACCACTA TGTGTGCCAC ATTTGCCAAC 360
CGTGAAGAAT TTATGTCTTC AGTTATATCC CTCTGAGGA CACATGACTT TGATGGTCTT 420
GACCTTTTCT TCTTATATCC TGGACTAAGA GGCAGCCCCA TGATGACCG GTGGACTTTT 480
CTCTTCTTAA TTGAAGAGCT CCGTGTGCCC TTCCGGAAGG AGGCACTGCT CACCATGCGC 540
COGAGGCTGC TGCTGTCTGC TGCTGTTTCT GGGGTCCAC ACATGTTCCA AACATCCTAT 600
GATGTGCGCT TTCTAGGAAG ACTCTGGAT TTCTATCAATG TCTGTCTTCA TGACTTACAT 660
GGAAGTTGGG AAAGGTTTCA AGGACATAAT AGCCCCCTCT TCTCTGTCG TGAAGACCCC 720
AAATCTTGGG CATATGCTAT GAATTATTGG AGAAAGCTTG GGGCACCCCTC AGAGAAGCTC 780
ATCATGGGGA TCCCCACCTA TGGACGTACC TTTGCGCTCC TCAAAGCCTC TAAGAATGGG 840
TTGACGGCCA GAGCGATCGG ACCAGCATCT CCAGGGAAGT ACACCAAGCA AGAAGGCTTC 900
TTGGCTTATT TTGAGATTGT TTCTTTGTC TGGGAGCGGA AGAAGCACTG GATTGATTAC 960
CAGTATGTCC CGTATGCCAA CRAAGGGGAA GAGTGGGTTG GCTATGACAA TGCCATCAGC 1020
TTCAATTACA AGGCATGGTT TATAAGGCGA GAGCATTTTG GGGGGGCCAT GGTGTGGACA 1080
TTGGACATGG ATGACGTGAG GGGCACTTTC TGTGGCACTG GCCCTTTCCC CCTTGTCTAC 1140
GTATTGAATG ATATCTGTGT TCAAGCACT GACCTGAAA GGCTGGCTGT GACCAAGGCA 1260
CTGTCACTCG CTGTGAATTC TTGCCCCCA GGAGGAGAGG CTGGGGTCA C TGAGATCCAC 1320
TGGACCACTG ATAGTAAGAT TTTGCCCTCA AGAGGTACAA CTGTGACCCC TACAAAGGAA 1380
GGAAGTGTGG AATAATGTAC TATAACCCCT AGAGGTACAA CTGTGACCCC TACAAAGGAA 1440
ACTGTATCCC TTGGAAGACA CACTGTAGCT CTAGGAGAGA AGACTGAGAT CACTGGGGCA 1500
ATGACCATGA CTTCTGTGGG TCATCAGTCC ATGACCCCTG GAGAGAAGGC CCTGACCCCT 1560
GTGGGTCATC AATCTGTGAC CACTGGACAG AAGACCCCTG CCTCTGTGGG TTATCAGTCT 1620
GTGACCCCTG GGGAAAAGAC CCTGACCCCT GTGGGTATC AGTCTGTGAC CCCTGTGAGT 1680
CATCAGTCTG TATGCTGTGG AGGAACGACT ATGACCCCTG TCCATTTTCA GACTGAGACC 1740
CTTAGACAGA ATACAGTGGC CCTAGAAAGG AAGGCTGTGG CCGGTGAAA GGTGACTGTC 1800
CCCTCCAGAA ACATCTAGT CACCCCTGAA GGGCAGACTA TGCCCTTAAG AGGGGAGAA 1860
TTGACTTCTG AGGTGGGCAC TCACCCAGG ATGGGTAAT TGGGTCTTCA GATGGAAGCT 1920
GAAAACAGGA TGATGCTGTG CTCCAGCCCC GTCATCCAGC TCCCGGAACA AACTCCTCTA 1980
GCTTTTGACA ACCGCTTTGT TCCCATCTAT GGAACCAATT CCTCTGTCAA CTCAGTAACC 2040
CCTCAACAAA GTCTCTTTCT TCTAAAAAAA GAAATCCAG AAAACTCTGC TGTGGATGAA 2100
GAGGCTTAAG CCCCTCTGGT GTCAAGAAC AGGGAAGACC CTGTCTTTT CTCTAAGTG 2160
ACATGTTGGA AGCCTTCTCA TCCCGGGGCA AAGCAGGCAT CAAACACAGA ATAGGCCAAT

```

CTCTTTTCCA TTAATAAAC TGTAACACA AGAACCCA

Seq ID NO: 632 Protein sequence  
 Protein Accession #: NP\_002548.1

5  
 10  
 15  
 20

1	11	21	31	41	51	
MWKL	LLVVL	VLV	LKH	HIDG	AHKL	VCYFTN
WAH	SRPG	PAS	ILPH	DLDP	FL	CTHL
IFAF	AS	60				
MNN	QIV	AKD	LQDE	KILY	PE	FNKL
KERN	RE	LKTL	LSIG	GW	NFGT	SRFT
TM	LST	FAN	REKF	120		
IAS	VIS	LLRT	HD	FDGL	DL	LF
LYP	GLRG	SPM	HDR	WTF	FL	LI
EEL	LF	AFKE	ALL	TM	PR	LL
180						
LSA	AVS	GVPH	IVQ	TSY	DV	RF
LG	RL	LD	FIN	LSY	DL	HGS
WE	RFT	GHN	SPL	FL	SL	PE
240						
YAM	YWR	KLG	AP	SEK	L	IMI
PTY	GRT	FR	LL	KAS	KN	LQAR
AIG	PAS	PG	KY	TQ	EG	FL
300						
EIC	SF	W	GAK	KH	WID	YQY
VP	YANK	GKE	WVG	YD	NAI	S
PSY	K	AW	FIR	RE	H	FG
GAM	V	W	T	L	D	M
360						
DVR	G	T	FC	GT	PF	PL
VY	V	I	AND	IL	V	RA
ES	S	T	SL	P	Q	W
LSS	A	V	N	S	S	T
420						
SK	L	P	G	G	E	A
GV	T	E	I	H	K	C
E	N	M	T	I	T	P
R	G	T	T	V	T	P
480						
SV	G	H	Q	S	M	T
P	E	K	A	L	T	P
V	G	H	Q	S	V	T
540						
SP	G	T	M	T	P	V
H	F	Q	T	E	T	L
R	N	T	V	A	P	R
K	A	V	A	R	K	V
600						
VG	T	H	P	R	M	G
N	L	G	L	M	E	A
E	N	R	M	L	S	S
P	V	I	Q	L	P	E
Q	T	L	A	F	D	N
660						
PL	S	L	K	K	E	I
P	E	A	D	E	E	A

Seq ID NO: 633 DNA sequence  
 Nucleic Acid Accession #: NM\_003885.1  
 Coding sequence: 98..1021

25  
 30  
 35  
 40  
 45

1	11	21	31	41	51	
AA	ACT	CAG	AA	TTT	TCG	CGG
C	G	G	G	G	G	G
60						
GC	AGG	GGG	CGC	AGC	ATG	CAG
C	A	C	C	C	C	A
120						
TC	CC	AGT	AC	CGA	AGG	CCA
C	G	C	T	G	T	T
180						
GG	CCG	TAC	AG	AC	AG	A
A	A	C	C	A	A	G
240						
CG	T	G	T	G	C	C
T	C	G	T	G	C	C
300						
GC	AG	C	T	A	C	A
A	A	C	A	A	C	A
360						
GT	CG	T	G	T	C	A
T	C	C	A	C	A	T
420						
AC	CC	C	G	G	T	T
C	C	C	A	G	G	G
480						
CC	TC	C	A	C	C	T
C	C	C	T	C	C	T
540						
C	A	G	T	A	G	T
T	G	G	T	A	G	T
600						
C	T	C	T	G	C	C
T	G	C	T	G	C	T
660						
G	G	C	T	G	C	A
G	A	C	A	G	G	C
720						
C	A	G	G	A	T	G
T	A	T	C	C	T	C
780						
A	T	G	C	T	G	T
A	C	T	C	T	A	C
840						
C	T	G	T	G	A	G
A	G	G	C	T	T	T
900						
G	A	G	C	T	A	A
A	T	G	C	T	G	C
960						
C	T	G	A	A	G	A
A	G	A	G	A	G	A
1020						
A	G	C	A	T	G	T
A	C	T	G	C	T	A
1080						
A	T	C	A	T	G	C
A	T	C	A	T	G	C

Seq ID NO: 634 Protein sequence  
 Protein Accession #: NP\_003876.1

50  
 55

1	11	21	31	41	51	
M	G	T	V	L	S	L
S	P	S	Y	R	K	A
60						
K	K	N	S	K	K	V
Q	P	N	S	S	Y	Q
120						
G	S	S	V	K	A	P
P	A	V	T	S	A	G
180						
V	D	R	S	L	L	Q
W	Q	D	G	F	I	P
240						
I	S	Y	P	L	K	F
L	V	I	N	L	M	S
300						
L	L	L	G	L	D	R

TABLE 79A:

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
15	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
	443646	AJ085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
20	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AJ910275	Hs.350470	trefoil factor 1 (breast cancer, estroge	Seq ID No. C10 & C226
	411789	AF245505	Hs.72157	Adican	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
25	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
30	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C23 & C238
35	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
40	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
45	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
50	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
55	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
	408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
60	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	Seq ID No. C48 & C263
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
65	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
70	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
	416965	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.54795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
75	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
80	421563	NM_005433	Hs.105806	granulysin	Seq ID No. C68 & C283
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-tRNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287



5	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	A1393742	Hs.199057	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
10	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
	431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	426440	BE382756	Hs.169502	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
	426484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85952	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	Seq ID No. C106 & C321
	440559	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AI015709	Hs.172089	PORIMIN Pro-oncogene receptor inducing me	Seq ID No. C120 & C335
50	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plaxin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
60	432874	W94322	Hs.279551	melanoma inhibitory activity	Seq ID No. C131 & C346
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
65	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
70	432596	AJ224741	Hs.278461	matritin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
75	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	Seq ID No. C146 & C361
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gaslin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C155 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	Seq ID No. C160 & C375
	436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179557	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
15	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (chofinergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW97938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AI732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
55	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.37796	EphB6	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

## 65 TABLE 79B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

70

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17858 D78863

75

## TABLE 79C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

80

Pkey	Ref	Strand	NL_position
------	-----	--------	-------------

5

404682	9797231	Minus	40977-41150
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence  
Nucleic Acid Accession #: NM\_005814  
Coding sequence: 345..1304

	1	11	21	31	41	51	
5	CTACCCCTTT	GTGAGCAGTC	TAGGACTTTG	TACACCTGTT	AAGTAGGGAG	AAGGCAGGGG	60
10	AGGTGGCTCG	TTTAAGGGGA	ACTTGAGGGA	AGTAGGGAAG	ACTCTCTTTG	GGACCTTTGG	120
	AGTAGGTGAC	ACATGAGCCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACCAGAC	AGCTCAGACC	TGTCTGGAGG	300
15	CTGCCAGTGA	CAGGTTAGGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAAGATGT	360
	GGCCTGTGTT	GTGGACACTC	TGTGCAGTCA	GGGTGACCGT	CGATGCCATC	TCTGTGGAAA	420
	CTCGCGCAGG	CGTTCTTCGG	GCTTCGCAGG	GAAAGAGTGT	CACCCCTGCC	TGCACCTACC	480
	ACACTTCCAC	CTCCAGTCGA	GAGGGACTTA	TTCAATGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGAAAGGGT	GGTCATCTGG	CGTTTTCAA	ACAAAACTA	CATCCATGGT	GAGCTTTATA	600
20	AGAATCGCGT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCCTCCATC	ACCATTGATC	660
	AGCTGACCAT	GGCTGACAAC	GGCAGCTACG	AGTGTTCGTG	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	GTCCGCTCGT	GTCCGCTCGT	TGGTCTCTGT	GCCACCTCC	AAACCAGAAT	780
	CGGGCATCGA	GGGAGAGACC	ATAATTGGGA	ACAACATCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCAGG	GATCAGCTGG	AGAGGTACAA	CATCCTGAAT	CAGGAGCAGC		900
25	CCCTGGCCCA	GCCAGCCTCA	GTCAGCCTG	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
	CGGGTTACTA	CATCTGTACC	TCCAGCAATG	AGGAGGGGAC	GCAGTTCTGC	AACATCACGG	1020
	TGGCCGTGAG	ATTCCTCTCC	ATGAACGTGG	CCCTGTATGT	GGGCATCGCG	GTGGGCGTGG	1080
	TTGCAAGCCT	CATTATCATT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGACG	1140
	ACAACACTGA	AGACAAGGAG	GATGCAAGGC	CGAACCGGGA	AGCCTATGAG	GAGCCACCCG	1200
30	AGCAGCTAAG	AGAACCTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAAGAAGAGC	1260
	AGAGGAGCAC	TGGGCGTGAA	TCCCGGAGCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGCGGAG	GAAGGGTTAG	GGGTTTATT	TCCGCTTCC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCCAG	ACATTGATGG	GGACATTCTT	TCCCCAGTGT	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
35	ACTGTCTGTT	GAAGTACCCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCTG	GCCCTCACTC	1560
	AAGACCAGGC	TGCAGCCTCC	ACTTCCCTCG	TAGTTGGCAG	GAGCTCCTGG	AAGCACAGCG	1620
	CTGAGCATGG	GGCGCTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCAGC	CTTGGGGGGT	1680
	GGGGGCTGTC	CTGCTCACCT	GTGTGCCAG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
	CACCTCCAC	ATCTTCTTTG	AATGAATGAA	AGAATAAGTG	AGTATGCTTG	GGCCCTGCAT	1800
40	TGGCCTGGCC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
	TCCAAACCCCT	CTTGGGAAGG	CCACCTCCCA	CTCCTGCTGC	ACAGGCCCTG	GGGAGCTTTT	1920
	GGCCACACAC	TTCCTCATCT	TGCCGTGCAA	TATCGTACCT	GTCCCTCCAG	GCCCATCTCA	1980
	AATCACAAGG	ATTCTCTCTA	CCCTATCCCTA	ATTGTCCACA	TACGTGGAAA	CAATCCTGTT	2040
	ACTCTGTCCC	ACGTCCAAAT	ATGGGCCACA	AGGCACAGTC	TTCTGAGCGA	GTGCTCTCAC	2100
45	TGTATTAGAG	CGCCAGCTCC	TTGGGGCAGG	GCCTGGGCTT	CATGGCTTTT	GCTTTCCCTG	2160
	AAGCCCTAGT	AGCTGGCGCC	CATCCTAGTG	GGCACTTAAG	CTTAATTGGG	GAAACTGCTT	2220
	TGATTGGTTG	TGCCCTCCCT	TCTCTGGTCT	CCTTGAGATG	ATCGTAGACA	CAGGGATGAT	2280
	TCCCAACCAA	ACCCAGTAT	TCATTCAAGT	AGTTAAACAC	GAATTGATTT	AAAGTGAACA	2340
	CACACACAGG	AGCTTCTCTG	CAGATGGTCT	GAGTTCTTGT	GTCCCTGGTA	TTCTCTCCCA	2400
50	GGCCAGAATA	ATTGGCATGT	CTCCTCAACC	CACATGGGGT	TCCCTGGTTG	TCTGCTATCC	2460
	CGATACCTCA	GCCTTGGCCC	TGCCAGAGCC	ATTGGGGCTC	TGGTTTCTGT	GTGGGGCTGT	2520
	CTGCTGGCCC	TCCCAAGAGC	TCCTTCTGTT	TGTCGAGCAT	TTCTTCTACT	CTTGAGAGCT	2580
	CAGGAGGCTG	TAGGGCTGCT	TAGGTCTCAT	GGACCAAGTG	CTGGTCTCAC	CCAACTGCAG	2640
	TTTACTATGT	CTATCTTTTC	TGGATGATCA	GAAAAATAAT	TCCATAAATC	TATTGTCTAC	2700
55	TTGCGATTTT	TTAAAAATG	TATATTTTAA	TATATATTGT	TAAATCCTTT	GCTTCATTCC	2760
	AAATGCTTTC	AGTAATAATA	AAATTGTGGG	TGG			2793

Seq ID NO: C2 DNA Sequence  
Nucleic Acid Accession #: E05 sequence  
Coding sequence: 1..3150

60	1	11	21	31	41	51	
	ATGGGGAGCC	GGACGCCAGA	GTCCCTCTCT	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
65	CGCGACCCCC	CGCTSSGTGC	GCTGCTGTGT	CTGCTSSGTG	CGCGGCCACC	CAGGGTCCGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTAA	CGGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACACAGCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTC	300
	TGGGCTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAGG	CTCTGGGCTC	360
70	CTGGAGTCTC	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCCCTGCAG	420
	TGGTTCGGGG	CAACAGTTCC	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600
	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAGT	GCGAGTTTCA	CCAAGACTGG	CGGTGTGGTT	660
75	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCTGCCAC	TCAGGAGCAG	720
	ATTGCAGAAT	CTTATTACCC	CGAGTACCTG	ATCAACCTGG	TTCAAGGGCA	GCTGCAGACT	780
	CGCCAGGCCA	GTTCATCTTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCAAGTGGT	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
	GGCTATGCTA	CATCCTTTAA	TGGCTCAGAC	ATTGATCCCC	TCTCAAACTT	CTCAGGGGAA	960
80	CAGATGGCCT	CCTACTTTGG	CTATGCAGTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
	GATGACTTGC	TGGTGGGGGC	ACCCCTGTCT	ATGGATCGGA	CCCCTGACGG	GCGGCTCTAG	1080
	GAGGTGGGCA	GGGTCTACGT	CTACCTGCAG	CACCCAGCCG	GCATAGAGCC	CAGCCCAACC	1140
	CTTACCCCTC	CTGGCCATGA	TGAGTTTGGC	CGATTTGGCA	GCTCCTTGAC	CCCCCTGGGG	1200
	GACCTGAGCC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCTTTGG	TGGGGAGAGC	1260
	CAGCAGGGAG	TAGTGTTTGT	ATTTCCTGGG	GGCCAGGAG	GGCTGGGCTC	TAAGCCTTCC	1320

5 CAGGTTCTGC AGCCCTCTGT GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380  
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCCTTTGGT 1440  
 GTGGACAGAG CTGTGGGTATA CAGGGGCGGC CCCATCGTGT CCGCTAGTGC CTCCTCACC 1500  
 ATCTTCCCCG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTCTGT 1560  
 GCCTGCATCA ACCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620  
 GGTTTTCACG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680  
 CTGTTCTCTG CCTCCAGGCA GGCAACCTTG ACCAGACCC TGCTCATCCA GAATGGGGCT 1740  
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800  
 10 CTCTGGCGGA TTCACATGCG TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860  
 CACGGCCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920  
 ATCTTGTCTG ACTGTGGAGA AGACAACATC TGTGTGCTTG ACCTGCAGCT GGAAGTGTIT 1980  
 GGGGAGCAGA ACCATGTGTA CTGGGTGAC AAGAATGCC TGAACCTCAC TTTCATGCC 2040  
 CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCAACGC CCCTCCAGAG 2100  
 15 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCTGAG CTGTGACTAC 2160  
 TTTGCCGTGA ACCAGAGCCG CTGTCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220  
 GCCAGTCTGT GGGGTGGCTT TGGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280  
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2340  
 TCCTTTCCGC TCTCCTGGA GGCTCAGGCC CAGGTCAACC TGAACGCTGT CTCCAAGCCT 2400  
 20 GAGGCAGTGC TATTCCAGT AAGCGACTGG CATCCCGAG ACCAGCTCA GAAGGAGGAG 2460  
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCC CAGCTCCATT 2520  
 AGCCAGGGTG ACTGTGAACT CAGCTGTCCC CAGGCTCTGG AAGGTCAACA GCTCCTATAT 2580  
 GTGACCAAGG TTAACGGACT CAACTGCACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640  
 GAGTTGGATG CCGAGGGTTC CTGCAACCA CAGCAAAAAC GGAAGCTCC AAGCCGACG 2700  
 25 TCTGCTTCTT CCGGACCTCA GATCCTGAAA TGCCCGAGGG CTGAGTGTIT CAGGCTGCGC 2760  
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTGA TTTCGAGTC 2820  
 TGGGCAAGA CTTTCTTGCA GGGGAGCAC CAGCCATTGA GCCTGCAGTG TGAGGCTGTG 2880  
 TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCA AAAAGAGCGT 2940  
 CAGGTGGCCA CAGCTGTGCA ATGGAACCA GCAAGAGGCA GCTATGGCGT CCCACTGTGG 3000  
 30 ATCATCATCT TAGCCATCTT GTTGGCCTC CTGCTCTAG GTCTACTCAT CTACATCCTC 3060  
 TCAAGCTTG GATTCTTCAA ACGTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120  
 CTCAGCCTC CAGCCACCTC TGATGCCCTGA 3150

Seq ID NO: C3 DNA Sequence

Nucleic Acid Accession #: NM\_002421.2

Coding sequence: 1..1410

35  
 40  
 45  
 50  
 55  
 60  
 65

1	11	21	31	41	51	
ATGCACAGCT	TTCTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTG	ACACAGCTTC	60
CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
TACTACAACC	TGAAGAATGA	TGGGAGGCAA	GTGAAAAGC	GGAGAAATAG	TGGCCCATGT	180
GTGAAAAAT	TGAAGCAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAAGT	240
GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCCTGATG	GGCTCAGTTT	300
GTCTCTCACT	AGGGGAACCC	TCGCTGGGAG	CAAAACATC	TGACCTACAG	GATTGAAAT	360
TACACGCCAG	ATTGCGAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACCT	420
TGGAGTAATG	TCACACCTCT	GACATTCAAC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACTCTCCTT	TTGATGGAAC	TGGAGGAAAT	540
CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
GAAAGGTGGA	CCACCAATTT	CAGAGAGTAC	AACCTACATC	GTGTTGCGGC	TCATGAACTC	660
GGCCATTCTC	TTGGACTCTC	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
ACCTTCACTG	TTGGAGTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
GGACGTTCCC	AAATCCTGT	CCAGCCCATC	GGCCACAAA	CCCCAAAAGC	ATGTGACAGT	840
AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900
TTCTACATGC	GCACAAATCC	CTTCTACCCG	GAAGTTGAGC	TCAATTTTAT	TTCTGTTTTC	960
TGGCCACAAC	TGCCAAATGG	GCTTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAAGT	1020
CGGTTTTC	TAAGGGAATA	GTACTGGGCT	GTTCAGGGAC	AGAATGTGCT	ACAAGGATAC	1080
CCCAAGGACA	TCATACGCTC	CTTTGGCTTC	CCTAGAACTG	TGAAGCATAT	CGATGCTGCT	1140
CTTTCTGAGG	AAAACACTGG	AAAAACCTAC	TTCTTTGTTG	CTAACAAATA	CTGGAGGTAT	1200
GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATAGCACA	TGACTTTTCT	1260
GGAAATGGCC	ACAAAGTTGA	TGCAGTTTTC	ATGAAAGATG	GATTTTTCTA	TTTCTTTTCT	1320
GGAACAAAGC	AATACAAATT	TGATCCTAAA	ACGAAGAGAA	TTTGTACTCT	CCAGAAAGCT	1380
AATAGCTGCT	TCAACTGCAG	GAAAAATTAG				1410

Seq ID NO: C4 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1410

70  
 75  
 80

1	11	21	31	41	51	
ATGCACAGCT	TTCTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTG	ACACAGCTTC	60
CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
TACTACAACC	TGAAGAATGA	TGGGAGGCAA	GTGAAAAGC	GGAGAAATAG	TGGCCCATGT	180
GTGAAAAAT	TGAAGCAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAAGT	240
GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCCTGATG	GGCTCAGTTT	300
GTCTCTCACT	AGGGGAACCC	TCGCTGGGAG	CAAAACATC	TGACCTACAG	GATTGAAAT	360
TACACGCCAG	ATTGCGAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACCT	420
TGGAGTAATG	TCACACCTCT	GACATTCAAC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACTCTCCTT	TTGATGGAAC	TGGAGGAAAT	540
CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
GAAAGGTGGA	CCACCAATTT	CAGAGAGTAC	AACCTACATC	GTGTTGCGGC	TCATGCCCTC	660
GGCCATTCTC	TTGGACTCTC	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
ACCTTCACTG	TTGGAGTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
GGACGTTCCC	AAATCCTGT	CCAGCCCATC	GGCCACAAA	CCCCAAAAGC	ATGTGACAGT	840
AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900

TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCGTGTTTC 960  
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCGGACAG AGATGAAGTC 1020  
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080  
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140  
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTGT CTAACAAATA CTGAGAGTAT 1200  
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCCT 1260  
 GGAATTGGCC ACAAGTTGA TGCACTTTTC ATGAAGATG GATTTTCTA TTTCTTTCAT 1320  
 GGAACAAGAC AATACAAAT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380  
 AATAGCTGGT TCAACTGCAG GAAAAATTAG 1410

Seq ID NO: C5 DNA Sequence  
 Nucleic Acid Accession #: NM\_014331.2  
 Coding sequence: 1..1506

15 1 11 21 31 41 51  
 ATGGTCAGAA AGCCTGTTGT GTCCACCATC TCCAAAGGAG GTTACCTGCA GGGAAATGTT 60  
 AACGGGAGGC TGCCCTCCCT GGGCAACAAG GAGCCACCTG GGCAGGAGAA AGTGCAGCTG 120  
 AAGAGGAAAG TCACCTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA 180  
 20 GGAATCTTCA TCTCTCTTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCTCTG 240  
 ACCATCTGGA CGGTGTGGG GGTCTGTGCA CTATTTGGAG CTTTGTCTTA TGCTGAATTG 300  
 GGAACAACCTA TAAAGAAATC TGGAGGTGAT TACACATATA TTTTGAAGT CTTTGGTCCA 360  
 TTACCACTT TTGTACGAGT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420  
 GTGATATCCC TGGCATTGCG ACGCTACATT CTGGAACCAT TTTTATTCA ATGTGAAATC 480  
 25 CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCTCTAAAT 540  
 AGCATGAGTG TCAGCTGGAG GCGCCGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA 600  
 GCAATCTGTA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCA AACGCAGAAC 660  
 TTTAAGAGCG CGTTTTCAGG AAGAGATTCA AGTATTACGC GGTGCCACT GGCTTTTAT 720  
 TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA 780  
 30 AACCTGAAA AAACCATTC CTTTGCATAA TGTATATCCA TGGCCATTGT CACCATTTGGC 840  
 TATGTCTGTA CAAATGTGGC TACTTTACG ACCATTAAAT CTGAGGAGCT GCTGCTTTCA 900  
 AATGCACTGG CAGTGACCTT TCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG 960  
 ATCTTTGTTG CCCTCTCTCG CTTTGGCTCC ATGAACGCTG GTGTGTTGC TGTCTCCAGG 1020  
 TTATTCTATG TTGCGTCTCG AGAGGGTCAC CTTCAGAAA TCCTCTCCAT GATTCATGTC 1080  
 35 CGCAAGCACA CTCCTTACC AGCTGTTATT GTTTTGCACC CTTTGACAAAT GATAATGCTC 1140  
 TTCTCTGGAG CCCTCGACAG TCTTTTGAAT TTCTCAGTT TTGCGAGGTG GCTTTTATT 1200  
 GGGCTGGCAG TTGCTGGGCT GATTATCTT CGATACAAAT GCCAGATAT GCATGCTCTC 1260  
 TTCAAGGTGC CACTGTTCAT CCCAGCTTTG TTTTCTTCA CATGCTCTT CATGTTTGGC 1320  
 CTTTCCCTCT ATTCCGACCC ATTTAGTACA GGGATTTGGT TCGTCATCAC TCTGACTGGA 1380  
 40 GTCCCTCGGT ATTATCTCTT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG 1440  
 TCAGAGAAAA TAACAGAAC ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500  
 TTATGAACCTA ATGGAATGTA GATCTTGCCA ATCTGCCAA GGGGAGACAC AAAATAGGGA 1560  
 TTTTCTACTC ATTTTCTGAA AGTCTAGAGA ATTACAACCT TGGTGATAAA CAAAAGGAGT 1620  
 CAGTTATTCT TATTATATATA TTTAGCATA TTGAACTAA TTTCTAAGAA ATTTAGTTAT 1680  
 45 AACTCTATGT AGTTATAGAA AGTGAATATG CAGTTATTCT ATGAGTCCGA CAATTCTTGA 1740  
 GTCTCTGATA CCTACTATT GGGGTTAGGA GAAAAGACTA GACAATTACT ATGTGTCAT 1800  
 TCTCTACAC ATATGTTAGC ACGGCAAGA ACCTTCAAT TGAAGACTGA GATTTTCTG 1860  
 TATATATGGG TTTTGTAAAG ATGGTTTAC AACTACAGA TGTCTATCT GTGAAAAGTG 1920  
 50 TTTTCAATTC TGAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATT 1980  
 ATTTTACATT GACATTCAT TGCTTCCCTT TAGATACCAA TTTAGATAAC AAACACTCAT 2040  
 GCTTAAATGG ATTATACCA GAGCACTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA 2100  
 TTAAGAAGA GTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGT ATGTTAAGT 2160  
 AAAAACTCTT GAGAATTTAT TATGTCAGAT GTTTTTCAT TCATTATCAG GAAGTTTATG 2220  
 55 TATCTGTCA TTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG 2280  
 AGCAAGAGTT AGTTTGGTAT TAAATCTCA TTAGAACAAC CACCTGTTT ACTAATAACT 2340  
 TACCCTGAT GAGTCTATCT AAACATATGC ATTTTAAAGC TTCAAAATT ACTATCAACA 2400  
 TGAGAGAAAT AACCAACAAA GAAGATGTTT AAAAATATAG TCCATATCT GTAATCATAT 2460  
 CTACATGCAA TGTTAGTAT TCTGAAGTTT TTTAAATTTA TGGCTATTT TACACGATGA 2520  
 60 TGAATTTTGA CAGTTTGTGC ATTTTCTTTA TACATTTTAT ATTCTTCTGT TAAATATCT 2580  
 CTTGAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATGCAA 2640  
 AAGAAATGTC GCTGTAAATA AGATTACAA CTGATGTTTC TAGAAAAATT CCACTTCTAT 2700  
 ATCTAGGCTT TGTGATTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA 2760  
 CTGATAAGAA GAAATTTGAA ATGAGAATCT GTGGATAAGT GTTTGTGTT AGAAGATGTT 2820  
 65 GTTTGCCAG TATTAGAAAA TACTGTGAGC CGGCATGGT GGCTTACATC TGTAATCCCA 2880  
 GCATTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCTGAC 2940  
 CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAATTT AGCTGGGCAT GGTGGCAT 3000  
 GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGAGGCG 3060  
 GAGGTTGCAG TGAGCCAAAG TTGACCACCT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120  
 70 CCATCTCCAA AAAAAAATA AAAA 3144

Seq ID NO: C6 DNA Sequence  
 Nucleic Acid Accession #: NM\_003246.1  
 Coding sequence: 112..3624

75 1 11 21 31 41 51  
 GGACGCACAG GCATTCCCCG CGCCCTTCCA GCCCTCGCGG CCTGCGCAC CGCTCCCGGC 60  
 CGCCGCGCTC CGGTACACAC AGGATCCCTG CTGGGCACCA ACAGCTCCAC CATGGGGCTG 120  
 80 GCCTGGGGAG TAGGGCTCTT GTTCTGATG CATGTGTGTG GCACCAACCG CATTCCAGAG 180  
 TCTGGCGGAG CAACACAGCGT GTTGTACATC TTTGAACTCA CCGGGGCGCG CCGCAAGGGG 240  
 TCTGGGCGCC GACTGGTGAA GGGCCCCGAC CCTTCCAGCC CAGCTTTCCG CATCGAGGAT 300  
 GCCAACCTGA TCCCCCTCTG GCCTGATGAC AAGTTCCAAG ACCTGGTGGG TGCTGTGCGG 360  
 GCAGAAAGG GTTCTCTCT TCTGGCATCC CTGAGGCAGA TGAAGAAGAC CCGGGGCACG 420

	CTGCTGGCCC	TGGAGGGGAA	AGACCACTCT	GGCCAGGTCT	TCAGCGTGGT	GTCCAATGGC	480
	AAGGCGGGCA	CCCTGGACCT	CAGCCTGACC	GTCCAAGGAA	AGCAGCACGT	GGTGTCTGTG	540
	GAAGAAGCTC	TCCTGGCAAC	CGGCCAGTGG	AAGAGCATCA	CCCTGTTTGT	GCAGGAAGAC	600
5	AGGGCCCGAG	TGTACATCGA	CTGTGAAAAG	ATGGAGAATG	CTGAGTTGGA	CCTCCCCATC	660
	CAAAGCGTCT	TCACCAGAGA	CCTGGCCAGC	ATCGCCAGAC	TCCGCATCGC	AAAGGGGGGC	720
	GTCAATGACA	ATTTCAGGAG	GGTGTGCTAG	AATGTGAGGT	TGTCTTTTGG	AACCACACCA	780
	GAAGACATCC	TCAGGAACAA	AGGCTGCTCC	AGCTCTACCA	GTGTCTCTCT	CACCTTGAC	840
	AACAACGTGG	TGAATGGTTC	CAGCCCTGCC	ATCCGCACTA	ACTACATTGG	CCACAAGACA	900
10	AAGGACTTGC	AAGCCATCTG	CGGCATCTCC	TGTGATGAGC	TGTCCAGCAT	GGTCTCGGAA	960
	CTCAGGGGCC	TGCGCACCAT	TGTGACCAAG	CTGCAGGACA	GCATCCGCAA	AGTGACTGAA	1020
	GAGAACAAAG	AGTTGGCCAA	TGAGCTGAGG	CGGCTCTCCC	TATGCTATCA	CAACGGAGTT	1080
	CAGTACAGAA	ATAACAGGGA	ATGAGCTGTT	GATAGCTGCA	CTGAGTGTCA	CTGTGAGAAC	1140
	TCAGTTACCA	TCTGCAAAAA	GGTGTCTCTG	CCCATCATGC	CCTGCTCCAA	TGCCACAGTT	1200
15	CCTGATGGAG	AATGCTGTCC	TGGCTGTTGG	CCCAGGAGCT	CTGCGGACGA	TGGCTGGTCT	1260
	CCATGCTCGG	AGTGGACCTC	CTGTTCTACG	AGCTGTGGCA	ATGGAATTCA	GCAGCGCGGC	1320
	CGCTCTGTGC	AGTTGGCTCA	CAACCGATGT	GAGGGCTCCT	CGGTCCAGAC	ACGGACCTGC	1380
	CACATTACAG	AGTGTGACAA	AAGATTAAAA	CAGGATGGTG	GCTGGAGCCA	CTGTCTCCCG	1440
	TGGTCACTTT	GTCTCTGAC	ATGTGGTGAT	GGTGTGATCA	CAAGGATCCG	GCTCTGCAAC	1500
20	TCTCCAGCC	CCAGATGAA	TGGGAAACCC	TGTGAAGGCG	AAGCGCGGGA	GACCAAGGCC	1560
	TGCAAGAAAG	ACGCTCGCCC	CATCAATGGA	GGCTGGGGTC	CTTGGTCAAC	ATGGGACATC	1620
	TGTTCTGTCA	AGTTGGGAGG	AGGGGTACAG	AAACGTAGTC	GTCTCTGCAA	CAACCCCGCA	1680
	CCCCAGTTTG	GAGCAAGGA	CTGCTTGGT	GATGTAACAG	AAAACAGGAT	CTGCAACAAG	1740
	CAGGACTGTC	CAATTGATGG	ATGCTGTGCC	AATCCCTGCT	TTGCCGCGGT	GAAGTGTACT	1800
25	AGCTACCCGT	ATGCGACGTG	GAAATGTGGT	GCTTGTCCCC	CTGGTTACAG	TGGAAATGGC	1860
	ATCCAGTGCA	CAGATGTTGA	TGAGTGCAAA	GAAGTGCCTG	ATGCCCTGCT	CAACCAACAAT	1920
	GGAGGAGCAC	GGTGTGAGAC	CACGGACCCC	GGCTACAACT	GCCTGCGCTG	CCCCCAACGC	1980
	TTCACCGGCT	CACAGCCCTT	CGGCCAGGGT	GTGGAACATG	CCAACGGCAA	CAACACAGGTG	2040
	TGCAAGCCCC	GTAACCCCTG	CACGGATGGG	ACCCACGACT	GCAACAAGAA	CGCCAACTGC	2100
30	AACTACCTGG	GCCACTATAG	CGACCCCATG	TACCGTGGG	AGTGCAAGCC	TGGCTACGCT	2160
	GGCAATGGCA	TCACTCTGGG	GGAGGACACA	GACCTGGATG	GCTGGCCCAA	TGAGAACCTG	2220
	GTGTGCGTGG	CCAATGGACG	TACCACTGCT	AAAAAGGATA	ATTGCCCCAA	CCTTCCCAAC	2280
	TCAGGGCAGG	AAGACTATGA	CAAGGATGGA	ATTGGTGATG	CCTGTGATGA	TGACGATGAC	2340
	AATGATAAAA	TTCAGATGA	CAGGGACAC	TGTCCATTCC	ATTACAACCC	AGCTCAGTAT	2400
35	GACTATGACA	GAGATGATGT	GGGAGACGCG	TGTGACAACT	GTCCCTACAA	CCACAACCCA	2460
	GATCAGGCAG	ACACAGACAA	CAATGGGGAA	GGAGACGCTT	GTGCTGCAGA	CATTGATGGA	2520
	GACGGTATCC	TCAATGAAAG	GGACAACTGC	CAGTACGCTT	ACAATGTGGA	CCAGAGAGAC	2580
	ACTGATATGG	ATGGGGTTGG	AGATCAGTGT	GACAATTGCC	CCTTGGAAAC	CAATCCGGAT	2640
	CAGCTGGACT	CTGACTCAGA	CGCATTTGGA	GATACCTGTG	ACAACAATCA	GGATATTGAT	2700
40	GAAGATGGCC	ACCAGAACAA	TCTGGACAA	TGTCCCTATG	TGCCCAATGC	CAACCAGGCT	2760
	GACCATGACA	AAGATGGCAA	GGGAGATGCC	TGTGACCACG	ATGATGACAA	CGATGGCATT	2820
	CCTGATGACA	CAGACAACCT	CAGACTGTGG	CCCAATCCCG	ACCAGAAGGA	CTCTGACGGC	2880
	GATGATCGAG	GTGATGCCCTG	CAAAGATGAT	TTTGACCATG	ACAGTGTGCC	AGACATCGAT	2940
	GACATCTGTC	CTGAGAATGT	TGACATCAGT	GAGACCGATT	TCCGCCGATT	CCAGATGATT	3000
45	CCTCTGGACC	CCAAAGGGAC	ATCCCAAAAT	GACCTTAAC	GGGTTGTACG	CCATCAGGGT	3060
	AAAGAACTCG	TCCAGACTGT	CAACTGTGAT	CCTGGACTCG	CTGTAGGTGA	TGATGAGTTT	3120
	AATGCTGTGG	ACTTCAGTGG	CACCTTCTTC	ATCAACACCG	AAAGGGACGA	TGACTATGCT	3180
	GGATTGTGCT	TTGGCTACCA	GTCCAGCAGC	CGCTTTTATG	TTGTGATGTG	GAAGCAAGTC	3240
	ACCCAGTCTT	ACTGGGACAC	CAACCCACCG	AGGGCTCAGG	GATACTCGGG	CCTTTCTGTG	3300
50	AAAGTTGTAA	ACTCCACCAC	AGGGCTTGGC	GAGCACCTGC	GGAAACGCGT	TGGGCACACA	3360
	GGAAACACCC	CTGGCCAGGT	GGCACCCTG	TGGCATGACC	CTGCTCACAT	AGGCTGGAAA	3420
	GATTTACAGC	CTGACAGATG	GGCTCTCAGC	CACAGGCCAA	AGACGGGTTT	CATTAGAGTG	3480
	GTGATGTATG	AAGGGAAGAA	AATCATGGCT	GACTCAGGAC	CCATCTATGA	TAAAACTTAT	3540
	GCTGTGGTGA	GACTAGGGTT	GTTTGTCTTC	TCTCAAGAAA	TGGTGTCTCT	CTCTGACCTG	3600
55	AAATACGAAT	GTAGAGATCC	CTAATCATCA	AATTGTTGAT	TGAAAGACTG	ATCATAAACC	3660
	AATGCTGTGA	TTCACCTTTC	TGGAATCATG	GGCTTGAGAA	AAACCCACAG	ATCACTTCTC	3720
	CTTGGCTTCC	TCTTTTCTTG	TGCTTGCAATC	AGTGTGGACT	CCTAGAACGT	GCGACCTGCC	3780
	TCAGAAAAAT	GCACTTTTCA	AAAAAGAGCT	CATCAGCATT	CAGCCTCCAA	TGAATAGAC	3840
	ATCTTCCAA	CATATAAACA	ATTGCTTTGG	TTTCTTTTGG	AAAAAGCATC	TACTTGCTTC	3900
60	AGTTGGGAAG	GTGCCCATTC	CACCTCTGCT	TTGTACAGAA	GCAGGGTGCT	ATTGTGAGGC	3960
	CATCTCT						3967

Seq ID NO: C7 DNA Sequence

Nucleic Acid Accession #: NM\_002192

Coding sequence: 86..1366

65	1	11	21	31	41	51	
	TCCACACACA	CAAAAAACCT	GGCGGTGAGG	GGGGAGGAAA	AGCAGGGCCT	TTAAAAAGGC	60
70	AATCAACACA	ACTTTTGTCTG	CCAGGATGCC	CTTGCTTTGG	CTGAGAGGAT	TTCTGTGTGGC	120
	AAGTTGCTGG	ATTATAGTGA	GGAGTTCCCC	CACCCACAGG	TCCGAGGGGC	ACAGCGGGGC	180
	CCCCGACTGT	CCGTCTGTGG	CGCTGGCGCG	CCTCCCAAGG	GATGTACCCA	ACTCTCAGCC	240
	AGAGATGGTG	GAGGCGGTCA	AGAAGCACAT	TTTAAACATG	CTGCACCTGA	AGAAGAGACC	300
	CGATGTACCC	CAGCCGGTAC	CCAAGGCGGC	GCTTCTGAAC	GCGATCAGAA	AGCTTCATGT	360
75	GGGCAAGTGC	GGGGAGAAGC	GGTATGTGGA	GATAGAGGAT	GACATTGGAA	GGAGGGCAGA	420
	AATGAATGAA	CTTATGGAGC	AGACCTCGGA	GATCATCAGC	TTTGCCGAGT	CAGGAACAGC	480
	CAGGAAGACG	CTGCACCTTG	AGATTTCCAA	GGAAGGCAGT	GACCTGTCA	TGGTGGAGCG	540
	TGCAGAGATC	TGGCTCTTCC	TAAAGTCCCC	CAAGGCCAAC	AGGACCCAGG	CCAAAGTCAC	600
	CATCCGCTCT	TTCCAGCAGC	AGAAGCACCC	GCAGGGCAGC	TTGGACACAG	GGGAAGAGGC	660
80	CGAGGAAGTG	GGCTTAAAGG	GGGAGAGGAG	TGAACCTGTTG	CTCTCTGAAA	AAGTAGTAGA	720
	CGCTCGGAAG	AGCACCTGCG	ATGCTCTCCC	TGTCTCCAGC	AGCATCCAGC	GGTGTGCTGA	780
	CCAGGGCAAG	AGCTCCCTCG	ACGTTCCGAT	TGCCTGTGAG	CAGTGCCAGG	AGAGTGGCGC	840
	CAGCTTGGTT	CTCTCTGGCA	AGAAGAAGAA	GAAAGAAGAG	GAGGGGGGAG	GGAAAAAGAA	900
	GGCGGAGGTT	GAAGGTGGGG	CAGGAGCAGA	TGAGGAAAAG	GAGCAGTGC	ACAGACCTTT	960
	CCTCATGCTG	CAGGCCCGGC	AGTCTGAAGA	CCACCCTCAT	CGCGGCGCTC	GGCGGGGCTT	1020

5  
10  
15

```

GGAGTGTGAT GGCAAGGTCA ACATCTGCTG TAAGAAACAG TTCTTTGTCA GTTTCAGGA 1080
CATCGGCTGG AATGACTTGA TCATTGCTCC CTCTGGCTAT CATGCCAACT ACTGCGAGGG 1140
TGAGTGCCCG AGCCATATAG CAGGCACGTC CGGGTCCTCA CTGTCCTTCC ACTCAACAGT 1200
CATCAACCAC TACCGCATGC GGGGCCATAG CCCCTTTGCC AACCTCAAAT CGTGCTGTGT 1260
GCCCCACCAAG CTGAGACCCA TGTCCATGTT GTACTATGAT GATGGTCAAA ACATCATCAA 1320
AAAGGACATT CAGAACATGA TCGTGGAGGA GTGTGGGTGC TCATAGAGTT GCCAGCCCCA 1380
GGGGGAAAGG GAGCAAGAGT TGTCCAGAGA AGACAGTGGC AAAATGAAGA AATTTTAAAG 1440
GTTTCTGAGT TAACAGAAA AATAGAAATT AAAACAAAA CAAAACAAA AAAAAACAA 1500
AAAAAACAA AAGTAAATTA AAAACAAACC TGATGAAACA GATGAAACAG ATGAAGGAAG 1560
ATGTGAAAT CTTAGCTTGC CTTAGCCAGG GTCAGAGAT GAAGCAGTGA AGAGACAGAT 1620
TGGGAGGGAA AGGAGAAATG GTGTACCTT TATTTCTTCT GAAATCACAC TGATGACATC 1680
AGTTGTTTAA ACGGGTATT GTCTTTCCTT CCCTTGAGGT TCCCTTGTA GCTTGAATCA 1740
ACCAATCTGA TCTGCAGTAG TGTGACTAG AACACCCAA ATAGCATCTA GAAAGCCATG 1800
AGTTTGAAG GGGCCATCAC AGGCACTTTC CTAGCTAAT 1840

```

Seq ID NO: C8 DNA Sequence

Nucleic Acid Accession #: NM\_000095.1

Coding sequence: 26..2299

20  
25  
30  
35  
40  
45  
50  
55  
60  
65

```

1      11      21      31      41      51
|      |      |      |      |      |
CAGCACCCAG CTCGCCGCCA CGGCCATGGT CCCCAGACAC GCCTGCGTTC TTCTGCTCAC 60
CCTGGCTGCC CTCGCCCGCT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
GCAGATGCTT CCGGAACATGC AGSAAACCAA CGCGGGGCTG CAGGACGTGC GGGACTGGCT 180
GGCGCAGCAG GTCAAGGAGA TCACGTTTCT GAAAAACACG GTGATGGAGT GTGACGCGTG 240
CGGGATGTCAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CGGCCCTCTG TCCACTGCGC 300
GCCCGGCTTC TGTTCGCCCG GCGTGGCCTG CATCCAGACG GAGAGCGGGG GCGCTGCGG 360
CCCTTGCCCC GCGGGCTTCA CGGGCAACGG CTCGCACTGC ACCGACGTCA ACGAGTGCAA 420
CGCCACCCCC TGCTTCCCCC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
GGCTTGCCCC CGGGGTATCA GCGGCCCCAC CCACAGGGC GTGGGGCTGG CTTCGCCAA 540
GGCCACACAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACTGCGT 600
CCCCAATCTC GTGTGCATCA ACACCGGGG CTCTTCCAG TCGCGCCCGT CCGAGCCCGG 660
CTTCGTGGGC GACCAGCGCT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGACGG 720
CTGCCCCAGC GAGTGCCAGC AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTGCGGGTC 780
GTGCGTGTGT CGGTTGGCT GGGCCGGCAA CGGATCCTC TGTGGTGGG ACATGACCT 840
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCGGAGCGCG CAGTGCCTGA AGGACAACTG 900
GTGATGCGG CCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCTG 960
CGATCCGGAT GCCGACGGG ACGGGGTCCC CAATGAAAAG GACAACCTGC CGTGGTGGG 1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGGG ACAACTGCGG 1080
GTCCAGAAAG AACGAGCAC AAAAGGACAC AGACAGGAC GGCOCGGGGG ATGCGTGCGA 1140
CGACGACATC GACGGGACAG GATTCGCAA CCGGGCCGAC AACTGCCCTA GGGTACCCAA 1200
CTCAGACGAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCA 1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACCTGT CCACTGGTCC 1380
TAACATGTCC CAGGGAAGCT CAGACCAAGA TGGCCAGGGT GATGCTGCG ACACGACGGA 1440
CGACATGACG GAGTCCCTG ACAGTGGGGA CAACTGCCGC CTGTGCTCTA ACCCGGCCA 1500
GGAGGACGCG GACAGGGAGC GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACTCTCA CCGACTTCAG 1620
GGCCTTCCAG ACAGTGTGTC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
GGTGTCTAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
GGGTATACCT GCCTTCAATG GCGTGGACTT CGAGGGCAGC TTCCATGTGA ACACGGTCAC 1800
GGATGACGAG TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGCT CTGTGGCCGA 1920
GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCGGGGGAAC AGCTGCGGAA 1980
CGCTCTGTGG CACTACAGG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
AAACGTGGGT TGGAAAGACA AGAAGTCTTA TCGTGTGTTT CTGCAGCACC GGGCCCCAAGT 2100
GGGCTACATC AGGTGCGAT TCTATGAGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
CTTGGACACA ACCATGCGGG GTGGCCGCTT GGGGTCTTCT TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGCTGGGG CAGGCTTAGG GACCAAGGTG AGGACCCGCC GATGACAGC CACCTTACC 2340
GCGGCTGGAT GGGGGCTCTG CACCAGCCCC AAGGGGTGGC CGTCTGAGG GGAAGTGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG 2439

```

Seq ID NO: C9 DNA Sequence

Nucleic Acid Accession #: XM\_057014

Coding sequence: 143..874

70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCTCGGAG 60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCTCGGT CTCTCCGCC TCCAGCTCCG 120
CGCTGCCCGG CAGCGGGAGC CCATGCGACC CCAGGGCCCC GCGCCCTCCC CGCAGCGGCT 180
CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCGCGC CGCTGAGGCG CCTCTGAGAT 240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
AATGTGCTTA CAGGGGCGAG CAGGAGTGCC TGGTCGAGAC GGGAGCCTGT GGGCCAAATG 360
CATTCGCGGT ACACCTGGGA TCCAGGTCC GATGGATTG AAAGGAGAA AGGGGGAATG 420
TCTGAGGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGT CATGGAGTT 480
ATTGAATTAT GGCATAGATC TTGGGAAAT TGCGGAGTGT ACATTTACAA AGATGCGTT 540
AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAATAATGA GAAATGCGAT 600
CTGTGCTTAT TGGTATTTC CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATGTA 660
AGCTATAATT TATTTGAGAC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTATCG 720

```



5  
10  
15

```

CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
CTGGGTGGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
TTCTCGCATC ATTATTGAAG AACTACCCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
TTTTTTTATT ATGCCTTGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTTTGTAGT 1080
TGTTAGAAAT ACTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT 1200
TGTAACAATT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
CAACCTTAAA AAAAAAAAAA AAAA 1284

```

Seq ID NO: C10 DNA Sequence  
Nucleic Acid Accession #: NM\_003225  
Coding sequence: 41..295

20  
25  
30

```

1      11      21      31      41      51
|      |      |      |      |      |
ATCCCTGACT CGGGGTGCGC TTTGGAGCAG AGAGGAGGCA ATGGCCACCA TGGAGAACAA 60
GGTGATGTGC GCCTGTGGTC TGGTGTCCAT GCTGGCCCTC GGCACCCCTG CCGAGGCCCA 120
GACAGAGACG TGTACAGTGG CCCCCCGTGA AAGACAGAAT TGTGGTTTTC CTGGTGTAC 180
GCCCTCCAG TGTGCAATA AGGGCTGCTG TTTGACGAC ACCGTTGCTG GGGTCCCTCG 240
GTGCTTCTAT CCTAATACCA TCGACGTCCC TCCAGAAGAG GAGTGTGAAT TTTAGACACT 300
TCTGCAGGGA TCTGCCTGCA TCCTGAGCGG GTGCCGTCCC CAGCACGGTG ATTAGTCCCA 360
GAGCTCGGCT GCCACCTCCA CCGGACACCT CAGACACGCT TCTGCAGCTG TGCCTCGGCT 420
CACACACAG ATTGACTGCT CTGACTTTGA CTACTCAAAA TTGCCTTAAA AATTAAAGA 480
GATCGATATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 540

```

Seq ID NO: C11 DNA Sequence  
Nucleic Acid Accession #: NM\_015419.1  
Coding sequence: 1..8487

35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCCCAAGC GCGCGCACTG GGGGGCCCTC TCCGTGGTGC TGATCCTGCT TTGGGGCCAT 60
CCGCGAGTGG CGCTGGCCCTG CCGGCATCCT TGTGCCTGCT ACGTCCCAG CCGAGTCCAC 120
TGACGTTCC GATCCCTGGC TTCCGTGCCG GCTGGCATTG CTAGACACGT GGAAAGAATC 180
AATTGCGGGT TTAATAGCAT ACAGGCCCTG TCAGAAACCT CATTTGCAGG ACTGACCAAG 240
TTGGAGCTAC TTATGATTCA CGGCAATGAG ATCCCAAGCA TCCCGATGG AGCTTTAAGA 300
GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT GATCACAGGA 360
CAGACCCCTC AGGGTCTCTC TAACTTAATG AGGCTGCACA TTGACCACAA CAAGATCGAG 420
TTTATCCACC CTCAGCTTTT CAACGGCTTA ACGTCTCTGA GGCTACTCCA TTTGGAAGGA 480
AATCTCTCCC ACCAGCTGCA CCCCAGCACC TTCTCCAGT TCACATTTT GATTATTTC 540
AGACTCTCCA CCATAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCTTCTGCCC 600
AGCATGTCTC GGAACATGCC GCTTCTGGAG AATCTTTACT TGCAGGGAAA TCGCTGGACC 660
TGCGATTGTG AGATGAGATG GTTTTGGGAA TGGGATGCAA AATCCAGAGG AATTCTGAAG 720
TGTAAGAAAG ACAGAGCTTA TGAAGGCGGT CAGTTGTGTG CAATGTGCTT CAGTCCAAAG 780
AAGTTGTACA AACATGAGAT ACACAAGCTG AAGGACATGA CTGTCTGAA GCCTTCAATA 840
GAGTCCCTC TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAAGA ACAGGAAGAG 900
GATGTGTGCA GCCAGCTCAT CCTGGAGAAA TTCCAAGTGC CCCAGTGGAG CATCTCTTTG 960
AATATGACCG AGGAGCAAGG GAACATGGTG AACTTGGTCT GTGACATCAA GAAACCAATG 1020
GATGTGTACA AGTATCACTT GAACCAACCG GATCCTCCAG ATATTGACAT AAATGCAACA 1080
GTTCCTTGGG ACTTTGAGTG TCCAATGACC CGAGAAAACAT ATGAAAAGCT ATGGAATTTG 1140
ATAGCATACT ACAGTGAAGT TCCCGTGAAG CTACACAGAG AGCTCATGCT CAGCAAGAGC 1200
CCCAGAGTCA GCTACCGATA CAGGCAGGAT GCTGATGAGG AAGCTCTTTA CTACACAGGT 1260
GTGAGAGCCC AGATTCTTGC AGAACCAAGG TGGGTCAATG AGCCATCCAT AGATATCCAG 1320
CTGAACCGAG CTACAGTACG GGCCAAGAGG GTGCTACTTT CCTACTACAC CCAATATTCT 1380
CAACAATAT CCACCAAGA TACAAGGCAG GCTCGGGGCA GAAGCTGGGT AATGATTGAG 1440
CCTAGTGGAG CTGTGCAAGG AGATCAGACT GTCTGGAAG GGGGTCCATG CCAGTTGAGC 1500
TGCAACGTGA AAGCTTCTGA GAGTCCATCT ATCTTCTGGG TGCTTCCAGA TGGCTCCATC 1560
GTGAAGCGC CCATGGATGA CCCAGACAGC AAGTTCTCCA TTCTCAGCAG TGGCTGGCTG 1620
AGGATCAAGT CCATGGAGCC ATCTGACTCA GGCTGTGACC AGTGCATTGC TCAAGTGAGG 1680
GATGAAATGG ACCGATGTT ATATAGGGTA CTGTGCAAT CTCCCTCCAC TCAGCCAGCC 1740
GAGAAAGACA CAGTGACAAT TGGCAAGAAC CCAGGGGAGT GGGTGACATT GCCTTGCAAT 1800
GCTTTAGCAA TACCCGAAGC CCACCTTAGC TGGATTCTTC CAACAGAAG GATAATTAAT 1860
GATTTGGCTA ACACATCACA TGTATACATG TTGCCAAATG GAACTCTTTC CATCCCAAAG 1920
GTCCAAGTCA GTGATAGTGG TTACTACAGA TGTGTGGCTG TCAACCAGCA AGGGGCAGAC 1980
CATTTTAGCG TGGGAATCAC AGTGACCAAG AAAGGGTCTG GCTTGCCATC CAAAAGAGGC 2040
AGACGCCAGG GTGCAAGGCG TCCTTCCAGA GTCAGAGAAG ACATCGTGGG GGATGAAGGG 2100
GGCTCGGGCA TGGGAGATGA AGAGAACACT TCAAGGAGAC TTCTGCTATC AAAGGACCAA 2160
GAGGTGTTC TCAAAACAAA GGATGATGCC ATCAATGGAG ACAAGAAAGC CAAGAAAGGG 2220
AGAAAGAAAG TGAACCTCTG GAAGCATTCG GAAAAAGAAC CAGAGACCAA TGTTGCAGAA 2280
GGTGCAGAG TGTTTGAATC TAGACGAAGG ATAAACATGG CAAACAAACA GATTAAATCCG 2340
GAGCGCTGGG CTGATATTTT AGCCAAAGTC CGTGGGAAAA ATCTCCCTAA GGCACAGAA 2400
GTACCCCGT TGATTAAAC CACAAGTCTT CCATCTTGA GCCTAGAAGT CACACCACCT 2460
TTTCTGTCTG TTTCTCCCC CTGACATCTT CCTGTGAGA CAGTAACCAAG TGCTGAAGAA 2520
TCTCAGCAG ATGTACTCTT ACTTGGTGAA GAAGAGCACG TTTTGGGTAG CATTTCTCTA 2580
GCCAGCATGG GGCTAGAAC CAACCAAAAT GGAGTTATTC TTTTGAATCC TGAAGTAACA 2640
AGCACACCTC TGGAGGAAGT TGTGTATGAC CTTTCTGAGA AGACTGAGGA GATRACTTCC 2700
ACTGAAGGAG ACCTGAAGGG GACAGCAGCC CCTACACTTA TATCTGAGCC TTATGAACCA 2760
TCTCTTACTC TGACACATT AGACACAGTC TATGAAAAGC CCACCATGA AGAGACGGCA 2820
ACAGAGGGTT GGTCTGCAGC AGATGTTGGA TCGTCAACAG AGCCCAATC CAGTGAGTAT 2880
GAGCTCCAT TGGATGCTGT CTCTTGGCT GAGTCTGAGC CCATGCAATA CTTTGACCCA 2940
GATTTGGAGA CTAAGTCAAC ACCAGATGAG GATAAGATGA AAGAAGACAC CTTTGACAC 3000
CTTACTCCAA CCCCACCAT CTGGGTTAAT GACTCCAGTA CATCACAGTT ATTTGAGGAT 3060

```

	TCTACTATAG	GGGAACCAAG	TGTCCCAAGC	CAATCACATC	TACAAGGACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAGCTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
	AAAGAGATGT	CTCAGACACT	ACAGGGAGGA	AATATGCTAG	AGGGAGACCC	CACACACTCC	3240
5	AGAAGTTCTG	AGAGTGAAGG	CCAAGAGAGC	AAATCCATCA	CTTTGCCTGA	CTCCACACTG	3300
	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGCGG	AAACCAAGT	TGGTACCCCTC	3360
	CTAGACAAGG	ACACCACAAC	AGTAACAACA	ACACCAAGGC	AAAAAGTTGC	TCCGTCACTCC	3420
	ACCATGAGCA	CTCACCCTTC	TGGAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCAAC	3480
	AAATTCCGCC	ACCGGCACAA	GCAAAACCCA	CCCACAACCT	TTGCCCATC	AGAGACTTTT	3540
10	TCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAA	GTCAAGTGGG	GAGTTCTCTG	3600
	GTTCTCTACG	CTTGGGTGGA	TAAACACAGT	AATACCCCA	AACAGTTGGA	AATGGAGAAAG	3660
	AATGCAGAAC	CCACATCCAA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCCTTCTAC	AGTGAGCTCA	AGAGCGTCCG	GATCCAAGCC	CAGCCCTTCT	3780
	CCAGAAAATA	AACATAGAAA	CATTGTTACT	CCCAGTTTCA	AACTATACT	TTTGCCTAGA	3840
15	ACTGTTTCTC	TGAAAACTGA	GGGCCCTTAT	GATTCCCTAG	ATTACATGAC	AAACCAACGA	3900
	AAAAATATAT	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCCACA	3960
	GCATCTAGAG	AATCAAAATA	AGATGATGTT	GCCACAAATG	TTGACAAACA	TAAAGTGAC	4020
	ATTTAGTCA	CTGGTGAATC	AATTACTAAT	GCCATACCAA	CTTCTGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AATTTAAGGA	AGAATCCTCT	CTGTAGGCT	TTCCAGGAAC	TCCAACCTGG	4140
20	AATCCCTCAA	GGACGGCCCA	GCCTGGGAGG	CTACAGACAG	ACATACCTGT	TACCACCTCT	4200
	GGGGAATAAT	TTACAGACCC	TCCCTTCTT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
	GAGTTTGTG	CCTCTTTGAC	AGTCTCCACA	CCATTTCAAC	AGGAAGAAGC	TGGTCTTCTC	4320
	ACAACCTCTC	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCTT	4380
	GATCAAGATC	ATCTTGAAAC	CACCTGTGCT	ATTCTCCTTT	CTGAAACTAG	ACCACAGAAT	4440
25	CACACCCCTA	CTGCTGCCCG	GATGAAGGAG	CCAGCATCCT	CGTCCCATC	CACAATCTCT	4500
	ATGTCTTTGG	GACAAACAC	CACCACTAAG	CCAGCACTTC	CCAGTCCAAG	AATATCTCAA	4560
	GCATCTAGAG	ATTCCAAGGA	AAATGTTTTC	TTGAATTATG	TGGGGAATCC	AGAAACAGAA	4620
	GCAACCCGAG	TCAACAATGA	AGGAACACAG	CATATGTCTG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCCG	ACCGGGATGC	ATTTAACTTG	TCTACAAAGC	TGGAATTGGA	AAAGCAAGTA	4740
30	TTTGTAGTA	GGAGTCTACC	ACGTGGCCCA	GATAGCCAAC	GCCAGGATGG	AAGAGTTCAT	4800
	GCTTCTCATC	AACATACAC	AGTCCCTGCC	AAACCCATCC	TACCAACAGC	AACAGTGAGG	4860
	CTACCTGAAA	TGTCCACACA	AAGCGCTTCC	AGATACTTTG	TAACTTCCCA	GTCACCTGT	4920
	CACCTGGACCA	ACAAACCGGA	AATAACTACA	TATCCTTCTG	GGGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACAA	CTCCAGATTT	ATCAAGTACA	ACAATTCCTC	TCCCATTGCA	CATGTCCAAA	5040
35	CCACAGATTC	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AATTCATAGG	TTACTCCAAA	5100
	GTGTTTGAAA	ATAACAACAT	CCCTGAGGGA	AGAAACCCAG	TTGGAAGGCC	TCCAGTCCCA	5160
	AGAAATCCGC	ATTATTCCAA	TGGAAGACTC	CCTTTCTTTA	CCAACAAGAC	TCTTTCTTTT	5220
	CCACAGTTGG	GAGTCAACCG	GAGACCCACG	ATACCCACTT	CTCCTGCCCC	AGTAATGAGA	5280
	GAGAGAAAAG	TTATTTCCAGG	TTCTTCAAC	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
40	GACTTTGGCC	CTCCGCAACC	TCCGTTGTTG	CACACTCOGC	AGACCAAGGG	ATACCCCTCA	5400
	ACTAAGCTTAC	AGAAATCCCC	TATGTTCTCT	TCCACCCAGA	GTTCTATCTC	CTTTATAACA	5460
	TCTTCTGTTC	AGTCTTACAG	AAGCTTCCAC	CAGAGCAGCT	CAAGTTCTT	TGCAGGAGGA	5520
	CCTCTGCTAT	CCAATTTCTG	GTCTCTTGGG	GAAAGGCCCC	AAATCCTCAC	CAAGTCCCCA	5580
	CAGACTGTGT	CCGTCAACCG	TGAGACAGAC	ACTGTGTTCC	CCTGTGAGGC	AACAGGAAAA	5640
45	CCAAAGCCTT	TCGTACTTGG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAATACC	5700
	AGGATACAA	GGTTTGAAGT	TCTCAAGAAC	GGTACCTTAG	TGATACGGAA	GGTTCAAGTA	5760
	CAAGATCGAG	GCCATATATG	GTGCAACGCG	AGCAACCTGC	ACGGCTTGGG	CAGGATGGTG	5820
	GTCTTGCTTT	CGGTACCCGT	GCAGCAACCT	CAAATCCTAG	CCTCCCACTA	CCAGGACGTC	5880
	ACTGTCTTACC	TGGGAGACAC	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCCAGCCCCC	5940
50	CAAAATTTCT	GGATCTTCCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	CGCATCACCC	TGCAAGAAA	CCGACCCCTT	TCCATCAAGG	AGGCGTCTTT	CTCAGACAGA	6060
	GGCGTGTGTC	CGCGCTGGG	CAGCAATGCA	GCCGGGGCGG	ACAGCTGGGC	CATCCGCTCG	6120
	CACGTGGCGG	CAGTGGCCCC	CGTTATCCAC	CAGGAGAGGC	TGGAGAACAT	CTCGTGGCCC	6180
	CCGGGGCTCA	GCATTACAT	TCACTGCACT	GCCAAGGCTG	CGCCCCCTCC	CAGCGTGGCC	6240
55	TGGGTGCTCG	GGGACGGTAC	CCAGATCOGC	CCCTCGCAGT	TCTCCACGG	GAACCTGTTT	6300
	GTTTTCCCCA	ACGGGACGCT	CTACATCOGC	AACTCGCGC	CCAAGGACAG	CGGGCGCTAT	6360
	GAGTGGGTGG	CGCCCAACTC	GGTAGGCTCC	GCGCGCAGGA	CGGTGCACTG	GAACGTGCGA	6420
	CGTGACGAG	CCAACGCGCG	CATCACGGGC	ACCTCCCGCG	GGAGGACGGA	CGTCAGGTAC	6480
	GGAGGAACCC	TCAAGCTGGA	CTGCAGCGCC	TCCGGGGACC	OCTGGCGCGC	CATCCTCTGG	6540
60	AGGCTGCGCT	CCAAGAGGAT	GATCGACGCG	CTCTTCAGTT	TTGATAGCAG	AATCAAGGTG	6600
	TTTGCCAATG	GGACCTGGT	GGTGAATCA	GTGACGGACA	AAGATGCGCG	AGATTACCTG	6660
	TGCGTAGCTC	GAAATAAGGT	TGGTGATGAC	TACGTGGTGC	TCAAAGTGGA	TGTGGTGATG	6720
	AAACCGGCCA	AGATTGAACA	CAAGGAGGAG	AACGACCACA	AAGTCTTCTA	CGGGGTGAC	6780
	CTGAAAGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCG	AGATCTCCTG	GAGCCTCCCA	6840
65	GACGGGAGTC	TGGTGAATCT	CTTCATGAC	TCCGATGACA	GCGGTGGAGC	CACCAAGCGC	6900
	TATGTGCTCT	TCAACAATGG	GACACTCTAC	TTTAAAGGAG	TGGGGATGAG	GGAGGAAGGA	6960
	GACTACACCT	GCTTTGCTGA	AAATCAGGTC	GGGAAGGACG	AGATGAGAGT	CAGAGTCAAG	7020
	GTGGTGACAG	CGCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGGTTC	GGTGCCTTAT	7080
	GGAGACGTGG	TCACTGTAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
70	TTGTCCCAAA	CCAACAAGGT	GATCCCCACC	TCCTCTGAGA	AGTATCAGAT	ATACCAAGAT	7200
	GGCACTCTCC	TTATTACAGAA	AGCCACGCGT	TCTGACAGCG	GCAACTACAC	CTGCCCTGGT	7260
	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	7320
	AAGATCAACG	GTAACCCCAA	CCCCATCACC	ACCGTGCGGG	AGATAGCAGC	CGGGGGCAGT	7380
	CGGAAACTGA	TTGACTGCAA	AGCTGAAGGC	ATCCCCACCC	CGAGGGTGT	ATGGGCTTTT	7440
75	CCGAGGGGTG	TGGTTCTGCC	AGCTCCATAC	TATGAAACCC	GGATCACTGT	CCATGGCAAC	7500
	GGTTCCCTGG	ACATCAGGAG	TTTGAGGAAG	AGCGACTCOG	TCCAGCTGGT	ATGCATGGCA	7560
	CGCAACGAGG	CGGGGAGGCG	GAGGTTGATC	GTGCAGCTCA	CTGTCTGGA	GCCCATGGAG	7620
	AAACCCATCT	TCCACGACCC	GATCAGCGCG	AAGATCACGG	CCATGGCGGG	CCACACCATC	7680
	AGCCTCAACT	GCTCTGCGCG	GGGGACCCCG	ACACCCAGCC	TGGTGTGGGT	CCTTCCCAAT	7740
80	GGCACCGATC	TGCAGAGTGG	ACAGCAGCTG	CAGCGCTTCT	ACCACAGGCG	TGACGCGCATG	7800
	CTACACATTA	GCGGCTCTCT	CTCGGTGGAC	GCTGGGGCCT	ACCGCTGCGT	GGCCCGCAAT	7860
	CGCGTGGGCC	ACACGAGAGG	GCTGGTCTCC	CTGAAGGTGG	GACTGAAGCC	AGAAGCAAAC	7920
	AAGCAGTATC	ATAACCTGGT	CAGCATCATG	AATGGTGAGA	CCCTGAAGCT	CCCTGCACCC	7980
	CCTCCCGGGG	CTGGGCGAGG	ACGTTTCTCC	TGGACGCTCC	CCAATGGCAT	GCATCTGGAG	8040
	GGCCCCAAAA	CCCTGGGAGG	GTTTCTCTT	CTGGACAATG	GCACCTTCAC	GGTTCGTGAG	8100

5  
10  
15  
20  
25

```

GCCTGGTGT TTGACAGGGG TACCTATGTA TGCAGGATGG AGACGGAGTA CGGCCCTTGG 8160
GTCACCAGCA TCCCGTGTAT TGTGATCGCC TATCCTCCCC GGATCACCAG CGAGCCCACC 8220
CCGGTCACTC ACACCCGGCC CGGGAACACC GTGAAACTGA ACTGCATGGC TATGGGGATT 8280
CCCAAAGCTG ACATCACGTG GGAGTTACCG GATAAGTCGC ATCTGAAGGC AGGGGTTTCA 8340
GCTCGTCTGT ATGGAACAG ATTTCTTAC CCCAGGGAT CACTGACCAT CCAGCATGCC 8400
ACACAGAGAG ATGCCGGCTT CTACAAGTGC ATGGCAAAAA ACATTCTCGG CAGTGACTCC 8460
AAAAACAATT ACATCCACGT CTTCTGAAAT GTGGATTCCA GAATGATTGC TTAGGAACTG 8520
ACAACAAAGC GGGGTTTGTG AGGGAAGCCA GGTGGGGGAA TAGGAGCTCT TAAATAATGT 8580
GTCACAGTGC ATGGTGGCCT CTGGTGGGTT TCAAGTTGAG GTTGATCTTG ATCTACAATT 8640
GTTGGGAAAA GGAAGCAATG CAGACACGAG AAGGAGGGCT CAGCCTTGCT GAGACACTTT 8700
CTTTTGTGTT TACATCATGC CAGGGGCTTC ATTCAGGGTG TCTGTGCTCT GACTGCAATT 8760
TTTCTTCTTT TGCAAAATGC ACTCGACTGC CTTCATAAGC GTCCATAGGA TATCTGAGGA 8820
ACATTACATCA AAAATAAGCC ATAGACATGA ACAACACCTC ACTACCCCAT TGAAGACGCA 8880
TCACCTAGTT AACCTGTGTC AGTTTTTACA TGATAGACTT TGTCCAGAT TGACAAGTCA 8940
TCTTTAGATT ATTTCTCTGT TCACCTCAA ACTCCAGCTT GCCCAATAAG GATTTAGAAC 9000
CAGAGTGACT GATATATATA TATATATTTT AATTCAAGT TACATACATA CAGCTACCAT 9060
TTTATATGAA AAAAGAAAAA CATTCTTCC TGGAACTCAC TTTTATATA ATGTTTTATA 9120
TATATATTTT TTCTTTCAA ATCAGACGAT GAGACTAGAA GGAGAAATAC TTTCTGTCTT 9180
ATTAAAAATA ATAAATTATT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA 9240
ATATAATTTT AAAAATTTTC TCTCCAACCT CCTTCAAATT CAGTACCAC TGTATATTA 9300
CCTTCTCCAG GAACCTTCCA GTGGGGAAGG CTGCGATATT AGATTTCCTT GTATGCAAG 9360
TTTTTGTGTA AAGCTGTGCT CAGAGGAGAG GAGAGGAGAA GAAGGAGAAA ACTGCATCAT 9420
AATCTTACAG AATTGAATCT AGAGTCTTCC CCGAAAAGCC CAGAACTTC TCTGCAGTAT 9480
CTGGCTGTGC CATCTGTGTC AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC 9540
CCATGAATAA TACACGACCT GTTATTCCA TGACTGCTT ACTGTATTTT TAAGTCAAT 9600
ATACTGTACA TTTGATAATA AAATAATATT CTCCAAAAA AAAAA 9645

```

30 Seq ID NO: C12 DNA Sequence  
Nucleic Acid Accession #: AK001903  
Coding sequence: none

35  
40  
45  
50  
55  
60  
65  
70

```

1 11 21 31 41 51
TATCATGCAT GTGGGAAGGT GGGTGTGGTG AGAAAAAGTTT TAAGGCAAGA GTAGATGGCC 60
ATGTTCAACT TTACAAATTT TCTTGGAAAA CTGGCAGTAT TTTGAAGTGC ATCTCTTTTG 120
GTACCGGAAC CTGCAGAAAC AGTGTGAGAA ATTAAGTCCT GGTTCAGTGC GCAGTAGCAA 180
AGATGGTCAA GGCCATGGAA AAAGCAGAAA TTTACCAAGA AAGCTGTATC CCATGTATAG 240
TTCCCACTCA TCTCAATATC ATCTGCTATC TTTTAAAGCT AAGTCTTAGA CATATCGGGG 300
ATAACATGGG GGTGATTAG TGACCACAGT TATCAGAAGC AGAGAAATGT AATTCATAT 360
TTTATTGAA ACTTATTTCA TATTTAATT GGATATTGAG TGATTGGGTT ATCAACACC 420
CACAAACTTT AATTTTGTTA AATTTATATG GCTTTGAAAT AGAAGTATAA GTTGCTACCA 480
TTTTTGTATA ACATTGAAAG ATAGTATTTT ACCATCTTTA ATCATCTTGG AAAATACAAG 540
TCCTGTGAAC AACCACCTCT TCACCTAGCA GCATGAGGCC AAAAGTAAAG GCTTTAAATT 600
ATAACATATG GGATTCTTAG TAGTATGTTT TTTTCTGAA ACTCAGTGGC TCTATCTAAC 660
CTTACTATCT CCTCACCTTT TCTCTAAGAC TAACTCTAG GCTCTTAAAT ATCTGCCAC 720
ACCAATCTTA GAAGCTCTGA AAAGAAATTG TCTTTAATA TCTTTAATA GTAACATGTA 780
TTTTATGGAC CAATTTGACA TTTTCGACTA TTTTCTCAA AAAAGTCAGG TGAATTTTCA 840
CACACTGAGT TGGGAATTTT TTATCCAGA AGACCAACCA ATTTCAATAT TATTAAAGAT 900
TGATTCCATA CTCGTTTTC AAGGAGAATC CTGCAGTCT CCTTAAAGGT AGAACAAATA 960
CTTCTATTTT TTTTCTTCC CATTTGGGGA TTGACTTTA AGAGGTGACT CTAAAAAAC 1020
AGAGAACAAA TATGCTCAG TTGTATTAG CACGGACCCA TATTATCATA TTCACTTAAA 1080
AAAATGATT CCTGTGCACC TTTTGGCAAC TTCTCTTTTC AATGTAGGGA AAAACTTAGT 1140
CACCTGAAA ACCCAAAAAA TAAATAAAAC TTGTAGATGT GGGCAGAGG TTTGGGGGTG 1200
GACATTGTAT GTGTTTAAAT TAAACCTGT ATCACTGAGA AGCTGTGTTA TGGGTGAGAG 1260
AAAATGAAGT CTTGAAGCT GTTCACTCT TCAAGACAG AAGCAACCA CATGTCTCAG 1320
CTATATTATT ATTTATTTT TATGCATAAA GTGAATCAT TCTTCTGTAT TAAATTTCAA 1380
AGGGTTTAC CCTCTATTTA AATGCTTTGA AAAACAGTGC ATTGACAATG GGTGTATATT 1440
TTTCTTAAA AGAAAAATAT AATTATGAAA GCCAAGATAA TCTGAAGCCT GTTTTATTTT 1500
AAAACTTTT ATGTTCTGTG GTTGTATGTT TTTGTTGTT TGTTCCTATT TTGTTGGTTT 1560
TTTACTTTGT TTTTGTGTTT GTTTGTTT GTTTTGCATA CTACATGCAG TTCTTTAACC 1620
AATGCTGTT TGGCTAATGT AATTAAAGTT GTTAATTTAT ATGAGTGCAT TTCAACTATG 1680
TCAATGGTTT CTTAATATT ATTTGTGAGA AGTACTGGTA ATTTTATAT TTACAATATG 1740
TTTAAAGAGA TAACAGTTTG ATATGTTTTC ATGTGTTTAT AGCAGAAGTT ATTTATTTCT 1800
ATGGCATTC ACCTGATATT TTGGTGTGTC CAGGAGATGC AGTCAATATT TTGTACAGTT 1860
AGTGACAGT ATTCAGCAAC GCCTGATAGC TTCTTTGGCC TTATGTTAAA TAAAAAGAC 1920
TGTTTGGGAT GT 1932

```

75 Seq ID NO: C13 Protein Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..5001

75  
80

```

1 11 21 31 41 51
ATGCCAGGCA CAAAACTAAC CCGAACAGGC GCCCCAGCAG ACTACAGAGT GATATTGAAG 60
ACCTCTCAAG AGGACGAATT GGATGTACCT GACGACATCA GCGTCCGGT TATGTCTACT 120
CAGTCTGTGC TTGTGTCCTG GGTGGATCCT GTTCTGGAAA AACAGAAGAA AGTTGTTGCA 180
TCAAGACAGT ACACCGTGGC CTATCGAGAG AAGGGGGAAT TGGCCAGGTG GGATTATAAG 240
CAGATCGCTA ACAGGCGTGT GCTGATTGAG AACCTGATTC CAGACACTGT GTATGAATTT 300
GCACTCCGTA TTTCAAGGG TGAAAGAGAT GGCAAAATGA GTACGTCACT CTCCAAAGA 360
ACACCAGAAT CTGCCCTTAC CACAGCTCCT GAAAACCTGA ACGTCTGGCC AGTCAATGGC 420
AAACCTACAG TTGTGCTGTC ATCTTGGGAT GCGCTACCAG AGACTGAGGG GAAAGTGAAA 480
GTCGTCTGTC TGGACACAGG ACTGTTTCA GTTCTCTCCT TCCAACCATC TGCCAAATCA 540

```

	TTTCAGAATA	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTGGAGCA	AAGTCCTCA	600
	CCTATCTCGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAACGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
5	TGCTATGTC	AACAAGAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
	ATCGATATCC	AAACCAAAAC	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
	CCATGTTTTT	TTTTCTACTT	CCTCACATTT	ATGCTGGATA	TTGGCGGCTT	TTCTTTCATT	900
	ATGTGCTATG	AAGACCCANN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACCTGAG	1020
10	CCTTCTCTAC	CTTCTCCGAG	AGTCCAGCT	TCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGCGC	CCCGAAAACC	CCAGCTTGCG	GCCAAGAAGG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCATGCGGGA	GGAGGAGCTG	GGTTCCCGGG	AGGACTCGCC	CATGTACACC	1260
	TCAGACACCC	AAGACCGAA	ACGGACCTTG	AGGCGCGCAA	GTAGACACGG	CCACTCGGTG	1320
15	GTGTCTCCCG	GACGAGCTGC	AGTGAGGGCC	CGGATGCCAG	CGCTGCCCGG	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCCGCC	CAGGGGGGCC	CCCTCGGCT	1440
	TCGGCTCTCT	TCGCCACCCA	CGGTCACACC	CAGGGCACCT	CTCATGCTCC	TTCCCTGCTT	1500
	GCCAGCTTGA	ATGACAAACA	CTTGCTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCGCTTT	CGCCAGCCCT	CGGCCAGCCC	TGTCCCCAG	CCGCCAGTCC	1620
20	CGCTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGACCCCG	CGCAAAAGCC	AGCTCGCGG	1680
	GCGCGGAGGA	CCCCCAATTC	AGGGGCGCGA	GAGGAAGATT	CCAGTGCCCTC	AGCCCCACCC	1740
	TCAGACTTTT	CTCCACCCCA	TGGGGATCA	TCTCGGCTGC	TGCCACCCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAAGGG	CGGGAAGSAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	GCAGCATCAC	GGTCCACCAT	GTCTCTCTCC	GTCTCTTCTC	ATCTCTCGTC	CAGGACGCG	1920
25	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGGCGA	TAGGGAAGAC	1980
	GCGGGAAGGG	AGGCGGAGGC	CACGGCCACG	ACGCTGCGGG	CCCGGCTGTC	CTCTGACAC	2040
	TTCCATTTGC	TCAGACACAA	ACCTTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTTCAG	2100
	ATTGGGCGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCTCCCGAT	2160
	GCCCCACCCA	GGGTTCCCTC	TCACCTGAT	TCCACCCCTA	AGCTTAGCTC	AGGTATCCAT	2220
30	GGAGACGAGG	AGAGTGAGAA	GCCGCTTCTC	GCCACCGTTG	TCAATGACCA	CGTGCTCTCC	2280
	TCTCTCAGGC	AGCCCATCTC	CCGGGCTTGG	GAGGACTTAA	GGAGAAGCCC	GCAGAGAGGG	2340
	GCCAGCTGCG	ATGCGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
	CATCTCTCAG	GCAAGTACTC	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTCA	ACAGAGCACA	2460
	GACGCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CCGCCACGGG	2520
35	TCCCTCTGCT	GTCTCTCCGC	AGCACGGTCA	CAGCAGATC	CCAGTGTTC	CAGAAAGGATG	2580
	ACACCCGCGC	GGGCCCCAGA	ACAGCAGCCC	CCTCTCTCCG	TGCCACGTC	CCAGCACCCAC	2640
	CCGGGACCTC	AGAGCAGAGA	CGGGGCTGG	TCACCTTCCC	AGCCAGGCT	CTCACTGACC	2700
	CAGGCGGGGC	GGCCCCGGCC	CAGCTGCGAG	GGCGCTCCCC	ACTCTCTCTC	GGACCTTAC	2760
	ACGGCGAGCT	CCAGAGGGAT	GCTCCCCACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCCG	2820
40	GGCAGCTACG	AGAGCGACAG	CACAGAAGTC	GAGGCCCCAG	ATGTGCGGGC	CCCGCGGCAC	2880
	GCCGCGCGCG	CCAAGGAGGC	AGCTGCTGCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
	ACAGGCGCAG	GGGCGGTTGG	GCACACAGG	TCCACGGCGG	GACATGCGGC	CTCCCCCGCC	3000
	AGGCCACGCC	GACCCGCGCG	CCCCCATGCC	CGCGCCCGGG	TCCCCAGCAG	GGCAGCGCGG	3060
	GGGAAGTGGG	AGCCTCTCTC	CAGCGGGCCC	CTGTCTTCCA	AGTCCCAGCA	GTCCGCTCTA	3120
45	CCGAGGACCG	AGGAGGAGGA	GGACGCGGGG	TTTTTTAAAG	GCGGGAAGA	AGACCTTCTG	3180
	CTTCTCTCTG	TGCCAAAGTG	GCCCTCTTCC	TCCACTCCCA	GGGGCGGCAA	AGACGCGCAT	3240
	GGGAGCCTCG	CCAAGGAAGA	GAGGGAGCCT	GCCATCGCGC	TTGCCCTCG	CGGAGGGAGC	3300
	CTGGCTCTCG	TGAAGCGACC	TCTCCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCTCTCCAC	3360
	GTCCCTTCCC	GACCGCGCGC	TGCGAGCGCT	GCCACCGTGA	GCCCGCTGCG	GGGCACCCAC	3420
50	CCCTGGCGCG	GGTACACCC	GGCGCGCCCV	CCTGGCCACT	TCTCCACAC	CCCGATGCTG	3480
	TCCTTGCGCG	AGAGGATGAT	GCATGCCAGA	TTCCGTAAAC	CTCTCTCCCG	ACAGCCTGCC	3540
	AGACCTCTCT	ACAGACAAGG	TTATAATGGC	AGACCAAATG	TAGAAGGGAA	AGTCTCTCT	3600
	GGTAGTAATG	GAAGACCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GTGTGGAGCT	TTGATCGTGG	GTATGATTAT	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
55	CATGGAATTC	CTCTTGGGAT	TAAACTAGGA	GGAGATGGTC	GAACCAATTG	AGATCTGGAA	3780
	GGGACCCCGG	TGCTGAGTCC	TGACGGCTCT	CCACTCTTTG	GGCAGGGGGG	ACATGGGACA	3840
	CCTCTGGCCA	ATGCGCAAGA	TAGGCCAATT	TTGAGTCTTG	GAGGAAGGCC	GCTGGTGGGC	3900
	TTGGAGGTCA	TCAAAAAAAC	CACCCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
	ACGACGCCCC	TGCTTACCAC	TACAACCCCG	AGGCCACCCA	CTGCCACCAC	CATGCAGCCC	4020
60	ACCACTACTA	CGACGCCCC	GCCTACCACT	ACACCGAGGC	CCACCACTGC	CACCAACCCG	4080
	CGCACGACCA	CCAGGGGCTC	AACAACCAAC	GTCCGAACCA	CTAGCGGAC	AACCAACACC	4140
	ACCAACCCCA	AACCCACCAC	TCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAAACGGAC	4200
	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260
	GATGAGTTCT	CAGGCTTGG	GACTGACACT	GCAGTAOCTA	CGGAAGAGGC	CTACGTTATA	4320
65	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCAA	CCACCACTGA	GCCTTGGACC	4380
	ACTGCTACCA	CACCGAGGGT	GATCCAGAG	GAAGGCGCCA	TCAGTTCCCT	TCCTGAAGAA	4440
	GAATTTGATC	TGGCTGGAAG	GAAACGATTT	GTGCTCCTT	ACGTGACGTA	CCTAAATAAA	4500
	GACCCATCAG	CCCCGTGCTC	TCTGACTGAT	GCATGGATC	ACTTCCAAGT	GGACAGCCTG	4560
	GATGAATACA	TCCCCAATGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCCGC	4620
70	AACATCACCG	TGGTGGCCGT	GGAAGGTTGC	CACTCATTGT	TCATTGTGGA	TTGGGACAAA	4680
	GCCACCCCGA	GAGATTGGT	CACAGGTTAT	TTGGTTTACA	GTGCATCCTA	TGAAGATTTC	4740
	ATCAGGAACA	AGTTTTCAC	TCAAGCTTCA	TCAGTAACCT	ACTTGCCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCAIT	TGTCACCGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGGCC	4920
75	CCAGGCGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAACAA	TGATCCGACT	TACACGGACT	4980
	GCCATGGAGC	GCAATATGTG	AAGCGCAGCT	GGTATCGAAA	GTTCGTGGGA	GTGTCTTTT	5040
	GTAATTTACT	GAGGTATAAA	ATCTACCTCA	GTGACAACCT	GAAAGATACA	TTCTACAGCA	5100
	TTGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAAGGC	TACTATCGCC	5220
80	AGTATCTGTA	GGAGCCTGTC	AGGTTTGGGA	ACATGGGCTT	CGGAACCCCG	TACTACTATG	5280
	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAGGTG	GTAATCACAG	GACCGTCACT	5340
	CTCAGACTCT	GCCTCGCCCA	GCCCAACCAA	CTAAGTOGCA	CTAGGGGCTG	TGAGCAAGA	5400
	CAGCCAGCAT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCAAGAT	GGACACTGGC	5460
	CATTCTGGTC	ATCTCAGTCT	GGAACTCAGT	CCCACTTCTT	GGCCTGGACA	ATGAACAGGA	5520
	TTCACTTTTG	CTGTTAACTT	TGCTTCTCTA	CTTTTTTTTG	TTTGTGTGTA	ATAGCACATC	5580

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65

CCAGAGACAT CAGAAACCAG CAACTGATTC AGTGTGATT CCCAGACTTT TTAGGCATGA 5640  
AATTCCGACA CTTCAGTATT TCCAGGAATA GCATATGCAC GCTGTTCTTG CTTCATGGAA 5700  
TGCTACATGC TTCTGTGTTT TCTCATTTTG GATTCTCCA AACTAAGCT AATTAAAGCT 5760  
TCAGGTCCCT TTGTATGCG TAGAAAGGAA TTATTAAGAA CACCACCAA GAAATAAAT 5820  
ATATCTACT TGAATTTAC TCTATGGACT TACCACTGC TAGAATAAAT GTATCAAATC 5880  
TTATTGTAA ATTCTCAATT TTGATATATA TATGTATATA TGCATATACA TATCCACACT 5940  
TGCTGCAAG AATATTGATT AAAATTGCTA AATTGTACT TGTTCACCAA AAAAAAAAAA 6000  
AAAAAA 6007

Seq ID NO: C14 DNA Sequence  
Nucleic Acid Accession #: NM\_003014  
Coding sequence: 238..1278

15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65

1 11 21 31 41 51  
GGCGGGTTCG CGCCCCGAAG GCTGAGAGCT GGCGCTGCTC GTGCCCTGTG TGCCAGACGG 60  
CGGAGCTCCG CGGCCGGACC CGCGGGCCCC GCTTTGCTGC CGACTGGAGT TTGGGGGAAG 120  
AAACTCTCCT CGCCCCAGA AGATTCTTTC CTGCGGAAG GGACAGCGAA AGATGAGGGT 180  
GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTGCGAG CGCAGAGAGG CAGTGCCATG 240  
TTCTCTCCA TCCTAGTGGC GCTGTGCTTG TGGCTGCACC TGGCGCTGGG CGTGGCGGG 300  
GGCGCCCTGG AGCGGTGGG CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCACGGG 360  
ATGCCCAACC ACCTGCACCA CAGCAGCGAG GAGAAAGCCA TCCTGGCCAT CGAGCAGTAC 420  
GAGGAGCTGG TGACGTGAA CTGCAGCGCC GTGCTGGCT TCTCTTCTG TGCCATGTAC 480  
GCGCCCATTT GCACCTGGA GTTCTGTCAC GACCTATCA AGCCGTGCAA GTCGGTGTGC 540  
CAACGCGCGC GCGACGACTG CGAGCCCTTC ATGAAGATGT ACAACCACAG CTGGCCCGAA 600  
AGCTGGCTCT GCGACGAGCT GCTGTCTAT GACCGTGGG TGTGCATTT GCCTGAAGCC 660  
ATCGTCAAGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACAGA CATGATGGTA 720  
CAGGAAGGCG CTCTGTATGT TGACTGTAAA CGCTAAGCC CGATCGGTG CAAGTGTAAA 780  
AAGGTGAAGC CACTTTGGG AACGTATCTC AGCAAAACT ACAGCTATGT TATTCATGCC 840  
AAAATAAAGC CTGTGAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900  
GAGATCTTCA AGTCCCTATC ACCCATCCCT CGAACTCAAG TCCCGCTCAT TACAAATCT 960  
TCTTGCCAGT GTCCACACAT CCGCCCCAT CAAGATGTT TCATCATGTG TTACAGTGG 1020  
CGTTCAGGA TGATGCTTCT TGAAAATTGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080  
AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140  
AAGAAACAG CCGGGCGCAC CAGTCGTAGT AATCCCCCA AACCAGAGG AAGCCCTCCT 1200  
GCTCCCAAC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGGCCA GAAGAGAAC 1260  
AACCCGAAA GAGTGTGAGC TAACTAGTTT CCAAGGGGGA GACTTCCGAC TTCCTACAG 1320  
GATGAGGCTG GGCATTGCTT GGGACAGCCT ATGTAAGGCC ATGTGCCCTC TGCCCTAAC 1380  
ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTTCTTAAG CTATGCTTCA 1440  
GTTTTCTTT GTAAGCCATC ACAAGCCATA GTGTAGGTT TGCCCTTTGG TACAGAAGGT 1500  
GAGTTAAAGC TGGTGAAGAA GGCCTATTGC ATTGCATTCA GAGTAACTG TGTGCATACT 1560  
CTAGAAAGT AGGGAATAAT ATGCTTGTTA CAATTCGACC TAATATGTGC ATTGTAAAT 1620  
AAATGCCATA TTTCAAACAA AACACGTAAT TTTTACAG TATGTTTAT TACCTTTGA 1680  
TATCTGTGT TGCAATGTTA GTGATGTTT AAAATGTGAT GAAATATAA TGTTTTAAAG 1740  
AAGGAACAGT AGTGAATGA ATGTTAAAG ATCTTTATGT GTTTATGGTC TGCAGAGGA 1800  
TTTTTGTGAT GAAAGGGGAT TTTTGAAGAA ATTAGAGAAG TAGCATATGG AAAATTATA 1860  
TGTGTTTTT TACCAATGAC TTCAGTTTCT GTTTTGTAGT AGAACTTAA AAAAAAAT 1920  
AATAATAAG AAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATT CTGTTTTTG 1980  
GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACCAGAA 2040  
ACAGTGAAT TGTCTGTACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100  
ATTTATACC CACAAGAGAG GTATGTCACT CATCTTACT CCCAGGACAT CCACCTGAG 2160  
AATAATTGA CAAGCTTAA AATGGCCTTC ATGTGAGTGC CAATTTTGT TTTTCTTCT 2220  
TTAAATATT TCTTTGCTTA AATACATGTG AGAGGAGTAA AATATAATG TACAGAGAG 2280  
AAAGTTGAGT TCCACCTCTG AATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340  
AAAAGAACT TATTGCGAGC ATTTTATCAA CAAATTTCT AATTGTGGAC AATTGGAGGC 2400  
ATTTATTTA AAAACAATT TTATTGGCCT TTTGCTAACA CAGTAAGCAT GTATTTTATA 2460  
AGGCATTCAA TAAATGCACA ACGCCCAAAG GAAATAAAT CCTATCTAAT CCTACTCTCC 2520  
ACTACACAGA GGTAACTCACT ATTAGTATT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580  
GCATTATAA AATGATTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640  
CTGCTCCTT TGCTTGGGCC TTTATTGAGA TAAGTTTCC TGTCAAGAAA GCAGAAACCA 2700  
TCTCAATTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760  
TATTGGATAC TTAGGTGTT TCTTCACTGA CAATACTGAA TAAACATCTC ACCGGAATTC 2820

Seq ID NO: C15 DNA Sequence  
Nucleic Acid Accession #: NM\_005940  
Coding sequence: 23..1489

70  
75  
80

1 11 21 31 41 51  
AAGCCCCAGCA GCCCGGGGGG GGATGGCTCC GGCGGCTGCG CTCCGAGCG CGGCCCGCG 60  
CGCCCTCTCT CCCCAGATGC TGCTGCTGCT GCTCCAGCCG CGCCCGCTGC TGGCCCGGG 120  
TCTGCGCGCG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180  
AGCCCTGCC AGTAGCCCGG CACCTGCCCC TGCCACGCGA GAAGCCCCCG GGCTGCCAG 240  
CAGCCTCAGG CCTCCCGGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300  
CCGACAGAA AGGTGTGTGC TTTTGCGCGG GCGCTGGGAG AAGACGAGAC TCACCTACAG 360  
GATCCTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGCAGACAGA TGGCAGAGGC 420  
CCTAAAGTTA TGGAGCGATG TGAGCCCACT CACCTTACT GAGGTGCACG AGGGCCGTGC 480  
TGACATCATG ATGCACTGCG CCAGTACTG GCATGGGAC GACCTGCGT TTGATGGGCC 540  
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600  
CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCGAGGC ACAGACCTGC TGCAGGTGGC 660  
AGCCCATGAA TTTGGCCAGG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720  
GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGGCT 780  
TCAACACAGA TATGGCCAGC CTGGCCCACT TGTCACCTCC AGGACCCAG CCTTGGGGCC 840  
CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC 900

5 CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960  
 GGGCTTTGTG TGGCGCCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCTC 1020  
 TCGCCACTGG CAGGGACTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080  
 CATTITGGTT TCCTAAGGTG CTCAGTACTG GGTGTACGAC GTGAAAAGC CAGTCTGTGG 1140  
 CCCCACCCCT CTCACCGAGC TGGGCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200  
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCCACCC 1260  
 CAGCACCCGG CGTGTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320  
 CTCTGAGATC GACGCTGCCT TCCAGGATGC TGTGGCTAT GCCTACTTCC TCGCGGCCCG 1380  
 10 CCTTACTGGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGTCTCGT 1440  
 GGGTCTGAC TTCTTTGGCT GTGCCGAGCC TGCCAAACAT TTCTCTGAC CATGGCTTGG 1500  
 ATGCCCTCAG GGGTGTGAC CCCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560  
 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGTCTCTGC AGGGGGATGG 1620  
 GGTGGGTAC AACCAACATG ACAACTGCCG GAGGGGCCAC GCAGGCTGTG GTCACTGCC 1680  
 15 AGGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740  
 GGGACCCGCT ATGCAGGTCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800  
 GTAGCACCAT GGCAGGACTG GGGGAACCTG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860  
 TCCTTCAGG GGTCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920  
 TGAGCAACTG GGTCTGAGGG CAGGGCCACT TCTGAGGTG AGGTCTTGTG AGGTGCTCTG 1980  
 20 ATCTGTCTGC CTCTGAGGCT ACAATCTCTG AATCTGTTC TCCAGATCC AGGCCAAAA 2040  
 GTTCACATG AATGGGGAG GGTATTCTT CATGCAGSAG ACCCCAGGCC CTGGAGGCTG 2100  
 CAACATACCT CAATCTGTG CCAGGCCGGA TCCTCTGAA GCCCTTTTCG CAGCACTGTG 2160  
 ATCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220  
 TTTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT 2260

25 Seq ID NO: C16 DNA Sequence  
 Nucleic Acid Accession #: NM\_024022  
 Coding sequence: 202..1563

30 1 11 21 31 41 51  
 | | | | |  
 ACCGGGCACC GAGCGGCTCG GGTACTTTGG TTCTTAATTA GGTCTATGCC GTGTGAGCCA 60  
 GGAAGGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAAT GAGGTAGAGG TGGAGGCGGA GCCCGATGTC 180  
 35 AGAGGTCTCG AATAGTGCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGGG CCTTGATGAT TTGAAAATAA GTCTGTGTGC ACCAGATGCA 300  
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATGTGC 360  
 ATTGGGATCA TTGCAATGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCT CTATCTCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 40 GAGGTCTCGG ATTGCAAAAG CCGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAG CCATGTGTCT CGATGACTGG 600  
 AAGGGTCACT ACACAAATGT TGCCTGTGCC CAACGTGGGT TCCCAAGCTA TGTGAGTTCA 660  
 GATAAGCTCA GAGTGTGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 45 TGTGCTCTGC GCCACGTGCT TACCTTGCAG TGCACAGCCT GTGTCTAG AGGGGGCTAG 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTGTGAC CTCGCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGTGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCCAC 1080  
 50 AGCAAGTCA AGCCAAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGCT GSCCGGGCCA 1140  
 CTCAGTTCA ATGAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GATGGAAAAG TGTGCTGGAC GTCCAGGATGG GGGGCCACAG AGGATGGAGG TGACGCTTCC 1260  
 CCTGTCTGTA ACCACGCGGC CGTCCCTTTG ATTTCCAAAC AGATCTGCAA CCACAGGGAC 1320  
 GTGTACGGTG GCATCATCTC CCCCTCCATG CTCTGCGGGG GCTACCTGAC GGGTGGCGTG 1380  
 55 GACAGCTGCC AGCGGGACAG CCGGGGGGCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440  
 TTAGTGGGAG CGACAGCTTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGTGTGAC 1500  
 ACCCGTGTCA CCTCTTCTCT GACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560  
 TGAAGAGGAA GGGGACAAGT AGCCACCTGA GTTCTGAGG TGTGAAAGAC AGCCCGATCC 1620  
 TCCCTTGGAC TCCCGTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTT 1680  
 60 CGGCAACAGT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740  
 GCTGCTTTT GTTTTTTGT TTTTGTAGGT GAGTCTGCG TCTGTGCCC AGGCTGGAGT 1800  
 GCAGTGGGGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAGC GATTCTCTTG 1860  
 CCTCAGCTTC CCCAGTAGCT GGGACCAAG GTGCCCGCCA CCACACCCAA CTAATTTTTG 1920  
 TATTTTGTAG AGAGACAGGG TTTCAACATG TTGGCCAGGC TGCTCTCAA CCCCTGACCT 1980  
 65 CAAATGATGT GCCTGCTTCA GCCTCCCAAC GTGCTGGGAT TACAGGCATG GGGCCACCA 2040  
 CCTAGCTCA CGCTCCTTTC TGATCTTCA TAAGAACAAA AGAAGCAGCA ACTTGCAAGG 2100  
 GCGGCTTTC CCACTGGTCC ATCTGTTTTT CTCTCCAGGG GTCTTGCAA ATTCTGACG 2160  
 AGATAAGCAG TTATGTGACC TCAGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220  
 CCAGCCAGA AGTGCAGAAC TGCACTCACT GCACTTTTC ATCTCTAGGG ACCAGAACCA 2280  
 70 AACCCACCT TTCTACTTCC AAGACTTATT TTCATGTG GGGAGGTTAA TCTAGGAATG 2340  
 ACTCGTTTAA GGCCTATTTT CATGATTTCT TTGTAGCATT TGGTGTGTA CGTATTATTG 2400  
 TCCTTTGATT CCAATAATA TGTTCCTTC CCTCAAAAA AAAAAA 2460  
 AAAAA

75 Seq ID NO: C17 DNA Sequence  
 Nucleic Acid Accession #: NM\_003220  
 Coding sequence: 63..1376

80 1 11 21 31 41 51  
 | | | | |  
 GAATTCGGCG TCTCTGGGTG AGAGACCGAG AGGGGCATAT CCGTTACGCG CGATCCATGA 60  
 AAATGCTTTG GAAATTSACG GATAATATCA AGTACGAGGA CTGCGAGGAC CGTCAACGAC 120  
 GCACCAAGCA CGGACCGGCA CGGTTGCCCC AGCTGGGCAC TGTAGGTCAA TCTCCCTACA 180  
 CGAGCGCCCC GCGGCTGTCC CACACCCCA ATGCGACTTA CCAGCCCCCA TACTTCCCCC 240  
 CACCCCTACCA GCCTATCTAC CCCCAGTCGC AAGATCCTTA CTCCACGTC AACGACCCCT 300

5  
10  
15  
20  
25

```

ACAGCCTGAA CCCCTGAC GCGCAGCGC AGCCGAGCA CCCAGGCTGG CCGGCCAGA 360
GGCAGAGCCA GGAGTCTGGG CTCCTGCACA CGCACCAGGG GCTGCTCAC CAGCTGTCGG 420
GCCTGGATCC TCGCAGGAGC TACAGGCGGC ACAGAGACCT CTGACACGGC CCACACGCGC 480
TCAGCTCAGG ACTCGGAGAC CTCTCGATCC ACTCCTTACC TCACGCCATC GAGGAGGTCC 540
CGCATGTAGA AGACCCGGGT ATTAACATCC CAGATCAAAC TGTAAATTAAG AAAGGCCCGC 600
TGTCCTGTGC CAAGTCCAAC AGCAATGCCG TCTCGCCAT CCCTATTAC AAGGACAACC 660
TCTTGGGCGG CGTGGTGAAC CCCAACGAAG TCTTCTGTTC AGTTCGGGT CGCTCTCGC 720
TCCTCAGCTC CACCTCGAAG TACAAGGTCA CGGTGGCGGA AGTGAGCGG CGGCTCTCAC 780
CACCCGAGTG TCTCAACGCG TCGCTGCTGG GCGAGGTGCT CCGGAGGCGG AAGTCTAATA 840
ATGGAGGAAG ATCTTTAAGA GAAAACTGG ACAAATAGG ATTAATCTG CCTGCAGGGA 900
GACGTAAAGC TGCCAACGTT ACCCTGCTCA CATCACTAGT AGAGGGAGAA GCTGTCCACC 960
TAGCCAGGGA CTTTGGGTAC GTGTGCGAAA CCGAATTTCC TGCCAAGCA GTAGCTGAAT 1020
TTCTCAACCG ACAACATTCC GATCCCAATG AGCAAGTGAC AAGAAAAAC ATGCTCCTGG 1080
CTACAAAAA GATATGCAAA GAGTTCACCG ACCTGCTGGC TCAGGACCGA TCTCCCTGG 1140
GGAACCTCAG GCCCAACCCC ATCTGAGAGC CCGGCATCCA GAGTGTCTG ACCCACTTCA 1200
ACCTCATCTC CCACGGCTTC GGCAGCCCCG CGGTGTGTGC CGCGGTCAAG GCCCTGCAGA 1260
ACTATCTCAC CGAGGCCCTC AAGGCCATGG ACAAATGTA CTCAGCAAC AACCCCAACA 1320
GCCACAGGGA CAACAACGCC AAAAGCAGTG ACAAAGAGGA GAAGCAGAGA AAGTGAGGCT 1380
TCTCTCCCG CCGGCCCTC CCACGCCCTC CCAGCCCCC GCGGCCAC CCGCCGCGG 1440
GTGACAGCTC CCGGATCAGC AACCTTCTCT GCTGTGCTA CTGCTGCTG TGTGCGCGC 1500
GCCGCCCGG CCGTGCCTCT TGGTCCCCC CGAGTCTCCG GAGTGCCTT CTGAGCTGTC 1560
AGTGGGCGAG CTTCTCGAC TCTGACCCG CCTGACCTC CCCACCGCT CCCACACCCC 1620
TGTGCCCCG GAATTC

```

Seq ID NO: C18 DNA Sequence  
Nucleic Acid Accession #: NM\_002988  
Coding sequence: 71..340

30  
35  
40  
45

```

1 11 21 31 41 51
| | | | |
CCGGCAGGAG AGGAGTTGTG AGTTTCCAAG CCCAGCTCA CTCTGACCAC TTCTCTGCCT 60
GCCAGCATC ATGAAGGGCC TTGCAGCTGC CCTCTTGTCT CTGCTCTGCA CCATGGCCCT 120
CTGCTCCTGT GCACAGTTTG GTACCAACAA AGAGCTCTGC TGCTCTGCT ATACCTCTCTG 180
GCAGATTCCA CAAAGTTTCA TAGTTGACTA TTCTGAAACC AGCCCCAGT GCCCAAGCC 240
AGGTGTCTAT CTCTTAACCA AGAGAGGCGG GCAGATCTGT GCTGACCCA ATAAGAAAGT 300
GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCCTGA GGGGCTGGA AGCTGCGAGG 360
GCCAGTGAAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420
CCACCTCGGA GGCCACCTCT TCTAAGAGTC CCATCTGCTA TGCCACAGCA CATTAACTAA 480
CTTTAATCTT AGTTTATGCA TCTATTTC TTTGAAATT GATTTCTATT GTTGAGCTGC 540
ATTATGAAT TAGTATTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTTCCCT 600
TTCCCTTCAA CTCTTGATC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTCTCAG 660
CAGACATTGT GCCATATGTA TCAATGACA AATCTTTAT GAATGGTTTT GCTCAGCACC 720
ACCTTTAAT ATATTGGCAG TACTATTAT ATAAAGGTA AACAGCATT CTCACTGTGA 780
AAAAAAAAA AAAAAAAAAA AAA

```

Seq ID NO: C19 DNA Sequence  
Nucleic Acid Accession #: NM\_004063  
Coding sequence: 121..2619

50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
AGGGAGTGTT CCCGGGGGAG ATACTCCAGT CAGTAGCAAGA GTCTCGACCA CTGAATGGAA 60
GAAAGGACT TTTAACCACC ATTTTGTGAC TTACAGAAAG GAATTTGAAT AAAGAAAACT 120
ATGATCTTC AGGCCCATCT TCACTCCCTG TGTCTTCTTA TGCTTTATT GGCAACTGGA 180
TATGGCCAG AGGGAAAGTT TAGTGGACCC CTGAAACCCA TGACATTTTC TATTATGAA 240
GGCCAGAAGC CGAGTCAAT TATATTCCAG TTTAAGGCCA ATCTCTCTGC TGTGACTTTT 300
GAACCTAAGT GGGAGACAGA CAACATATT GTGATAGAAC GGGAGGGACT TCTGTATTAC 360
AACAGACCTC TGGACAGGGA AACAGATCT ACTCACAATC TCCAGTTTGC AGCCCTGGAC 420
GCTAATGGAA TTATAGTGGG GGGTCCAGTC CCTATCACCA TAGAAGTGAA GGACATCAAC 480
GACATCGAC CCAGTCTTCT CCAGTCAAAG TACGAAGGCT CAGTAAGGCA GAACCTCTGC 540
CCAGAAAGC CCTTCTTGTA TGTCAATGCC ACAGACCTGG ATGATCCGGC CACTCCCAAT 600
GGCCAGCTT ATTACAGAT TGTCAATCCG CTTCCTCATG TCACAATGT CATGTACTTT 660
CAGATCAACA ACAAACCGGG AGCCATCTCT CTACCCGAG AGGGATCTCA GGAATTGAAT 720
CCTGCTAAGA ATCTTCTCTA TAATCTGGTG ATCTCAGTGA AGGACATGGG AGGCCAGAGT 780
GAGAACTCTC TCAGTGATAC CACATCTGTG GATATCATAG TGACAGAGAA TATTGGAAA 840
GCACCAAAAC CTGTGGAGAT GGTGAAAAAC TCACTGATC CTCACCCAT CAAATCACT 900
CAGGTGCGGT GGAATGATCC CGGTGCACAA TATTCCTTAG TTGACAAAGA GAAGCTGCCA 960
AGATTCCCAT TTTCAATTGA CCAGGAAGGA GATATTACG TGACTCAGCC CTGGACCGA 1020
GAAGAAAAGG ATGCAATGT TTTTATGCA GTTGCAAAGG ATGAGTACGG AAAACCACTT 1080
TCATATCCGC TGGAAATTC TGTAAAGTT AAAGATATTA ATGATAATCC ACCTACATGT 1140
CCGTCAACG TAACCGTATT TGAGGTCCAG GAGAATGAAC GACTGGGTAA CAGTATCGGG 1200
ACCTTACTG CACATGACAG GGATGAAGAA AATACTGCCA ACAGTTTCT AAACACAGG 1260
ATTGTGAGC AAACCTCCAA ACTTCCCATG GATGGACTCT TCCTAATCCA AACCTATGCT 1320
GGAATGTAC AGTTAGCTAA ACAGTCCCTG AAGAAGCAAG ATACTCTCA GTACAACCTA 1380
ACGATAGAGG TGTCTGACAA AGATTTCAG ACCCTTGTG TGTGCAAAAT CAACGTATT 1440
GATATCAATG ATCAGATCCC CATCTTGAA AAATCAGATT ATGGAACCT GACTTGTGCT 1500
GAAGACACAA ACATTGGGTC CACCATCTTA ACCATCCAGG CCACTGATGC TGTGAGCCA 1560
TTTACTGGGA GTTCTAAAAA TCTGTATCAT ATCATAAAGG GAGACAGTGA GGGACGCTG 1620
GGGTGTGACA CAGATCCCCA TACCAACACC GGATATGTCA TAATTAATAA GCCTCTTGAT 1680
TTTGAACAGC CAGCTGTTTC CAACATTGTG TTCAAAGCAG AAAATCCTGA GCCTCTAGTG 1740
TTTGTGTGA AGTACAATGC AAGTTCTTTT GCCAAGTTCA CGCTATTGT GACAGATGTG 1800
AATGAAGCAC CTCAATTTTC CCAACACGTA TTCCAAGCGA AAGTCAAGTGA GGATGTAGCT 1860
ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGGTCTGGA CATAAGCTAT 1920
TCACTGAGGG GAGACACAA AGGTGTGGCT AAAATTGACC ACGTGACTGG TGAGATCTTT 1980

```



5	AGTGTGGCTC	CATTGGACAG	AGAAGCCGGA	AGTCCATATC	GGGTACAAGT	GGTGGCCACA	2040
	GAAGTAGGGG	GGTCTTCCCT	GAGCTCTGTG	TCACAGTTC	ACCTGATCCT	TATGGATGTG	2100
	AATGACAACC	CTCCCAGGCT	AGCCAAGGAC	TACACGGGCT	TGTTCTTCTG	CCATCCCCTC	2160
	AGTGCACCTG	GAAGTCTCAT	TTTCGAGGCT	ACTGATGATG	ATCAGCACTT	ATTTCCGGGT	2220
	CCCCATTTTA	CATTTTCCCT	CGGCAGTGGG	AGCTTACAAA	ACGACTGGGA	AGTTTCCAAA	2280
	ATCAATGGTA	CTCATGCCCG	ACTGTCTACC	AGGCACACAG	AGTTTGAGGA	GAGGGAGTAT	2340
	GTCGTCTTGA	TCCGCATCAA	TGATGGGGGT	CGGCCACCCT	TGGAAGGCAT	TGTTTCTTTA	2400
	CCAGTTACAT	TCTGCAGTTG	TGTGGAAGGA	AGTTGTTTCC	GGCCAGCAGG	TCACCAGACT	2460
10	GGGATACCA	CTGTGGGCAT	GGCAGTTGGT	ATACTGCTGA	CCACCCTTCT	GGTGATTGGT	2520
	ATAATTTTAA	CAGTGTGTGT	TATCCGCATA	AAGAAGGATA	AAGGCAAGA	TAATGTTGAA	2580
	AGTGCTCAAG	CATCTGAAGT	CAAACCTCTG	AGAAGCTGAA	TTTGAAAAGG	AATGTTTGAA	2640
	TTTATATAGC	AAGTGCTATT	TCAGCAACAA	CCATCTCATC	CTATTACTTT	TCATCTAAAG	2700
	TGCATTATAA	TTTTTTAAAC	AGATATTCCC	TCTTGTCTCT	TAATATTTCG	TAAATATTTC	2760
	TTTTTTGAGG	TGGAGTCTTG	CTCTGTGCCC	CAGGCTGGAG	TACAGTGGTG	TGATCCAGC	2820
15	TCACTGCAAC	CTCCGCTCC	TGGGTTTACA	TGATTTCTCT	GCCTCAGCTT	CCTAAGTAGC	2880
	TGGGTTTACA	GGCACCCACC	ACCATGCCCA	GCTAATTTTT	GTATTTTAA	TAGAGACGGG	2940
	GTTCGCCAT	TGCGCCAGGC	TGGTCTTGAA	CTCCTGACGT	CAAGTGATCT	GCCTGCCCTG	3000
	GTCTCCCAT	ACAGGCATGA	ACCACTGCAC	CCACTACTT	AGATATTTC	TGTGCTATAG	3060
20	ACATTAGAGA	GATTTTTCAT	TTTTCCATGA	CATTTTTCCT	CTCTGCAAT	GGCTTAGCTA	3120
	CTGTGTTTT	TCCCTTTTGG	GGCAAGACAG	ACTCATTAAA	TATTCGTAC	ATTTTCTCT	3180
	TATCAAGGAG	ATATCTCAGT	GTGTCTCAT	AGAACTGCCT	GGATCCATT	TATGTTTCTT	3240
	CTGATTCCAT	CCTGTGTCCC	CTTCATCCTT	GACTCCITTG	GTATTTCACT	GAATTTCAAA	3300
	CATTGTTCAG	AGAAGAAAA	CSTGAGGACT	CAGGAAAAAT	AAATAAATA	AAGAACAGCC	3360
25	TTTTCCCTTA	GATTTTAAAC	AAATGTTTCT	GTGTCAITAA	CCATCTTAA	TCAATGTGAC	3420
	ATGTTGCTCT	TGCGCTGAAA	TTCTTCAACT	TGGAAATGAC	ACAGACCCAC	AGAAGGTGTT	3480
	CAAAACAAC	CTACTCTGCA	AACCTTGGTA	AAGGAACCA	TCAGCTGGCC	AGATTTCTCT	3540
	ACTACCTGCC	ATGCATACAT	GCTGCGCATG	TTTTCTTCAT	TOGTATGTTA	GTAAGGTTTT	3600
	GGTTATTATA	TATTTAACAT	GTGGAAGAAA	ACAAGACATG	AAAAGAGTGG	TGACAAATCA	3660
30	AGAATAAACA	CTGGTTGTAG	TCAGTTTGT	TTGTTAA			3697

Seq ID NO: C20 DNA Sequence  
Nucleic Acid Accession #: NM\_004443  
Coding sequence: 28..3024

35	1	11	21	31	41	51	
	GGCTCGGCTC	CTAGAGCTGC	CACGGCCATG	GCCAGAGCCC	GCCCGCCGCC	GCCGCGGTGG	60
	CCGCGCGCGG	GGCTTCTGCG	GCTGCTCCCT	CGCTGCTGTC	TGCTGCCGCT	GCTGCTGCTG	120
40	CCCGCGCGCT	GCCGCGGCGT	GGAAGAGACC	CTCATGGACA	CAAAATGGGT	AACATCTGAG	180
	TGCGCGTGA	CATCTCATCC	AGAAAGTGGG	TGGGAAGAGG	TGAGTGGCTA	CGATGAGGCC	240
	ATGAATCCCA	TCCGCACATA	CCAGGTGTGT	AATGTGCGCG	AGTCAAGCCA	GAACAACCTG	300
	CTTCGACCGG	GGTTCATCTG	CGCGCGGGAT	GTGCAGCGGG	TCTACGTGGA	GCTCAAGTTC	360
45	ACTGTGCGTG	ACTGCAACAG	CATCCCAAC	ATCCCGGCT	CCTGCAAGGA	GACCTTCAAC	420
	CTCTTCTACT	ACGAGGCTGA	CAGCGATGTG	GCCTCAGCCT	CCTCCCGCTT	CTGGATGGAG	480
	AACCCCTAAG	TGAAAGTGA	CACCATTGCA	CCGATGAGA	GCCTTCTGCG	GCTGGATGCC	540
	GGCCGTGTCA	ACACCAAGGT	GCGCAGCTTT	GGGCCACTTT	CCAAGGCTGG	CTTCTACCTG	600
	GCCTTCCAG	ACCAGGGGCG	CTGCATGTGG	CTCATCTCCG	TGCGCGCCTT	CTACAAGAG	660
50	TGTGATCCA	CCACGCGCAG	CTTCGCACTC	TTCCCGAGA	CCCTCACTGG	GGCGGAGCCC	720
	ACCTGCTGCG	TCAATTGCTC	TGGCAGCTGC	ATCCCTAAGC	CGGTGGAGGT	GTCGGTGCCA	780
	CTCAAGCTCT	ACTGCAAGCG	OGATGGGGAG	TGGATGGTGC	CTGTGGGTGC	CTGCACCTGT	840
	GCCACCGGCC	ATGAGCCAGC	TGCCAAGGAG	TCCAGTGGCC	GCCCTGTGTC	CCCTGGGAGC	900
	TACAAGGCGA	AGCAGGGAGA	GGGGCCCTGC	CTCCCATGTC	CCCCCAACAG	CCGTACCACC	960
55	TCCCGAGCCG	CCAGGACTCT	CACCTGCCAC	AATAACTTCT	ACCGTGCGAG	CTCGGACTCT	1020
	CGCGGACAGT	CCTGTACCA	CGTGCCATCT	CCACCCGAG	GTGTGATCTC	CAATGTGAAT	1080
	GAAACCTCAC	TGATCTCTGA	GTGAGTGTAG	CCCCGGGACC	TGGGTGGCCG	GGATGACCTC	1140
	CTGTACAATG	TCATCTGCAA	GAAGTGCCAT	GGGGCTGGAG	GGGCCTCAGC	CTGCTCAGGC	1200
	TGTGATGACA	ACGTGGAGTT	TGTGCCCTCG	CAGCTGGGCC	TGACGGAGCG	CGGGTCCAC	1260
60	ATCAGCCATG	TGCTGGCCCA	CACGCGCTAC	ACCTTTGAGG	TGCAGGCGGT	CAACGCTGTC	1320
	TGCGGCAAGA	GCCTCTGCGC	GCCTCGTTAT	GCGGCGGTGA	ATATCAACCA	AAACAGGCTC	1380
	GCCCGTCTG	AAGTGCCAC	ACTACGCTG	CACAGCAGCT	CAGGCAGCAG	CCTCACCTTA	1440
	TCCTGGGCAC	CCCCAGAGCG	GCCCAACGGA	GTCTCTCTGG	ACTACGAGAT	GAAGTACTTT	1500
	GAGAAGAGCG	AGGACATCGC	CTCCACAGTG	ACCAGCCAGA	TGAATCTCGT	GCACTGGGAC	1560
65	GGCTTTCGCG	CTGACGCCCG	CTATGTGGTC	CAGGTCCGTG	CCCGCACAGT	AGCTGGCTAT	1620
	GGGCACTACA	GCCGCCCTGC	CGAGTTTGAG	ACCACAAGTG	AGAGAGGCTC	TGGGGCCAG	1680
	CAGCTCCAGG	AGCAGCTTCC	CCTCATCGTG	GGCTCCGCTA	CAGCTGGGCT	TGCTCTGGTG	1740
	GTGGCTGTG	TGTCATCGC	TATCGTCTGC	CTCAGGAAGC	AGCGACACGG	CTCTGATTCT	1800
	GAGTACACGG	AGAAGCTGCA	GCAGTACATT	GCTCCTGGAA	TGAAGGTTTA	TATTGACCTT	1860
70	TTTACCTACG	AGGACCTTAA	TGAGGCTGTT	CGGAGTTTGG	CCAAGGAGAT	CGAAGTGTCC	1920
	TGCGTCAAGA	TGAGGAGGAT	GATCGGAGCT	GGGGAATTTG	GGGAAGTGTG	COGTGGTGA	1980
	CTGAACACAG	CTGGCGCGCG	AGAGGTGTTT	GTGGCCATCA	AGACGCTGAA	GGTGGGCTAC	2040
	ACCGAGAGGC	AGCGCGGGGA	CTTCCTAAGC	GAGGCCCTCA	TCATGGGTCA	GTTTGATCAC	2100
	CCCAATATAA	TCCGGCTCGA	GGGCGTGGTC	ACCAAAAGTC	GGCCAGTTAT	GATCCTCACT	2160
75	GAGTTTCATG	AAAACCTGCG	CCTGGACTCC	TTCTCTCGCG	TCAACGATGG	GCAGTTCAAG	2220
	GTGATCCAGC	TGTTGGGCGAT	GTGCGGGGCG	ATTGCTGCGG	GCATGAAGTA	CCTGTCCGAG	2280
	ATGAACCTATG	AGCAACGCGA	CCTGGCTGCT	CGCAACATCC	TTGTCAACAG	CAACCTGGTC	2340
	TGCAAGTCT	CAGACTTTGG	CCTCTCCCGC	TTCTGTGAGG	ATGACCCCTC	CGATCCTACC	2400
	TACACCAAGT	CCCTGGGCGG	GAAGATCCCC	ATCGCTGGA	CTGCCCCAGA	GGCCATAGCC	2460
80	TATCGAAGT	TGACTTCTGC	TAGTATGTGC	TGGAGCTACG	GAATTGTTCAT	GTGGGAGGTC	2520
	ATGAGCTATG	GAGAGGAGCC	CTACTGGGAC	ATGAGCAACC	AGGATGTTCAT	CAATGCCGTG	2580
	GAGCAGGATT	GAGGCTGGCG	ACCAACCATG	GACTGTCCCA	CAGCACTGCA	CCAGCTCATG	2640
	CTGGACTGCT	GGGTGCGGGA	CCGGAACCTC	AGGCCCAAT	TCTCCAGAT	TGTCAATACC	2700
	CTGGACAAGC	TCATCCGCAA	TGCTGCCAGC	CTCAAGGTCA	TTGCCAGCGC	TCAGTCTGGC	2760
	ATGTACAGC	CCCTCTGTGA	CCGCAAGGTC	CCAGATTACA	CAACCTTCA	GACAGTTGGT	2820



5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

GATTGGCTGG ATGCCATCAA GATGGGGCGG TACAAGGAGA GCTTCGTGAG TGGGGGTTT 2880  
GCATCTTTTG ACCTGTGTGG CCAGATGACG GCAGAAGACC TGCTCGGTAT TGGGGTCACC 2940  
CTGGCCGGCC ACCAGAAGAA GATCCTGAGC AGTATCCAGG ACATGCGGCT GCAGATGAAC 3000  
CAGACGCTGC CTGTGCAGGT CTGACACCGG CTCCACGGG GACCTTGAGG ACCGTGCAGG 3060  
GATGCCAAGC AGCGGCTGG ACTTTCGGAC TCTTGGACTT TTGGATGCCT GGCCTTAGGC 3120  
TGTGGCCCAAG AAGCTGGAAG TTTGGGAAAG GCCCAAGCTG GGACTTCTCC AGGCCTGTGT 3180  
TCCCTCCCCA GGAAGTGC GC CCAAACTC TTCAATTGA AGATGGATTA GGAGAGGGGG 3240  
TGATGACCCC TCCCACAGCC CCTCAGGGCC CAGACCTTCC TGCTCTCCAG CAGGGGATCC 3300  
CCACAACCTC ACACCTGTCT GTTCTTCAGT GCTGGAGGTC CTGGCAGGGT CAGGCTGGGG 3360  
TAAGCCGGGG TTCCACAGGG CCCAGCCCTG GCAGGGGTCT GGCCCCCAG GTAGCGGGAG 3420  
AGCAGTCCCT CCCTCAGGAA CTGGAGGAGG GGACTCCAGG AATGGGAAA TGTGACACCA 3480  
CCATCTGAA GGCAGCTTGC ACCTCCAGTT TGACAGGGA TTTGTCTGG GGGCTGAGGG 3540  
CCCTGTCCCC ACCCCCGCCC TTGGTGTCTGT CATAAAAGGG CAGGCAGGGG CAGGCTGAGG 3600  
AGTTGCCCTT TGCCCCCAG AGACTGACTC TCAGAGCCAG AGATGGGATG TGTGAGTGTG 3660  
TGTGTGTGTG TGTGCGCGCG CGCGCGCGTG TGTGTGTGCA CGCACTGGCC TGACACAGAG 3720  
GCATGGGTGA GCGTGTAAAA GCTTGGCCCT GTGCCCTACA ATGGGGCCAG CTGGGCCGAC 3780  
AGCAGAATAA AGGCAATAAG ATGAA 3805

Seq ID NO: C21 DNA Sequence  
Nucleic Acid Accession #: NM\_001804  
Coding sequence: 82..879

1 11 21 31 41 51  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

AGGTGAGCGG TTGCTGCTCG TCGGGGCGGC CGGCAGCGGC GGCTCCAGGG CCCAGCATGC 60  
GCGGGGGACC CCGCGGCCAC CATGTATGTG GGCTATGTGC TGGACAAGGA TTCGCCCTGT 120  
TACCCCGGCC CAGCCAGGCC AGCCAGCCTC GGCTTGGGCC CGGCAAACTA CGGCCCCCGG 180  
GCCCGGCCCG CGGCGCCCCC GCAGTACCCC GACTTCTCCA GCTACTCTCA CGTGGAGCOG 240  
GCCCCCGCCG CCCCAGCGCG CTGGGGGGCG CCTTCCCTG CGCCCAAGGA CGACTGGGCC 300  
GCCGCTTAGC GCGCGGCCCG CGCGGCCCTC CAGCTTCGCT GGCATTGCGG 360  
CCCCCTCCAG ACTTTAGCCC GGTGCGCGCG CCCCCTGGGC CGGCCCCGGG CTTCTGCGG 420  
CAGCCCCCTG GGGGCCCGGG CACACCGTCC TGSCCCGGAG CGCAGAGGCC GAGGCCCTAC 480  
GAGTGAATGC GCGCGACGCT GCGCGCCGGA GCGCGCGGTG GCAGCGGTAA GACTCGGACC 540  
AAGGACAAGT ACCCGCTGGT CTACACCGAC CACCAAGGCC TGGAGCTGGA GAAGGAGTTT 600  
CATTACAGCC GTTACATCAC AATCCGCGCG AAATCAGAGC TGGCTGCCAA TCTGGGGCTC 660  
ACTGAACGGC AGGTGAAGAT CTGGTTCCAA AACCGCGCGG CAAAGGAGCG CAAAGTGAAC 720  
AAGAAGAAAC AGCAGCAGCA ACAGCCCCCA CAGCGCCGGA TGGCCACGA CATCAGGCC 780  
ACCCAGCCCG GGCATCCCT GGGGGGCTTG TGTCCAGCA ACACAGCCT CTTGGCCACC 840  
TCCTCTCCAA TGCTGTGAA AGAGGAGTTT CTGCCATAGC CCGATGCCCA GCCTGTGCGC 900  
CGGGGACCTG GGGGATACGG GTGCTGGGAG TGTGCTCCT GTGGGCCAG GAGGTCTGGT 960  
CGAGTCTCA GCCCTGACCT TCTGGGACAT GGTGGACAGT CACCTATCCA CCTCTGCAT 1020  
CCCCTTGGCC CATTTGTGTG AGTAAGCCTG TTGGATAAAG ACCTTCCAGC TCCTGTGTTT 1080  
TAGACCTCTG GGGGATAAAG GAGTCCAGGG TGGATGATCT CAATCTCCCG TGGGATCTCT 1140  
AAGCCCAAAA TGGTTGGGG AGGGGCCCTAG ACAAGGCTCC AGGCCCCACC TCCTCTCCA 1200  
TACGTTGAGA GTTGACAGTG GAGGCTGTG TGGGACCACT ACTGATCTCT GAGAAAAGGG 1260  
ATGAGAGCTGA AAAAGATGGA ATGCTTGCA AGCATGACCT GAGGAGGGAG GAACGTGGTC 1320  
AACTCACACC TGCTCTTCT GCAGCCTCAC CTCTACCTGC CCGCATCATA AGGGCACTGA 1380  
GCCCTTCCCA GGGGTGATAC TAAGCACAAA GCCCATAGCA CTGGGCTCTG ATGGCTGCTC 1440  
CACTGGGTTA CAGAATCACA GCCCTCATGA TCAATCTCAG TGAGGGCTCT GGAATTGAGAG 1500  
GGAGGCGCTG GAGGAGGAGA AGGGGGCAGA GTCTTCCCTA CCAGGTTTCT ACACCCCGC 1560  
CAGGCTGCCC ATCAGGCCCC AGGGAGCCCC CAGAGGACTT TATTGAGACC AAGCAGAGCT 1620  
CACAGCTGGA CAGGTGTGT ATATAGAGTG GAATCTCTTG GATGCAGCTT CAAGATAAA 1680  
TTTTCTTCT CTTTTCAAA 1699

Seq ID NO: C22 DNA Sequence  
Nucleic Acid Accession #: NM\_021978  
Coding sequence: 36..2603

60  
65  
70  
75  
80

1 11 21 31 41 51  
GACGCTGTG AGACCCGCGA GCGGCTGCG GGACCATGGG GAGCGATCGG GCCCGCAAGG 60  
GCGGAGGGGG CCGAAGGAG TTGCGCGCGG GACTCAAGTA CAACCTCCCG CACGAGAAAG 120  
TGAATGGCTT GGAGGAAGGC GTGAGTTTCC TGCCAGTCAA CAACGTCAA AAGGTGAAA 180  
AGCATGGCCC GGGGCGCTGG GTGGTGTCTG CAGCCGTGCT GATCGGCTCT CTCTTGTCT 240  
TGCTGGGGAT CGGCTTCTG GTGTGGCATT TGCACTACCG GGAAGTGGCT GTCCAGAAGG 300  
TCTTCAATGG CTACATGAGG ATCACAATG AGAATTTTGT GGATGCCTAC GAGAACTCCA 360  
ACTCCACTGA GTTTGTAAGC CTGGCCAGCA AGGTGAAGGA CGCGCTGAAG CTGCTGTACA 420  
GCGGAGTCCC ATTCTTGGC CCTTACCACA AGGAGTCCGG TGTGAAGGCC TTCAGGAGG 480  
GCAGGTCAT CGCCTACTAC TGCTCTGAGT TCAGCATCCC GCAGCACCTG GTGGAGGAGG 540  
CGAGCGCGGT CATGCGCGAG GAGCGGTAG TCATGCTGCC CCGCGGGGCG CGCTCCCTGA 600  
AGTCTTTGT GGTCACTCA GTGGTGGCTT TCCCAACGGA CTCCAAAACA GTACAGAGGA 660  
CCAGGACCAA CAGCTGCAGC TTTGGCTTGC ACCCCGCGG TGTGGAGCTG ATGCCCTTCA 720  
CCAGCGCCCG CTTCCCTGAC AGCCCTTACC CCGCTCATGC CGCTGCCAG TGGGCCCTGC 780  
GGGGGAGCGC CGACTCAGTG CTGAGCCTCA CCTTCCGAG CTTTACCTT GCGTCTGCG 840  
ACGAGCGCGT CATGCGCGAG GTGACGTTGT ACAACACCTT GAGCCCCATG GAGCCCCAG 900  
CCCTGGTGA GTTGTGTGGC ACCTACCTTC CCTCTACAA CCGTCACTTC CACTCTCTCC 960  
AGAACGTCTT GCTCATACA CTGATAACCA ACATGAGCG GCGCATCCG GGCCTTGAGG 1020  
CCACCTTCTT CCAGTGCCTT AGGATGAGCA GCTGTGGAGG CCGCTTACGT AAAGCCAGG 1080  
GGACATTCAA CAGCCCCCTAC TACCCAGGCC ACTACCCACC CAACATTGAC TGACATGGA 1140  
ACATTGAGGT CGGCCAACAC CAGCATGTGA AGGTGCGCTT CAATTTCTT TACCTGCTGG 1200  
AGCCCGCGGT GCTCGCGGGC ACCTGCCCA AGGACTACGT GGAGATCAAT GGGGAGAAAT 1260  
ACTGCGAGA GAGGTCCAGG TTGCTGTCA CCAGCAACAG CAACAAGATC ACAGTCTGCT 1320  
TCCACTCAGA TCAGTCTTAC ACCGACACCG GCTTCTTAGC TGAATACCTC TCCTACGACT 1380

5  
10  
15  
20  
25  
30

```

CCAGTGAACC ATGCCCGGG CAGTTACGTT GCCGCACGGG GCGGTGTATC CGGAAGGAGC 1440
TGCGCTGTGA TGGCTGGGCC GACTGCACCG ACCACAGCGA TGAGCTCAAC TGCAGTTGCG 1500
ACGCCGGCCA CCAGTTTCACG TGCAAGAACA AGTTCTGCAA GCCCCTCTTC TGGGTCTGCG 1560
ACAGTGTGAA CGACTGCGGA GACAACAGCG ACGAGCAGGG GTGCAGTTGT CCGGCCGAGA 1620
CCTTCAGGTG TTCCAATGGG AAGTGCCTCT CGAAAGCCA GCAGTGAAT GGGAGGACG 1680
ACTGTGGGGA CGGGTCCGAC GAGGCTCTCT GCCCAAGGT GAACTGCTC ACTTGTACCA 1740
AACACACCTA CCGCTGCCCTC AATGGGCTCT GCTTGAGCAA GGGCAACCCT GAGTGTGAG 1800
GGAAAGAGGA CTGTAGCGAC GGCCTCAGATG AGAAGGACTG CGACTGTGGG CTGCGGTCTAT 1860
TCACGAGACA GTTGGGTGTT GTTGGGGGCA CGATGCGGA TGAGGGCGAG TGGCCCTGGC 1920
AGGTAAGCCT GCATGCTCTG GGCAGGGGCC ACATCTGCGG TGCTTCCCTC ATCTCTCCA 1980
ACTGGCTGGT CTCTGCCGCA CACTGCTACA TCGATGACAG AGGATTGAGG TACTCAGACC 2040
CCACGCACTG GACGCGCTTC CTGGGCTTGC ACGACCAGAG CCAGCGCAGC GCCCCTGGGG 2100
TGCAGGAGCG CAGGCTCAAG GGCATCATCT CCCACCCCTT CTTCATGAC TTCACTTTCG 2160
ACATATGACAT CGCGCTGCTG GAGCTGGAGA AACCGGCAGA GTACAGCTCC ATGGTGGCGC 2220
CCATCTGCCT GCCGACGCC TCCATGTCT TCCCTGCCGG CAAGGCCATC TGGGTCAAGG 2280
GCTGGGGACA CACCCAGTAT GGAGGCACTG GCGCGTGAT CCTGCAAAAG GGTGAGATCC 2340
GCGTCATCAA CCAGACCACC TGCGAGAACG TCCTGCGGCA GCAGATCAGC CCGCGCATGA 2400
TGTGCGTGGG CTTCCTCAGC GCGCGCTGGG ACTCCTGCCA GGGTGATTCC GGGGGACCCC 2460
TGTCCAGCGT GGAGGCGGAT GGGCGGATCT TCCAGGCGGG TGTGGTGAGC TGGGGAGACG 2520
GCTGCGCTCA GAGGAACAAG CCAGGCGTGT ACACAAGGCT CCCTCTGTTT CGGGACTGGA 2580
TCAAAGAGAA CACTGGGGTA TAGGGGCGCG GGCACCCCAA ATGTGTACAC CTGCGGGGCC 2640
ACCCATCGTC CACCCGAGTG TGCAACGCTG CAGGCTGGAG ACTGGACGCG TGACTGCACC 2700
AGCGCCGCCA GAACATACAC TGTGAACATA ATCTCCAGGG CTCCAAATCT GCCTAGAAAA 2760
CCTCTCGCTT CCTCAGCCTT CAAAGTGGAG CTGGGAGGTA GAAGGGGAGG AACTGCTGG 2820
TTCTACTGAC CCAACTGGGG GCAAAAGTTT GAAGACACAG CCTCCCGCGC CAGCCCCAAG 2880
CTGGGCCGAG GCGCGTTTGT GTATATCTGC CTCCCTGTCT TGTAAAGGAG AGCGGGAAAG 2940
GAGCTTCGGA GCCTCTCTAG TGAAGGTGGT GGGGCTGGCG GATCTGGGCT GTGGGGCCCT 3000
TGGGCCAGCG TCTTAGGAGG GCCCAGGCTC GGAGGACCCT GGAACACAGA CGGGTCTGAG 3060
ACTGAAATG GTTTACGAGC TCCAGGTGA CTTAGTGTG TGTATTGTG AAATGAGTAA 3120
AACATTTTAT TTCTTTTAA AAAAAAAA 3149

```

Seq ID NO: C23 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2268

35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ATGCCCCCTT TCCTGTGCT GGAAGCCGTC TGTGTTTCC TGTTTCCAG AGTGCCCCCA 60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
AGCAAAATGA TGTGTGCTC GGCTGCACTG GACATCATGT TTCTGTAGA TGGGTCTAAC 180
AGCGTGGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTTG CCATCAGAGT CTGTGACGCT 240
CTGGACATCA GCCCGAGAGG GGTGAGAGTG GAGCAGTTCC AGTTGAGTTC CACTCTCTAT 300
CTGGAATTCG CCTTGAATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
ATGGTTTTC AAGGAGGGCG CACGAGAGCG GAACCTGCTC TGAATACTCT TCTGCACAGA 420
GGGTTCGCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480
AAGTCCGAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
TTTGTGTGGG GGGTCAGGTT TCCAGGTGG GAGGAGCTGC ATGCACTGCG CAGCGAGCCT 600
AGAGGGCAGC ACCTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACCG CCTCTTCAGC 660
ACCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAAGGT CGAGGCTCAC 720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGAGTTTCG CTGGCAATGC CCCATGCTGG 780
AGAGGATCGC GGGGACCCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900
TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAA GACTGGACGG CTACCAAGTGC 960
CTCTGCCCCG TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC 1020
AGGGTCGACC TCCTCTTCTT GCTGGACAGC TCTGCGGCA CCACTCTGGA CGGCTTCTCT 1080
CGGGCCAAAG TCTTCTGTGA GCGGTTTGTG CCGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCGCTG GGGGGAGTAC 1200
CAGGATGTGC CTGACCTGCT GTGGAGCCTC GATGCGATTG CCTTCCGTGG TGGCCCCACC 1260
CTGACGGGCA GTGCCTTGGC GCAGGCGGCA GAGCGTGGCT TCGGGAGGCG CACCAAGGAC 1320
GGCCAGGACC GGCCAGCTAG AGTGTGGT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
GTTGCGGGCC CAGCGCTGCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCACT 1440
GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGACGCC CAAAGCATGT GATGGTCTAC 1500
TCGGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
CAGCGGCCAG GGTGCGGAGC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CAOCTCTGCC 1620
TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
TTTGAGGTGA ACCCTGAGCT GACACAGTGC GGCTGCTGGG TGTATGGCAG CCAGGTGCAG 1740
ACTGCTTCG GGTGAGACAC CAAACCCACC CCGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCGCCA AAGCTGTGGT GGTGCTCACA 1920
GGCGGAGAG GCGCAGAGGA TGACGCGGTT CTGCCCAGA AGCTGAGGAA CAATGGCATC 1980
TCTGTCTTGG TCGTGGGCGT GGGGCTGTCT CTAAGTGAAG GTCTGCGGAG GCTTGCAAGT 2040
CCCGGGGATT CCCTGATCCA CGTGGCAGCT TACGCGACC TGCGGTACCA CCAGGACGTG 2100
CTCATTGAGT GGCTGTGGG AGAAGCCAA GCGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
TGCAATGAAT AGGGCAGCTG CGTCTGAGC AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
GGCTGGGAGG GCGCCCACTG CGAGAACCGA TTCTTGAGAC GCGCCCTGA 2268

```

Seq ID NO: C24 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2424

80

```

1 11 21 31 41 51
| | | | |
ATGCCCCCTT TCCTGTGCT GGAGGCGTCT TGTGTTTCC TGTTTCCAG AGTGCCCCCA 60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120

```

5	AGCAAAATGA	TGTGGTGCTC	GGCTGCAGTG	GACATCATGT	TTCTGTTAGA	TGGGTCTAAC	180
	AGCGTCGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTTG	CCATCACAGT	CTGTGACGGT	240
	CTGGACATCA	GCCCCGAGAG	GGTCAGAGTG	GGASCATTCC	AGTTCAGTTC	CACCTCTCAT	300
	CTGGAATTCC	CCTTGGATTG	ATTTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
	ATGGTTTTCA	AAGGAGGGCG	CACGGAGACG	GAACCTTGCTC	TGAAATACCT	TCTGCACAGA	420
	GGGTTGCCCTG	GAGGCAGAAA	TGCTTCTGTG	CCCCAGATCC	TCATCATCGT	CACCTGATGG	480
	AAGTCCACAG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
	TTTGCTGTGG	GGGTGAGTTT	TCCCAGGTGG	GAGGAGCTGC	ATGCACTGGC	CAGCGAGCCT	600
10	AGAGGGCAGC	CGTACTGTGT	GGCTGAGCAG	GTGGAGGATG	CCACCAACGG	CCTCTTCAGC	660
	ACCCCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGGAACGT	GGAGATGGTC	CGGGAGTTGG	CTGGCAATGC	CCCATGCTGG	780
	AGAGGATCGC	GGCGGACCTT	TGCGGTGCTG	GCTGCACACT	GTCCCTTCTA	CAGCTGGAAG	840
	AGAGTGITCC	TAAACCCACC	TGCCACCTGC	TACAGGACCA	CCTGCCCCAG	CCCTGTGAC	900
15	TGCGAGCCCT	GCCGAATGG	AGGCACATGT	GTTCAGGAAG	GACTGGACGG	CTACCACTGC	960
	CTCTGCCCGC	TGGCCTTTGG	AGGGGAGGCT	AACTGTGCCC	TGAAGCTGAG	CCTGGAATGC	1020
	AGGGTTCGAG	TCTCTTCTCT	GCTGGACAGC	TCTGGGGGCA	CCACTCTGGA	CGGCTTCCTG	1080
	CGGGCCAAAG	TCTTGTGAA	GCGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
	CGAGTGGGTG	TGGCCACATA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCCTGT	GGGGGAGTAC	1200
20	CAGGATGTGC	CTGACTGTGT	CTGGAGCCTC	GATGGCAATC	CCTTCGTGGG	TGGCCCCACC	1260
	CTGACGGGCA	GTGCCCTTGG	GCAAGGCGCA	GAGCGTGGCT	TGGGGAGCGC	CACCAAGACA	1320
	GGCAGGAGC	GGCAGAGCTG	AGTGGTGGTT	TTGCTCACTG	AGTCAACTC	CGAGGATGAG	1380
	GTTCGGGGCC	CAGCGCGTCA	CGCAAGGGCG	CGAGAGCTGC	TCCTGTCTGG	TGTAGGCAGT	1440
	GAGGCGGTGC	GGGAGAGCTG	GGAGGAGATC	ACAGGCAGCC	CAAAGCATGT	GATGGTCTAC	1500
25	TGCGATCCCT	AGGATCTGTT	CAACCAATC	CCTGAGCTGC	AGGGGAAGCT	GTGCAGCCGG	1560
	CAGCGGCCAG	GGTGGCGGAC	ACAAGCCCTG	GACCTGTGCT	TCATGTTGGA	CACCTCTGCC	1620
	TCACTAGGAG	CCGGAATTTT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
	TTTGAGGTGA	ACCTCGACGT	GACACAGSTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCAG	1740
	ACTGCCTTCC	GGCTGGACAC	CAAAACCCACC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
30	GCCCCCTTAC	TAGGTGGGTG	GGGCTCAGCC	GGCACCGCCC	TGCTGCACAT	CTATGACAAA	1860
	GTGATGACCG	TCCAGAGGGG	TGCCCGGCCCT	GGTGTCCCCA	AAGCTGTGGT	GGTGTCTACA	1920
	GGCGGGAGAG	GGCGAGAGGA	TGCAGCCGTT	CCTGCCCAGA	AGCTGAGGAA	CAATGGCATC	1980
	TCTGTCTTGG	TGCTGGGCGT	GGGCGCTGTC	CTAAGTGAGG	GTCTGCGGAG	GCTTGCAGGT	2040
	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGAGCTG	2100
35	CTCATTGAGT	GGCTGTGTGG	AGAAGCCAAG	CAGCCAGTCA	ACCTCTGCAA	ACCCAGCCCG	2160
	TGCATGAATG	AGGGCAGCTG	CGTCTGCGAG	AATGGGAGCT	ACCGCTGCAA	GTGTGCGGAT	2220
	GGCTGGGAGG	GCCGCCACTG	CGAGAACCGT	GAGTGAAGCT	CTTGCTCTGT	ATGTGTGAGC	2280
	CAGGATATGA	TTCTTGAGAC	GCCCTGAGG	CACATGGCTC	CGGTGCAGGA	GGGCAGCAGC	2340
	CGTACCCCTC	CCAGCAACTA	CAGAGAAGGC	CTGGGCACTG	AAATGGTGCC	TACCTTCTGG	2400
40	AATGTCTGTG	CCCCAGGTCC	TTAG				2424

Seq ID NO: C25 DNA Sequence  
Nucleic Acid Accession #: XM\_097386.3  
Coding sequence: 142..795

45	1	11	21	31	41	51	
	CTGCAGAAC	CACCTGGACT	CTGTCCGTGT	CTGTCCCCCG	GCCTCCAGGG	CTCCTCTCCC	60
	GGGACCCCGG	TCCACGCCCT	GGGCCCCGCG	CGGGGGGAAG	CGCTCTGTGC	CTATCTCTGT	120
50	CTACCTCAGG	TCTGACTTTT	GATGCCAAAA	TCTGAGCCCC	TGGGTGCTCT	CTCCCCGGCC	180
	TCCCGTGCAC	CAGGGTCTGC	AGCAGCCACT	GGGGCCTGGC	TGCTCTGTGC	ATCTGGCGGC	240
	CTTGACCCCG	TGGGGCCCCC	GTGCACCTGC	CCACTCTGGA	GCTTGGGGAG	GGGCGGTGCA	300
	GGGTGAGGGG	CTGGGTCTGT	TCCCTCGGGC	TGCGTGTGTG	TGTGCGGAAT	CCTGCGTGTG	360
	GTGTCTGTGG	GCATCCGGC	CTCCCGCGCG	TGGGTGGACC	TGGATTCTAA	CTCAGAGGAC	420
55	TTGAGCCTGC	TGTTAACTCC	GATGATTGTA	GGGACAGGCG	GGGTGGGTGG	GGGGTGGGCG	480
	CGAGGCTGGG	TCCCGGCCCA	GGAGAAGGAA	GTGCTGAAG	GCAGTGGCCA	TGCTGGCGGT	540
	GGAAATGGGA	GGCGGTGCA	GAGGCTCTAT	GGGGCCCGGT	CCTGGATACT	CGGCAGGAAG	600
	CCGTGTCTGC	AGAGGCTCCT	CCCTGCCTCA	GGTGGCCCG	TTCAACCCCA	GCGTGCCTCA	660
	TCTCCTGCCA	CCGCTGTCTG	GTGGGGGTTT	AAATTCGGTG	TGGCTTTCTG	GGGTGCAGCT	720
60	CAGCACCCCC	CCTATGCGAG	ACTGGGAGGG	GGTGGGGCAG	TCCCTCAGC	CAGAGGAGCC	780
	CTGATGGGTG	TCTAGTTCAC	TTGGGACCGT	GGGGCCTGGC	TGCGTACTGA	GTGGGTGCCC	840
	CACAGTCAAG	GCCCAACGGG	GCTCCCCCTG	CTCTGAGATG	TTGGGAGAAA	GGCGGCTTCT	900
	GGAACTCTCC	GTGGGAGCCG	TAGTGGCTG	TCCAGAAAGG	CGGGAGGGTG	GGCAGGGGGC	960
	ACGGGGGGCA	GCTGGGTCTG	TTGTTAAGGG	TCAACCATCT	GTACAGTTGA	ATTTCCTTTC	1020
65	TCTTATCATG	TTTACCCAC	CTGTCCCTT	TTTTCCCAA	TTGTGCTTTT	GCAATTTTTT	1080
	CCTTGGCAAA	TGTAACCTCA	GCCTTTCAAT	CATGAOGTGT	GAAATTTTCA	TTTCTCTGGA	1140
	GTTTGTGAGA	CGGCGTGGGA	ACCAAGCCTG	AAACTCAGGT	AATAGGAGGA	AAAAAAAAAA	1200
	AACCTAAAAA	AATTTTAAAA	AAACATAAAA	CTACTCTCTA	CCTCTGGCTG	GGCCAGCCTT	1260
	GTCTGSCCCT	GGCGCGGGCA	GGGTGGCCTG	TAACAATTTT	AGTTTTCGCA	GAACATTGAG	1320
70	GTATTAAAAA	GAAAAA					1337

Seq ID NO: C26 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 95..2128

75	1	11	21	31	41	51	
	GGGGTAGTTT	GTAGGGAGCG	AGCTCTCCAC	GTGCGGAGCT	GCGAGGCTGG	ACGCTACGGG	60
	CTCTCGGAAA	GGAGAGACAC	CAGCATTTCG	CACATGCTG	TCATCCACTG	ACTTTACATT	120
80	TGCTTCTCTG	GAGCTTGTGG	TGCGGTTTGA	CCATCCCAAT	GAGAGCAGC	AGAAAGACGT	180
	CACACTGAGA	GTATCTGGAG	ACCTTCATGT	TGGAGGAGTG	ATGCTCAAGT	TAGTAGAACA	240
	GATCAATATA	TCCCAAGACT	GGTCAGACTT	TGCTCTTTGG	TGGGAACAGA	AGCAATTGCTG	300
	GCTTCTGAAA	ACCCACTGGA	CCCTGGACAA	ATATGGGGTC	CAGGCAGATG	CAAAGCTTCT	360
	CTTACCCCTT	CAGCATAAAA	TGCTGCGCCT	TCGTCTGCGG	AATTTGAAGA	TGGTGAAGTT	420
	GCGAGTCAGC	TTCTCAGCTG	TGGTTTTTAA	AGCTGTCACT	GATATCTGCA	AAATCTTGAA	480

TATTAGAAGA TCAGAAAGAGC TTTCCTTGTT AAAGCCGCTT GGTGACTATT TTAAGAAGAA 540  
 GAAGAAAAAA GACAAAAATA ATAAGGAACC CATAATTGAA GATATTCTAA ACCTGGAGAG 600  
 TTCTCCAACA GCTTCAGGTT CATCAGTAAG TCCTGGTTTA TACAGTAAAA CCATGACCCC 660  
 TATATATGAC CCCATCAATG GAACACCAGC ATCATCCACC ATGACTTGGT TCAGTGACAG 720  
 CCCTTTGACG GAACAAAAC TGCAGATCCT CGCATTGAGC CAACCCCCC AGTCCCCAGA 780  
 AGCACTTGCG GATATGTACC AGCCTCGGTC TCTGGTTGAT AAAGCCAAGC TCAATGCAGG 840  
 TTGGCTAGAC TCCTCAGGCT CCCTTATGGA ACAAGGCATC CAAGAGGATG AGCAGCTGCT 900  
 CTTACGATTT AAATATTATT CTTTCTTCGA CTTGAATCCT AAATATGATG CTGTCGGAAT 960  
 AAACCAACTC TATGAGCAAG CCAGGTGGGC CATTCTCTTA GAAGAAATTG ATTGCACAGA 1020  
 GGAAGAAATG TTGATCTTTG CAGCTCTACA GTACCACATT AGCAAACTGT CGTTGCTGTC 1080  
 TGAACACACG GATTTTGCGA GCGAGTCCGA GGTGATGAA ATAGAAGCGG CGCTTCTAA 1140  
 TTTGGAAGTA ACCCTAGAAG GTGAAAAGC GGACAGCCTT TTGGAGGACA TTAAGTATAT 1200  
 CCCTAAACTT GCAGATAATC TCAAAATTAT TAGGCCCAAG AAGTTACTAC CAAAAGCTTT 1260  
 CAACAATAT TGGTTTATCT TTAAGACAC ATCCATAGCA TACTTTAAAA ATAAGGAAC 1320  
 TGAACAGGA GAACCACTAG AAAAATAAAA TCTTAGAGGC TGCGAAGTTG TGCCCGATGT 1380  
 AAATGTAGG GCGGCCCCG TGGGAATCAA GTTACTAATC CCTGTTGCGG ATGGTATGAA 1440  
 TGAATGTAT TTGAGATGTG ACCATGAGAA TCAATACGCC CAATGATGCG CTGCTGCAT 1500  
 GTTGGCATCG AAGGGCAAAA CCATGGCAGA CAGCTCTAC CAGCCAGAGG TCCTCAACAT 1560  
 CCTTTCATT CTGAGGATGA AAAACAGGAA CTCTGCATCT CAGGTGGCTT CCAAGTCTGA 1620  
 AAACATGGAT ATGAACCCAG AATGTTTTGT GTACCCAGCG GTGCAAAA GACACAAATC 1680  
 CAACAGCTG GCGGCCCGGA TCTGGAGGC GCACCAAGAC GTGGCCAGA TGCCCTGGT 1740  
 CGAAGCCAAG CTGCGTTCA TCCAGGCGTG GCAGTCACTG CCTGAGTTTG GCCTCACCTA 1800  
 CTACCTTGTC AGATTTAAAG GAAGCAAAA AGATGACATT CTGGGAGTTT CATATAACAG 1860  
 GTTGATTAAA ATTGATGCGA CCACCGGAT TCCAGTGACA ACATGGAGAT TCACAAATAT 1920  
 CAAACAGTGG AATGTAACCT GGGAAACCGG GCAGGTGGTC ATCAGTTTG ACCAAAACTG 1980  
 CTTTACTGCT TTACCTGCTG TGAGTGCAGA TTGCAAGATT GTGCACGAGT ACATTGGCGG 2040  
 CTACATTTTC TTGTCCACCC GCTCCAAGGA CCAGAATGAA ACATCGATG AGGACTTGT 2100  
 CCACAAATG ACCGCGGGTC AGGATTGAAA CAAGCAGCGG TGCTCGGCTC ACACCAACAA 2160  
 GGCAGGCCAA AGGCGCCCTT CCCCAGAGGG ATCCCTAACG TGCCAGCAT GTAGATTCTG 2220  
 GACTAACAGA CAACATACAT TCACCGCTGG TCACCCAGAT CCTCATTCAA ACCCACTGCT 2280  
 GGCACATGCC TTCTCTACT TTGCCCTGTG CTACAGCCA CGGAAGGAGC CTCTCTGTT 2340  
 TTTTCTATAA AATGGGTAGG CAGGAGAAA GCAGGTGCCC TAAGATTGCT CTAAGGCCCA 2400  
 GCATGTGGTT ACAGTCTCT GACTTGCAGA ACCTGCCAGG TGTATGGCTA CAAGTTATCC 2460  
 TGTGCTGAT CTGTCTCATT ACTAAGTCAA TGGAGAAGAC AGAAAGGTAA AAATCACGTG 2520  
 TAGCAAGAAC AACTCTTATT TCACAACTC AGGTATGAAA CGAAACGCTT GTCCCTCATG 2580  
 GAAGTGTCTT TAGCTCTGT CTCTTCAAAA TGGCAGAGG AGTTCTTACA CACACTTTTT 2640  
 CCCTGGAGGC CAAGGTCTAG GGGTAGAAG GGGAGGGGTG GGGCTACCAG GTAGCAGTTG 2700  
 ACAACCCAG GTCAGAGGAG TGGCCCTCAG GTCTATCTGT CCACAGTGAT ACCTGCCAAG 2760  
 ATGACCACTG ACCCACATCT GGTCTTAGTC ATTGCTCTCC TCAGATTCTT GGGGCCACCT 2820  
 GCAAGCCCCA TTCAATCTCT ACAGATCTCT CAGCCACCTG TAAGTCTTT GTGAAGATGT 2880  
 GGGTGACCA GGGGACAGG AAAACCCATT TCTCAACCCA GATCCATGTC TCCACTGCTT 2940  
 CTACTCTGGG TTGGATTCA GGAAGACAGG CACAGTCTCT TCTGTTTATA GAAACACCTG 3000  
 CCAGTGTCAA GGATTCAGT CAGGTGTCTA TCCCAACTGG TCAGGGAGAG AAGGGCAGAC 3060  
 CCATTCTCAA AGACACCAT GTCCAAGGTC TGACAGCTCC CCACTGGCTG CCCCCACAGG 3120  
 GGCCTTAGGC TGGCTGGGT CATGGGGAAG CGTCCCTCT ATCGCTGGTC TGTGTTCTCC 3180  
 TGGATTTGGT ATCTATGTTG GTACGACTCC TGGCCTTTA TCTAAAGGAC TTTGGCTTTT 3240  
 GTAATACACA AGCCAATAAT AGACTTTTT CTCCCCCTCT GTTTTTGCT GTGTCTCTC 3300  
 TGCCTTGAGA CTGCTTGAG ACAGTGCTTG CCTTGAGAGA GTGAGCCAAT TAACAGCTGC 3360  
 CTGAATTGTC ATTTTCCATT TTGGTTGTT AGAGGTGGGA GGGGTGGGTT TTGAGAAGT 3420  
 CAAAGCAAT ACCAGAAGTA AAGGGAATA TCAGACAATA TTTTATTATT TTTTCATAGA 3480  
 TGTCTGCCA CACAAAGAAC TTGGGGTGA AGGATAAGGC AAAAGCTCCA ATCCCATTTT 3540  
 TCAGTTCTCC TAGGATGCAC CCTCAGGGA GCCTGGCCAG AGTTCGAGG CCGTGAGCG 3600  
 TCAGCTGTTG CTTTATTTTC CATCAAAGCC CTCTGAGAAG TGAGACCTCA GCAATTCGG 3660  
 GAGCCACATA AGACAGACT TGGCAAGGGA CCCCCTGGTT CTGAGCCAGT AGCTGCCATC 3720  
 TGGAAATTC TCTTTAGCC TCTCCTTAGA GGTGAATGTG AATGAAGCCT CCCAGGCAAC 3780  
 CGCTGAATT CTGAGGCCCT GCTTAAAGCT CAGAAGTGGT TTAGGCATTG GGAATCTG 3840  
 GTTCACATCA TAAAGAACT GATTGAAAT GTTTTCTATA GAAACAAGTG CTAAGTGATC 3900  
 CGTATTATC TTGATGTTG TCATTTCTCA GTCTTATTT TCAGTTCTAT TATTTTAGAA 3960  
 CCTAGTCAGT TCTTAAAGAT TATAACTGGT CCTACATTAA AATAATGCTT CTGATGTCA 4020  
 GATTTTACCT GTTGTGCTG GAGAACATCT CTGCCATAAT TACCAAGGCC AGACCTTCAG 4080  
 TTCAACATG TCCCTTAGCT TTTCATAGT GTCTGACATT TCCATGAAAA CAAAGGAACC 4140  
 AACTTTGTT TAACCAACT TTGTTTGGT ACAGTTTCA GGGAGCGTT TCTTCCATGA 4200  
 CACACAGCAA CATCCAAAG AAATAACAA GTGTGACAAA AAAAAAATA AACAAACCTA 4260  
 AATGCTACTG TTCCAAAGAG CAACCTGATG GTTTTTTTA ATACTGAGTG CAAAAGGTCA 4320  
 CCCAAATTC TATGATGAAA TTTTAAATTA ATGGGCACCT TTCAACATCA TTTGCTTCT 4380  
 TATCTACAGT TGATTGAGAA ATCTGCATT TTTATCTTT TATATGACTT TTAAGTAAAA 4440  
 GATTATATG GATTGAAAA AAAAAAAAAA A 4471

Seq ID NO: C27 Protein Sequence  
Protein Accession #: NP\_005161.1

1 11 21 31 41 51  
 | | | | |  
 MDGGLPRSA PPAPFPVFGC AARRRPASPE LLRCRRRRR ATABTGGGAA AVARRNERER 60  
 NRKLVNLFQ QALRHVPHG GASKKLSKVE TLRSAYEYIR ALQRLAEHD AVRNALAGGL 120  
 RPQAVRPSAP RGPPGTTTVA ASPSRASSP GRGGSSEPGS PRSAYSSDDS GCEGALSPAE 180  
 RELLDPSWL GGY 193

Seq ID NO: C28 DNA Sequence  
Nucleic Acid Accession #: NM\_017763  
Coding sequence: 169..2520

1 11 21 31 41 51  
 | | | | |

5	AAAAA	AACTTTAGAG	AAAGGAAGGG	CCAAA	ACTAC	GACTTGGCTT	TCTGAAACGG	60
	AAGCATAAAT	GTTCTTTTCC	TCCATTTGTC	TGGATCTGAG	AACCTGCAAT	TGGTATTAGC		120
	TAGTGGAGGC	AGTATGTATG	GTTGAAGTGC	ATTGCTGCAG	CTGGTAGCAT	GAGTGGTGGC		180
	CACCAGCTGC	AGCTGGCTGC	CCTCTGGCCC	TGGCTGCTGA	TGGCTACCCCT	GCAGGCAGGC		240
	TTTGGACGCA	CAGGACTGGT	ACTGGCAGCA	GCGGTGGAGT	CTGAAAGATC	AGCAGAACAG		300
	AAAGCTGTTA	TCAGAGTGAT	CCCCTTGAAA	ATGGACCCCA	CAGGAAAACT	GAATCTCACT		360
	TTGGAAGGTG	TGTTTGTCTGG	TGTTGTCTGAA	ATAACTCCAG	CAGAAGGAAA	ATTAATGCAG		420
	TCCACCCAC	TGTACTGTGT	CAATGCCAGT	GATGACGACA	ATCTGGAGCC	TGGATTTCATC		480
10	AGCATCGTCA	AGCTGGAGAG	TCCTCGACGG	GCCCCCCC	CCTGCCTGTC	ACTGGCTAGC		540
	AAGGCTCGGA	TGGCGGGTGA	GCGAGGAGCC	AGTGTCTGCC	TCTTTGACAT	CAGTGGAGAT		600
	CGAGCTGCTG	CTGAGCAGCT	GCAGCAGCCG	CTGGGGCTGA	CCTGGCCAGT	GGTGTTGATC		660
	TGGGTAATG	AGCTGAGAAA	GCTGATGGAG	TTTGTGTACA	AGAACCAAAA	GGCCCCATGTG		720
	AGGATTGAGC	TGAAGGAGCC	CCCGGCCCTGG	CCAGATTATG	ATGTGTGGAT	CCTAATGACA		780
	GTGGTGGGCA	CCATCTTTGT	GATCATCTCTG	GCTTCGGTGC	TGGCATCCG	GTGCCGCC		840
15	CGCCACGCA	GGCGGATCC	GCTTCAGCAG	AGAACAGCCT	GGGCCATCAG	CCAGCTGGCC		900
	ACCAGGAGGT	ACCAGGCCAG	CTGCAGSCAG	GCCCCGGGTG	AGTGGCCAGA	CTCAGGGAGC		960
	AGCTGCAGCT	CAGCCCCCTGT	GTGTGCCATC	TGTCTGGAGG	AGTTCCTCTGA	GGGCGAGGAG		1020
	CTACGGGTCA	TTTCTGCTCT	CCATGAGTTC	CATCGTAATC	GTGTGGACCC	CTGGTTACAT		1080
	CAGCATCGGA	CTTGCCTCTG	CTGCGTGTTC	AACATCACAG	AGGGAGATTTC	ATTTTCCAG		1140
20	TCCTTGGGAC	CCTCTCGATC	TTACCAAGAA	CCAGGTGCGA	GACTCCACCT	CATTGCGCAG		1200
	CATCCCGGCC	ATGCCCACTA	CCACCTCCCT	GCTGCCTACC	TGTTGGGCC	TTCCCGGAGT		1260
	GCAGTGGCTC	GGCCCCCAGG	ACCTGGTCCC	TTCTGCCAT	CCCAGGAGCC	AGGCATGGGC		1320
	CCTGGGATC	ACCGCTTCCC	CAGAGCTGCA	CATCCCCGGG	CTCCAGGAGA	GCAGCAGCGC		1380
25	CTGGCAGGAG	CCCATGACCC	CTATGCACAA	GGCTGGGGAA	TGAGCCACCT	CCAATCCACC		1440
	TCACAGCACC	CTGCTGCTTG	CCAGTGGCCC	CTACGCGGGG	CCAGGCCCCC	TGACAGCAGT		1500
	GGATCTGGAG	AAAGCTATTG	CACAGAACGC	AGTGGGTACC	TGGCAGATGG	GCCAGCCAGT		1560
	GACTCCAGCT	CAGGGCCCTG	TCATGGCTCT	TCCAGTGACT	CTGTGTTCAA	CTGCACGGAC		1620
	ATCAGCCTAC	AGGGGGTCCA	TGGCAGCAGT	TCTACTTTCT	GCAGCTCCCT	AAGCAGTGAC		1680
30	TTTGACCCCC	TAGTGTACTG	CAGCCCTAAA	GGGGATCCCC	AGCGAGTGGG	CATGCAGCCT		1740
	AGTGTGACCT	CTGGGCTCG	TTCTTGGAC	TGGGTGGTGC	CCACAGGGGA	AACCCAGGTT		1800
	TCCAGCCATG	TCCACTACCA	CCGCCACCGG	CACCACTACT	ACAAAAAGCG	GTTCAGTGG		1860
	CATGGCAGGA	AGCCTGGCCC	AGAAACCGGA	GTCCCCCAGT	CCAGGCCCTCC	TATTCCTCGG		1920
	ACACAGCCCC	AGCCAGAGCC	ACCTTCTCCT	GATCAGCAAG	TCACGGGATC	CAACTCAGCA		1980
35	GGCCCTTCGG	GGCGGCTCTC	TAAACACAG	TGCCCCAGGG	CCCTCCCTGA	GCCAGCCCTC		2040
	GGCCAGTTG	ACGCTCCAG	CATCTGCCCC	AGTACCAGCA	GTCTGTTCAA	CTTGCAAAAA		2100
	TCCAGCCTCT	CTGCCCGACA	CCACAGAGG	AAAAGCGGGG	GGGTCCCTC	CGAGCCCAAC		2160
	CCTGGCTCTC	GGCCCCAGGA	TGCAACTGTG	CACCCAGCTT	GCCAGATTTT	TCCCATTTAC		2220
	ACCCCACTG	TGGCATATCC	TTGGTCCCCA	GAGGCACACC	CCTTGATCTG	TGGACCTCCA		2280
40	GGCCTGGACA	AGCGCTGCTG	ACCAGAAACC	CCAGGCCCTC	GTTACTCAAA	TTACAGCCA		2340
	GTGTGGTTGT	GCCTGACTCC	TGCCAGCCCC	CTGGAACCAAC	ATCCACCTGG	GGAGGGGCTC		2400
	TCTGAATGGA	GTTCTGACAC	CGCAGAGGGC	AGGCCATGCC	CTTATCCGCA	CTGCCAGGTG		2460
	CTGTCCGCC	AGCCTGGCTC	AGAGGAGGAA	CTCGAGGAGC	TGTGTGAACA	GGCTGTGTGA		2520
	GATGTTGAG	CCTAGCTCCA	ACCAAGAGTG	TGCTCCAGAT	GTGTTTGGGC	CCTACCTGGC		2580
45	ACAGAGTCT	GCTCCTGGGA	AAGGAAAGGA	CCACAGCAAA	CACCAATCTT	TTTGCCGTAC		2640
	TTCTAGAAAG	CATGGAAGA	GGACTGGTGA	TGGTGGAGGG	TGAGAGGGTG	CCGTTTCTCTG		2700
	CTCCAGCTCC	AGACCTTGTC	TGCAGAAATC	ATCTGCAGTG	CAGCAATCC	ATGTCCAGCC		2760
	AGGCAACCAG	CTGCTGGCTG	TGGCGTGTGT	GGGCTGGATC	CCTTGAAGGC	TGAGTTTTTG		2820
	AGGGCAGAAA	GCTAGCTATG	GGTAGCCAGG	TGTTACAAAG	GTGCTGCTCC	TTCTCCAACC		2880
50	CCTACTTGGT	TTCCCTCACC	CCAAGCCTCA	TGTTTATACC	AGCCAGTGGG	TTGAGCAGAA		2940
	CGCATGACAC	CTTATCAGCT	CCCTCCTTGG	GTGAGCTCTG	AACACCAGCT	TTGGCCCCCTC		3000
	CACAGTAAGG	CTGCTACATC	AGGGGCAACC	CTGGCTCTAT	CATTTCCTT	TTTTGCCAAA		3060
	AGGACCACTA	GCATAGGTGA	GCCCTGAGCA	CTAAAAGGAG	GGGTCCCTGA	AGCTTTCCCA		3120
	CTATAGTTG	GAGTTCTGTC	CCTGAGGTGG	GTACAGCAGC	CTTGGTTCTC	CTGGGGGTTG		3180
55	AGAATAAGAA	TAGTGGGGAG	GGAAAACTC	CTCCTTGAAG	ATTTCCTGTC	TCAGAGTCCC		3240
	AGAGAGGTAG	AAAGAGGAAA	TTTCTGTGG	ACTTTATCTG	GGCAGAGGAA	GGATGGAATG		3300
	AAAGTAGAAA	AGGCAGAAAT	ACAGCTGAGC	GGGACAAACA	AAGAGTTCTT	CTCTGGGAAA		3360
	AGTTTTGTCT	TAGAGCAAGG	ATGGAAAATG	GGGACAAACA	AGGAAAGCA	AAGTGTGACC		3420
	CTTGGGTTTG	GACAGCCAGC	AGGCCAGCT	CCCCAGTATA	AGCCATACAG	GCCAGGGACC		3480
60	CACAGGAGAG	GAGATTAGAG	CACAAGTCTG	GCCTCACTGA	GTGGACAAGA	GCTGATGGGC		3540
	CTCATCAGGG	TGACATTAC	CCCAAGGGCAG	CCTGACCACCT	CTTGGCCCTC	CAGGCATTAT		3600
	CCCATTGGA	ATGTGAATGT	GSTGGCAAG	TGGGCAGAGG	ACCCACCTG	GGAACCTTTT		3660
	TCCCTCAGTT	AGTGGGGAGA	CTAGCACCTA	GGTACCACA	TGGGTATTTA	TATCTGAACC		3720
	AGACAGACGC	TTGAATCAGG	CATATGTGA	AGAAATATAT	TTATTGCTA	ATATATTTAT		3780
65	CCACAAAAA	AAAAAAAAA	AA					3802

Seq ID NO: C29 Protein Sequence  
Protein Accession #: NP\_004280.2

70	1	11	21	31	41	51	
	MNSSAHYHVN	FSQAISQDVN	LHEAILLCPN	NTFRDRPTAR	TSQSQEPFLQ	LNSHITNFEQ	60
	TLPGTNLTGF	LSPVDNMRN	LTSQDLLYDL	DINIFDEINL	MSLATEDNFD	PIDVSQLFDE	120
	PDSDGLSLSD	SSHNNTSVIK	SNSSHVCD	GAIGYCTDHE	SSSHDLLEGA	VGGYYPEPSK	180
75	LCHLDQSDSD	PHGDLTFQHV	FINHTYHLQP	TAPESTSEPF	PWPGKSQKIR	SRYLEDTRN	240
	LSRDEQRAKA	LHIFPVSDEI	VGMPVDSFNS	MLSRYLTLDL	QVSLIRDIRR	RGNKVAQN	300
	CKRRLDIIIL	NLEDDVCNLQ	AKKETLKRQ	AQCNKAINIM	KQKLHDLVHD	IFSRRLDDQG	360
	RPVNPNNHYAL	QCTHDSILI	VPKELVASGH	KKETQKGRK			400

80 Seq ID NO: C30 DNA Sequence  
Nucleic Acid Accession #: NM\_004442  
Coding sequence: 19..2982

1 11 21 31 41 51

1216

5  
10  
15  
20

```

TTGCCATTCT AACTGGTGTG AGATGGTATC TCATTGTGGG TTTGATTGCG ATTTCTCTAA 5040
TGACCAAGTA AGATGAGCTT TTTTTCATAT GTTTGTGTGC CACATGTTTG TTGTTTCTTT 5100
TGAGAAAGTG CTGTTTCATAA CCTTCACCAA TTTTGTATGA GGTGTTTGTG TCTTTTCTTG 5160
TAAACTTAAT GAAATAAAGC ATGAAGACAA GATTAGAAGA AAAAGAATGA AAAGGAACAA 5220
ACAAAGGCGT CAAGAAATAT GGGACTATGT GACAAGAAC AACTTACGTT TGACTGGTGT 5280
GCTGAAAATG ACAGGGAGAA TGAACCAAG TTGGAACAAC CTCCTCAGGA TATTATCCAG 5340
GAGAACTTCT CCAACCTAGC AAGACAGACC AACGTTCAAA TTCAGGAAAT ACAGAGAACA 5400
CCCAAAGATA TTTCTCGAGA AGAGCAACCC GAAGACACAT AATTGTGAGA TTCACCAAGG 5460
TTGAAATGAA GGAATAAATG CTAAGGGCAG CCAGAGAGAA AGGTACAGGT ACTCACAAAA 5520
GGAAGCCCAT CAGACTAACA GCAGATCTCT CTGCAGAAAC CCTACAACCT AGAAGAGAGT 5580
GGGGACCAAT ATTCAACATT CACAAAGAAA AGAATTTTCA ATCCAGAAAT TCATATCCAG 5640
CCAAACTAAG CTCATAAGC AAAGGAGAAA TAAATCCCTT TACAGACAAG CAAATCTGG 5700
GAGATTTTGT CACCACCAGG CCTGCCTTAC AAGACATCCT GAAGGAAGCA CTAATATGG 5760
AAAAGAAAAA CTGGTGCCAG CCACTGCAAA AAATACCAAA TTGTAGAGAC CATTGACACT 5820
ATGAAGAAC CGTGTCAACT AATGGGCAAA ATAACCAGCT AGTATCATAA TGACAGGATC 5880
AGATTACAC ATAACAATAT TAACCTTATA TCTAAATGGG CTAATCCCC CAATTAAAG 5940
ACGCAGACTG CCAAAATGGT TAAAGAGTCA AGACTCATTG GTGTGCGGTA TTCAGGAGAC 6000
CCATCTCAG TGCAAGACA CACATAGGCT CAGAGTAAAA GGGATACAGG GGAATTC 6057

```

Seq ID NO: C31 DNA Sequence  
Nucleic Acid Accession #: NM\_031942.1  
Coding sequence: 145..1260

25  
30  
35  
40  
45  
50  
55  
60  
65  
70

```

1      11      21      31      41      51
|      |      |      |      |      |
CCCGAGCCCC GCCCCTCGGG GCGCGGGTGG GCGCGCCCAG CCTGCCAGCC GCGCTGCTGC 60
TGCTCTCTCT GCTGTGGGAC CGCTGACGCG GCGGCTGCTC CGCTCTCCCC GCTCCAAGCG 120
CCGATCTGGG CACCGGCCAC CAGCATGGAC GCTCGCGCGG TGCCGCGAGAA AGATCTCAGA 180
GTAAAGAGA ACTTAAAGAA ATTCAAGATAT GTGAAGTTGA TTTCATGGA AACCTCGTCA 240
TCCTCTGATG ACAGTTGTGA CAGCTTTGCT TCTGATAATT TTGCAACAC GAGGCTGCAG 300
TCAGTTCGGG AAGGCTGTAG GACCCGCAGC CAGTGCAGGC ACTCTGAGCC TCTCAGGGTG 360
GCGATGAAGT TTCCAGCGCG GAGTACCAGG GGAGCAACCA AAAAAAAGC AGAGTCCGCG 420
CAGCCCTCAG AGAATTCGT GACTGATTCC AACTCCGATT CAGAAGATGA AAGTGGAAATG 480
AATTTTGTGG AGAAAAGGGC TTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC 540
ATGTTCTGAAT TAGAAGCTT CCTTGGCTCG TTCCGTGGAA GACATCCCTT CCCAGGCTCC 600
GACTCACAAAT CAAGGAGACC GCGAAGGCGT ACATTCGCGG GTGTTGCTTC CAGSAGAAAC 660
CCTGAACGGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCTCGG GTCCCTTGAC 720
GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGTGTGAG AAAGAGGAAG 780
ACCGTGATG GCTCATGAA TGAAGATGAC CTGCCAGAA GCGCTCGCTC CAGATCATCC 840
GTGACCCCTC CGCATATAAT TGCCCGAGTG GAAGAAATTA CAGAGGAGGA GTTGGAGAAC 900
GTCTGCAGCA ATTCTCGAGA GAAGATATAT AACCGTTCAC TGGGCTCTAC TTGTCATCAA 960
TGCGGTGAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGCGGTT 1020
CGAGCCAGT TCTGTGGCCC CTGCCCTTGA AACCGTTATG GTGAAGAGGT CAGGGATGCT 1080
CTGCTGGATC CGAACTGGCA TTGCCCGCCT TGTGAGGAA TCTGCAACTG CAGTTTCTGC 1140
CGGCAAGGAG ATGGACGGTG TGCGACTGGG GTCCTTGTGT ATTAGCCAA ATATCATGGC 1200
TTTGGGAATG TGCAATGCCA CTGAAAAGC CTGAAACAGG AATTGAAAT GCAAGCATAA 1260
TATCTGGAAA ATTTGCTGCC TGCCCTTCTAC TTCTCAATC TTCTCTGTA AAGTTTCCAA 1320
TTTTTCACT GAAACCTGAG TTAATAATCT TGATGATCAG CCTGTTTCAT AAGAACTCC 1380
AATCAAGTAT ACTTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGTGA TATTGCTAGT 1440
TACACTTTCG CCTCTCGAG TTTCTTCTCT GCTCCCAACC CCTATCTCAT AGCATCCCC 1500
TCTATTTCCA ATGCTCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTAA ATTACAGTTT 1560
TATGAAAGCA TATTTTATTT ACTTGGTGTT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
GAAACACAAAT AATAGTATTA ACTAAGTACA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
CTTGTTTACA CAAAACGAG TATGATTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
TCAAGGCACA AAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
CTCTCAATCC CATGTATTGC GCATTATGTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860
CTCTCAATTT CTCTGCGCG AAGGGTAAGT GGTGCGTCCA GCTTACAGCA TCATAATTCA 1920
AAGGTTGAGT GGCATGTAA TACTTAATTA AATAATGAT GGAAGAGCTA TCTGGAGATT 1980
ATGAGTAAGC TGATTGAAAT TTTCAGTATA AAATCTTAGT ATAATTGATG TTTGCAAGT 2040
TTATTTCACT TCACATGTAA GGTATTGCAA ATAAATCTT GGACAATTTT GTATGGAAAC 2100
TTGATATTAA AAACAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACAGGCA 2160
CAAGGTTCAA GTTTAGATT TAAGCACTT TATAACAATG ATAAGTGCCT TTTTGGAGAT 2220
GTAACCTTTA GCAGTTTGT AACTTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
CTGTGTCAGT ATTCCTCTC CTCTTTGCAT TAATCAAGGT ATTGGTGAAG GGTGGAATCT 2340
AAGTGTGTTG ATGTCCAAT TACTTGCTA TGTAACCAT TGCTTGCCA TTCAATGTTT 2400
GTGCTAATAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTGATC GTAATGCTTT 2460
TATACAAAAG TTTATTTTAA TAATAAAATG TTTGTTCTAA AAAAAAATA 2510

```

Seq ID NO: C32 DNA Sequence  
Nucleic Acid Accession #: NM\_012445.1  
Coding sequence: 276..1271

75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
GCACGAGGGA AGAGGGTGAT CCGACCCGGG GAAGGTGCGT GGGCAGGGCG AGTTGGGAAA 60
GCGGCAGCCC CGCGCGCCCC CGCAGCCCTT TCTCTCTCTT TCTCCACGT CATTCTGCC 120
TCTCGCTGGA GGCAGGCGCG TGCAGCATCG AAGACAGGAG GAACCTGAGC CTCATTGGCC 180
GGCCCGGGGC GCGCGCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCCGACC 240
GCTGCGGGCC GCGCTCCGCG TGCTCCTGCC GGGTGATGGA AAACCCAGC CGCGCCGCGC 300
CCCTGGGCAA GGCCTCTGCG GCTCTCTCTC TGGCCACTCT GCGCGCGGCC GGCAGCCTC 360
TTGGGGGAGA GTCCATCTGT TCGCCAGAG CCGCGGCAA ATACAGCATC ACCTTCAGCG 420
GCAAGTGGAG CAGACGCGCC TTCCCAAGC AGTACCCCTT GTTCGCGCCC CCTGCGCAGT 480
GGTCTCGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCAAT 540
ACGTCAGTAA CGGGCTGCGC GACTTTGCGG AGCGCGGCGA GCGCTGGGCG CTGATGAAG 600

```

5  
10  
15  
20

```

AGATCGAGGC GCGCGGGGAG GCGCTGCAGA GCGTGCACGC GGTGTTTTCG GCGCCCGCGG 660
TCCCCAGCGG CACCGGGCAG ACCTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720
TCTCGTTTTG GGTGGGCATC GTGCCAGGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG 780
ACCTGTGCGA CGGGGACCGT TGGCGGAAC AGGCGGGCTT GGACCTGTAC CCTACGACG 840
CQGGAGCGGA CAGCGGCTTC ACCTTCTCCT CCCCACACTT CGCCACCATC CCGCAGGACA 900
CGGTGACCGA GATAACGTCC TCCTCTCCCA GCCACCCGGC CAACTCCTTC TACTACCCGC 960
GGCTGAAGGC CCTGCTCCCT ATGSCCAGGG TGACACTGGT GCGCTGCGA CAGAGCCCCA 1020
GGGCTTCATC CCTCCCGGCC CAGTCTCTGC CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080
CCTCAGTTCC AGAAAGCGCG CTGGACTGCG AGGTCTCCCT GTGGTCGTTC TGGGACTGT 1140
GCGGAGGCCA CTGTGGGAGG CTGCGGACCA AGAGCAGGAC TCGTACGTC CCGGTCCAGC 1200
CGGCCAACAA CGGGAGCCCC TGCCCGAGC TCGAAGAAGA GCTGAGTGC GTCCCTGATA 1260
ACTGCGTCTA AGACAGAGC CCCGAGCCCC CTGGGCCCC CGAGCCATG GGGTGTGCGG 1320
GGCTCTCTGT CAGGCTCATG CTGCGGCGG CCGAGGCACA GGGGTTTCG CGCTGCTCCT 1380
GACCGCGGTG AGCGCGCGCC GACCATCTCT GCACTGAAGG GCGCTCTGGT GCGCGGCAGG 1440
GGCATTGGGA AACAGCTCCT TCCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG 1500
TCTGCTCTCA GCCTCTCTCT CTGCGAGGAT AAAGTCTATC CCAAGGCTCC AGCTACTCTA 1560
AATTATGGTC TCCTTATAAG TTATGTCTGC TCCAGSAGAT TGTCTTCAT CGTCAGGGG 1620
CCTGGCTCCC ACGTGGTTCG AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680
CTCTCCCGAG GCGCGGAGG AGCGGGGCC ACTTGAGAA GGAATAAATG GGGCGGTTTC 1740
GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC 1867

```

25  
Seq ID NO: C33 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1314

30  
35  
40  
45  
50

```

1 11 21 31 41 51
ATGTTACAGG ATCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
AAACCCCGTA TCCCATGGA GACCTTCAGA AAGTGGGGA TCCCATCAT CATAGCACTA 120
CTGAGCCTGG CGATATCAT CATGTGGTT GTCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTT GCGGCGAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGAAGGAGAG 240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTTC CAAGGACCGA TCCCACTGC AGGTGCTGGA CTCGGCCACA 360
GGGAACCTGT TCTCTGCTGT TTGAGACAAC TTCAGAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTGCTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCC GTGTGGTGGG TGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGAGCC CCACTGGGTC 720
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCGA CTTOCCATCC CTGGCTGTGG CCAAGATCAT CATATTGAA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCGCCTCA TGAAGTGCA GTTCCCACTC 900
ACTTTCTCAG GACACATGAG GCGCATCTGT CTGCTCTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACATG TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GGGTACCAGG GGAAGTACG CGAGAAGATG ATGTGTGCGA GCATCCCGGA AGGGGCTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATGT TTGATCTGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
AAGGTCTCAG CTAATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA 1314

```

55  
Seq ID NO: C34 DNA Sequence  
Nucleic Acid Accession #: NM\_003045.1  
Coding sequence: 148..2037

60  
65  
70  
75  
80

```

1 11 21 31 41 51
CGATCCTGCC GGAGCCCCGC CGCGCCCGGC TTGGATTCTG AAACCTTCTT TGTATCCCTC 60
CTGAGACATC TTGTCTGCAA GATCGAGGCT GTCTCTGGT GAGAAGGTGG TGAGGCTTCC 120
CGTCATATTC CAGCTCTGAA CAGCAACATG GGTGCAAAAG TCCTGCTCAA CATTTGGCAG 180
CAGATGCTGC GCGGGAAGGT GGTGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCCTCGGG GTGGGCGACA CACTGGGTGC TGGTGTCTAC 300
GTCCTGGCTG GAGCTGTGGC CCGTGAGAA TGCAGGCCCT CCATTGTCTAT CTCCTTCTCT 360
ATCGCTGGCG TGGCTCTAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTGGGTC 420
CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTACCG TTGGAGAGCT CTGGGCCCTC 480
ATCACCGGCT GGAACCTAAT CCTCTCTAC ATCATGGTA CTTCAGCGT AGCGAGGGCC 540
TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC 600
ATGACTCTGA ACGCCCCCGG CGTGTGGCT GAAACCCCG ACATATTGCG AGTGATCATA 660
ATTCTCATCT TGACAGGACT TTAACTCTT GGTGTGAAG AGTCGGCCAT GGTCAACAAA 720
ATATTCACTT GTATTAAAGT CCTGGTCTCT GGCTTCATAA TGGTGTCTAG ATTGTGAAA 780
GGATCGGTTA AAAACTGGCA GCTCAGGAG GAGGATTTTG GGAACACATC AGGCGGCTC 840
TGTTTGAACA ATGACACAAA AGAAGGGAAG CCGGTTGTG GTGGATTCAT GCCCTTCGGG 900
TTCTCTGGTG TCCTGTGGGG GGCAGGAGCT TGCTTCTATG CCTTCTGGG CTTTGAAGTC 960
ATCGCCACCA TGGCTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCGT GGGGATGCTG 1020
GCGTCCCTCT TGATCTGCTT CATCGCTTAC TTTGGGCTGT CCGCTGCGCT CAGCTCATG 1080
ATGCCCTACT TCTGCTCTGA CAATAACAGC CCGCTGCCC ACCTCTTTAA GCAAGTGGGC 1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCCA TGTTTCCCAT GCCTCGGGT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
TTTAAATCTT TAGCCAAAGT CAATGATAGG ACCAAAACAC CAATAATCGC CACATTAGCC 1320
TCGGGTGCGC TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380
ATGTCTATG GCACTCTCCT GCCTTACTCG TTGGTGGCTG CTTGTGTGTT GGTCTTACGG 1440
TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTTCC AGCTGGGGTT TTTACCAGAG 1560
CGAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAAA ACATGGAGCC TTCCAARATC 1620

```



5 TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680  
 ATTGTGACCG TGCTTGGAGG GGAGGCTCTC ACCAAAGGGG CGCTGTGGGC AGTCTTCTGC 1740  
 CTCGAGGGT CTGCGCTCTC CTGTGCGCTG GTACAGGGGC TCATCTGGAG GCAGCCCGAG 1800  
 AGCAAGACCA AGCTCTCAT TAAGGTTCCC TTCCTGCCAG TGCTCCCAT CCTGAGCATC 1860  
 TTCTGTAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTTGCTGTG 1920  
 TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980  
 TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAGTG CAAGTGACGC 2040  
 ACAGCCCGCG CCCCAGGAGG TGGCAGCAGC CCGAGGGGAC GCCCCAGAGG GACCGGGAGG 2100  
 CACCCACACC TCCCCACACC TGCAACAGAA ACCACCTGGG TCCACACCTT CACTGCA 2157

Seq ID NO: C35 DNA Sequence  
 Nucleic Acid Accession #: NM\_002776.1  
 Coding sequence: 82..912

15 1 11 21 31 41 51  
 ACCAGCGGCA GACCACAGGC AGGGCAGAGG CAGCTCTGGG TCCCTCTCCCT CCTTCTATTC 60  
 GGCGACTCCC AGATCCTGGC CATGAGAGCT CCGCACCTCC ACCTCTCCGC CGCTCTGGC 120  
 20 GCGCGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGCG 180  
 GCGCTGTCTC CCAAAACGCA CACGCGCTTG GACCCGGAAG CCTATGGGCG CCGTGTGCGG 240  
 CGCGGCTGCG AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGGCGGGT 300  
 GTCTGGTGG ACCAGAGTTG GGTGCTGACG GCGCGGCACT GCGGAAACAA GCCACTGTGG 360  
 GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTACAGGGC AGCAGCTCCG CCGGACGACT 420  
 CGCTCTGTTG TCCATCCCAA GTACCAACAG GGCTCAGGCC CCATCTGGCC AAGGCGAAGC 480  
 25 GATGAGCAGC ATCTCATGTT GCTAAGCTG GCCAGGCCCG TAGTGGCGGG GCCCGCGCTC 540  
 CGGGCCCTGC AGCTTCCCTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTGTGCTGG 600  
 TGGGCGACCA CGGCGCGCGG GAGAGTGAAG TACAACAAGG GCCTGACCTG CTCAGCATC 660  
 ACTATCTCTG GCCTTAAAGA GTGTGAGGTC TTCTACCTCG GCGTGGTTCAC CAACAACATG 720  
 ATATGTGCTG GACTGACCG GGGCCAGGAC CCTTGCCAGA GTGACTCTGG AGGCCCGCTG 780  
 30 GTCTGTGACG AGACCTCCA AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC 840  
 CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA 900  
 CGCTCCAAC TATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CCTGCTGATC 960  
 CAGATGCCCA GAGGCTCCAT CGTCCATCCT CTTCTCCCTC AGTGGCTGA ACTCTCCCTT 1020  
 TGTCTGCACT GTTCAAACTT CTGCCGCCCT CCACACTCTT AAACATCTCC CCTCTCACT 1080  
 35 CATTCGCCCA CCTATCCCA TTCTCTGCTC GTACTGAAGC TGAATGCGAG GAAGTGGTGG 1140  
 CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTCTACAC CCAGCCTCTG AGAGCAGTTA 1200  
 CTGGGGTCA CCAACCTGAC TTCTCTGCC ACTCCCGCT GTGTGACTTT GGGCAAGCCA 1260  
 AGTGCCTCT CTGAACCTCA GTTCTCTCAT CTGCAAAATG GGAACAATGA CGTGCTTACC 1320  
 40 TCTTAGACAT GTTGTGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATT 1380  
 GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTCTGACT AAAGTTTACC TGTGTGCTG 1440  
 AAAAAAAAAA AAAA 1454

Seq ID NO: C36 DNA Sequence  
 Nucleic Acid Accession #: XM\_095088  
 Coding sequence: 1..4074

45 1 11 21 31 41 51  
 ATGACCGGGG CCGCGACAGC CGAGCGGGGC CGCGTGTCTC CCGCTCGCC CGCGCGCAGC 60  
 ACGCGGGGCC TGCGCGCGGC CTCTCTGAGC AGCCTGCGCA CCTGTGTAGA CATCTGGAC 120  
 50 GACTGCGAGC GCGGCTCGGT GCACCTGCGA GAGATCCAGT CCTCTGGGT CGAAGCGCGG 180  
 GAGCTGCCAA GCGGGGTGCT GGAGGGGCTG AGCCAGCGGC GCGGGCGCGA GCCGGAGCA 240  
 GCTGTACGCT CCGCGCGAGG CGCGCGCAGT CCGCGCGGGG CCGGAGCGGT TCCAGAGCGC 300  
 55 TGCGCTGGAA CCGAGACCGG CGCGGAGCGC AGGTGCGAGG GCCTGCGAGG CCTTGGAGGC 360  
 GGATTCAGGG GATGCCCGGC GGACCCCTGT GCCCGAGGGG AACACCGGAG GCACACCATC 420  
 ACCAGCGCGG TGACTGTGGG CCGTCTGAAG CAGATGAAG AGCTGGAGCA GGAGAAGGAG 480  
 GTGCTGCTAC AGGGTTTGGG GATGATGGCG CAGGGCGCGG ATTGGTACCA GCAGCAGCTG 540  
 CAACAAGTGC AGGAGCGCCA GTGCGCGCTG GGCCAGAGCA GAGCCAGCGC CGACTTTGGG 600  
 60 GCGTGGGGA GCCCTCGCCC ACTGGGACGG CTACTGCCCC AGGTACAGGA GGTGGCCCGG 660  
 TGGCTGGGGT AGCTGTGGC TGAGGCTGTG GCCGTGCGGG CCTTGCCTCC ATCTCTCTCC 720  
 GGGCCCCCTT GCTCTGCCCT GACGTCCACC TGTTCCCGG GCTGGCAGCA GCAGATCATC 780  
 CTATGCTGA AGGAGCAGAA CCGACTCCTC ACCCAGGAGG TGACCGAGAA GAGTGAGCGC 840  
 ATCAOGCAGC TGGAGCAGAA GTGCGCGCTC ATTAAGCAGC TATTTGAGGC CCGCGCCCTG 900  
 65 AGCCAGCAGG ATGGGGGCTT GTCCCGGCTT GGCCCCACA TTGAGCCCTT GACTGGGTTT 960  
 CGGCTTCGGG TGCTGACATG GGTGGGGCTT CTCTTGTGTC CGCATAGTCC GCAGTACTA 1020  
 CTGCGCGCTG CAGCGGACAG TGGGGGACCC CTCACGAGT TACCAGATAC CTGTTTCCA 1080  
 GCGGTGCTGC TTTGGGTCCC ATCTCCAGGG AAAAGAACTG CTCACGCCG GCTGCACCTC 1140  
 CACCAAGGCG CAGCAGAGGG CGCGTGGCAG CTGCGATGCG GCGCTGAGGC TCGCGCGGAG 1200  
 70 ACCTGAGGGA CGCTGCCCA CTTTGAGTCC CACAAAACAA CCTGTAGGCC TGACTCCCTC 1260  
 GGAGGGCCCT GTCCCGAGGA GGGGGATCGC AGCTGGAGCC ACCTGGGCGC AGCGTTTGAT 1320  
 GTGCGACCTG CAGTGGCCAA AGTGACACCC AACGTGAGG ACGCTGAGG GAGTGGGCAC 1380  
 GGAGACATCT GTCCCTCTG TCCCAAGGGA CTGTTGACAT TCAGAGACAT AGCTATAGAA 1440  
 TTCTCTCTGG CCGAGTGGCA ATGCTTGGAT CATGCTCAGC AGAATTTATA TAGAGATGTG 1500  
 75 ATGTTAGAGA ACTAGAGAAA CCTGTTCTCC CTGGGTATGA CTGTCTCTAA GCCAGACTTG 1560  
 ATCGCTGTG TGGAGCAAAA TAAAGAGCCC CAGAATATAA AGAGAAATGA GATGGCAGCC 1620  
 AAACACCCAG TTACATGTTT TCATTTCAAC CAAGACCTTC AGCCAGAGCA GAGCATAAAA 1680  
 GATTCACTCC AAAAAGTAAT ACCAAGAACA TATGGAAAT GTGGACATGA GAATTTACAA 1740  
 TTAAAAAAT GTTGTAAAAG AGTAGATGAG TGTGAGGTGC ACAGAGGAGG TTATAATGAC 1800  
 80 CTTAAACCAAT GTTGTCAAA TACCAAAAC AAAATATTTC AGACTATAA ATGTGTCAAA 1860  
 GTCTTCAGTA AATTTTCAAA TTCCAATAGA CACAATGCAA GATATACTGG AAAGAAACAT 1920  
 TGAATAATGA AAAAATGAG CAAATCATTT TGCAATGTTT CACACCTAAA TCAACATCAG 1980  
 ATAATTCATA CTAAGAGAA GTCCCTACAAA TGTGAAGAAT GTGGCAATC CTTTAAACCAC 2040  
 TCCTCAAGCG GTACTACACA TAAAGAAAT CTTACTGGAG AGAAACCTTA CAGATGTGAG 2100  
 GAATGTGGCA AAGCCTTTAG GTGGCCCTCA AACCTTACTA GACATAAGAG AATTCACACT 2160

5	GGAGAGAAAC	CCTACGCATG	TGAAGAATGT	GGCCAAGCCT	TTAGGCGCTC	CTCAACACTT	2220
	ACTAACCACA	AGAGAATTCA	TACTGGAGAG	AGACCCCTACA	AATGTGAAGA	ATGTGGCAAA	2280
	GCCTTTAGCG	TATCCTCAGC	CCTCATTTAC	CACAAGAGAA	TTCACTAGG	AGAGAAACCC	2340
	TACACATGTG	AAGAATGTGG	CAAGGCCTTT	AACTGCTCCT	CGACTCTTAA	GACACATAAG	2400
	ATAATTTCATA	CTGGAGAGAA	ACCCTACACA	TGTGAAGAAT	GTGGCAGAAC	CTTTAACTGC	2460
	TCCTCAACTG	TAAAGGCACA	TAAGAGAATT	CATACTGGAG	AGAAACCAT	CAAAATGTGA	2520
	GAATGTGACA	AAGCTTTTAA	GTGGCAATTCA	AGTCTTGCTA	AACATAAGAT	AATTCACACT	2580
	GGAGAGAAAC	CCTACAAATG	CAGTGACAGC	AAAGCCTTAG	CCAAATCATC	AGAAATGCAA	2640
10	AAGGTCTACT	CTGGAGATGG	GGAAATGGA	ATCCGTGTAC	ATAAGAAAAA	GGAGACACAG	2700
	GGCTGGCTTG	TGAGAAACAA	GAACGAAAT	AGAACAGGGC	TGTTCCAGAT	CCGGGCTGCC	2760
	GTGAGACCTA	ACAGGGACCC	TTCTATGGGA	CAGCAAGAG	GTTCACCTGAC	TGACCCCAAT	2820
	CAGAGGAAGG	AGGAACCTGA	CCTTCAAAAT	CACATGACC	ATCAGAAATG	CTTAGAAGAT	2880
	CAAAGAAATA	CTGGAGTGGG	TGGACTGTG	ACATTGAGAG	ATGTAGTCAT	AGAATTCTCT	2940
15	CTGGAGGAGT	GGCAATGCCT	GGATCAGCT	CAGCAGAAAT	TATATAGAGA	TGTGATGTTA	3000
	GAGAACTACA	GAAACCTGGT	CTCCCTGGGT	ATTGCTGTCT	CTAAGCCAGA	CTTGATCACC	3060
	TGTCTGGAGC	AAAATAAAGA	GCCTTGGAA	ATAAAGAGAA	ATGAGATGGT	AACCAACAC	3120
	CCAGACCTTC	CGCCAGAGCT	AGGCATAAAA	GATTCACTCC	AAAAAGTAAT	ACCAAGAAGA	3180
	TATGGAAAAA	TGGGACATGA	CAATTTACAA	GTAAGAAAT	GTAAGAAAT	GGGTGAGTGT	3240
20	GAGGTGCAAA	AAGGAGGTTG	TAATGAAGTT	AACCAATGTT	TGTCAACTAC	CCAAAAACAA	3300
	ATATTTTCAG	CTCATAAATG	TGTCAAAGTC	TTGGGCAAT	TTTCAAAATC	CAATAGACAT	3360
	AAGACAAGAC	ATACTGGAAA	GAAACATTTC	AAATGTAAAA	AATATGGCAA	ATCATTTTGC	3420
	ATGGTTTCAC	AACTACATCA	ACATCAGATA	ATTCTACTA	GGGAGAAATC	CTACCAATGT	3480
	GAAGAAATCG	GCAAAACCTT	CAACTGCTCT	TCAACCTTT	CTAAACATAA	AGAATTTCT	3540
25	ACTGGAGAGA	AACCTACAG	ATGTGAGGAA	TGTGGCAAAG	CTTTTACCTG	GTCTTCAACC	3600
	CTTACTAAAC	ATAGGAGAA	TCATCTGGA	GAAAAACCTT	ACACATGTGA	AGAATGTGGC	3660
	CAAGCCTTTA	CGCGCTCCTC	AACACTTGCT	AACCAACAGA	GAATTCATAC	TGGAGAGAAA	3720
	CCATACACAT	GTGAAGAATG	TGGCAAAAGC	TTTAGCTTAT	CCTCATCCCT	CACCTTACCAC	3780
	AAGAGAAATA	TAATCTGGGA	GAAACCTTAC	ACATGTGAAG	AATGTGGCAA	AGCCTTTAAC	3840
30	TGCTCCTCAA	CCCTTAAGAA	ACATAAGATA	ATTCTACTG	GAGAGAAACC	CTACAAATGT	3900
	AAAGAAATGT	GGAAAGCCTT	TGCCTTCTCC	TCAACTCTTA	ATACTCATAA	GAGGATTCAT	3960
	ACTGGAGAGG	AACCTTACAA	ATGTGAAGAA	TGTGACAAAG	CTTTTAAGTG	GTCTTCAAGT	4020
	CTTGCTAATC	ATAAGAGTAT	GCATCTGGA	GAGAAACCTT	ACAAATGTGA	ATAA	4074

Seq ID NO: C37 DNA Sequence  
Nucleic Acid Accession #: NM\_032044  
Coding sequence: 182..658

40	1	11	21	31	41	51	
	AAAGATATAAA	AGCTCCAGAA	ACGTTGACTG	GGACCACTGG	AGACACTGAA	GAAGGCAGGG	60
	GCCCTTAGAG	TCTTGGTTGC	CAAAACAGATT	TGCAGATCAA	GGAGAACCCA	GGAGTTTCAA	120
	AGAAGCGCTA	GTAAGGCTCT	TGAGATCCTT	GCACTAGCTA	CATCCTCAGG	GTAGGAGGAA	180
	GATGGCTTCC	AGAAGCATGC	GGCTGCTCCT	ATTGCTGAGC	TGCTTGCCCA	AAACAGGAGT	240
45	CCTGGGTGAT	ATCATCATGA	GACCCAGCTG	TGCTCCTGGA	TGGTTTTACC	ACAAAGTCAA	300
	TGCTATGGT	TACTTCAGGA	AGCTGAGGAA	CTGGTCTGAT	GCGAGCTCG	AGTGTCAATC	360
	TTACGGAAAC	GGAGCCACAC	TGGCATCTAT	CCTGAGTTTA	AAGGAAGCCA	GCACCATAGC	420
	AGAGTACATA	AGTGCTATC	AGAGAAGCCA	GCAGATATGG	ATTGGCCTGC	ACGACCCACA	480
	GAAGAGGCAG	CAGTGGCACT	GGATTGATGG	GGCCATGTAT	CTGTACAGAT	CTGGTCTGG	540
50	CAAGTCCATG	GGTGGGAACA	AGCACTGTGC	TGAGATGAGC	TCCAATAACA	ACTTTTTAAC	600
	TTGGAGCAGC	AACGAATGCA	ACAAGCGCCA	ACACTTCTCT	TGCAAGTACC	GACCATAGAG	660
	CAAGAATCAA	GATTCTGCTA	ACTCTGTCAC	AGCCCGCTCC	TCTTCTTTTC	TGCTAGCCTG	720
	GCTAAATCTG	CTCATTTATT	CAGAGGGGAA	ACCTAGCAAA	CTAAGAGTGA	TAAGGGCCCT	780
	ACTACACTGC	CTTTTATAGG	CTTAGAGACA	GAAACTTTAG	CATTGGCCCA	GTAGTGGCTT	840
55	CTAGCTCTAA	ATGTTTGCCC	CGCCATCCCT	TTCCACAGTA	TCTTCTTCCC	CTCCTCCCTC	900
	GTCTCTGGCT	GTCTGAGGCA	GTCTAGAAGA	GTGCATCTCC	AGCCTATGAA	ACAGCTGGGT	960
	CTTTGGCCAT	AAGAATGATA	GATTTGAAGA	CAGAAGGAAG	AAACTCAGGA	GTAAGCTTCT	1020
	AGACCCCTTC	AGCTTCTACA	CCCTTCTGCC	CTCTCTCCAT	TGCTGACACC	CCACCCAGC	1080
	CACCTCAACT	CTGCTTGTTT	TTCTTTGGC	CATAGGAAGG	TTTACAGTA	GAATCTTGC	1140
60	TAGGTTGATG	TGGGCCATAC	ATTCTTTTAA	TAAACCAATG	TGTACATAAG	AAAAAATAAA	1200

Seq ID NO: C38 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 52..3042

65	1	11	21	31	41	51	
	GCTCACCAG	GAAAAATATG	CAATCGTCCC	ATTGATATAC	AGGCCACTAC	AATGGATGGA	60
	GTTAACTCTA	GCACCGAGGT	TGCTTACAAA	AAAGGCCAGG	ATTATAGGTT	TGCTTGCTAC	120
	GACCGGGGCA	GAGCCTGCGG	GAGCTACCGT	GTACGGTTCC	TCTGTGGGAA	GCCTGTGAGG	180
70	CCCAAACTCA	CAGTCACCAT	TGACACCAAT	GTGAACAGCA	CCATTCTGAA	CTTGGAGGAT	240
	AATGTACAGT	CATGGAATCC	TGGAGATACC	CTGGTCATTG	CCAGTACTGA	TTACTCCATG	300
	TACCAGGCAG	AAGAGTTCCA	GGTGTCTCCC	TGCAGATCCT	GCGCCGCCAA	CCAGGTCAAA	360
	GTGGCAGGGA	AACCAATGTA	CCTGCACATC	GCGGAGGAGA	TAGACGCGGT	GGACATGCGG	420
75	GCGGAGGTTG	GGCTTCTGAG	CCGGAACATC	ATAGTATGGG	GGGAGATGGA	GGACAAATGC	480
	TACCCCTACA	GAAACCCATC	CTGCAATTTT	TTTGACTTCG	ATACCTTTGG	GGGCCACATC	540
	AAGTTTGCTC	TGGGATTATA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTCAAGT	CCCGATTAC	TTCCACCTGG	CGGGTATGAT	AGAAGAAAGG	660
	GGAGGTTATG	AACCAACCCAC	ATACATCAGG	GACCTCTCCA	TCCATCATAC	ATTCTCTGCG	720
80	TGCGTCAAG	TCCATGGCTC	CAATGGCTTG	TTGATCAAGG	ACGTTGTGGG	CTATAACTCT	780
	TTGGGCCACT	GCTTCTTAC	GGAAGATGGG	CCGGAGGAAC	GCAACACTTT	TGACCACTGT	840
	CTTGGCTTCC	TTGTCAAGTC	TGGAACCTTC	CTCCCTCGG	ACCGTGACAG	CAAGATGTGC	900
	AAGATGATCA	CAGGAGACTC	CTACCCAGGG	TACATCCCCA	AGCCAGGCA	AGACTGCAAT	960
	GCTGTGTCCA	CTTCTGGGAT	GGCCCAATCCC	AACAACAACC	TCATCAACTG	TGCCGTGCA	1020
	GGATCTGAGG	AAACTGGATT	TTGGTTTATT	TTTACCACCG	TACCAACGGG	CCCCCTCGTG	1080

	GGAATGTACT	CCCCAGGTTA	TTGAGAGCAC	ATTCCACTGG	GAAAATTCTA	TAACAACCGA	1140
	GCACATTCCA	ACTACCGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCTGCCAAGG	ACAAGCGGGC	GTTCCTCTCA	ATCATCTCTG	CCAGATACAG	CCCTCACCAG	1260
5	GACGCCGACC	CGCTGAAGCC	COGGGAGCCG	GCCATCATCA	GACACTTCAT	TGCTTACAAG	1320
	AACCAGGACC	ACGGGGGCTG	GCTGCGCGGC	GGGATGTGT	GGCTGGACAG	CTGCCGGTTT	1380
	GCTGACAATG	GCATTGGCCT	GACCCCTGGC	AGTGGTGAA	CCTCCCGTA	TGACGACGGC	1440
	TCCAAGCAAG	AGATAAAGAA	CAGCTTGTTT	GTGGCGAGA	GTGGCAACGT	GGGGACGGAA	1500
	ATGATGGACA	ATAGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCTCCCTT	1560
10	ATAGGCCAGA	ATTTTCCAAT	TAGAGGAATT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACTT	TCCGAAAGTT	TGTGGCCCTG	GAGGGCCGGC	ACACCAGCGC	CCTGGCCTTC	1680
	GGCTGGAATA	ATGGCTGGCA	GAGCTGCCCC	CATAACAACG	TGACCGGCAT	TGCCCTTGAG	1740
	GAGGTTCCGA	TACTTCCAG	AGTGTCTTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTT	CATGACGTCG	ACGGCTCCGT	GTCGAGTAC	1860
	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGGTCC	GGCACCAGAA	CTGCATCAAT	1920
15	GTTCGCCACT	GGAGAGGGGC	CATTTCAGT	GGGTGCTATG	CACAGATGTA	CATTCAAGCC	1980
	TACAAGAGCA	GAGCTCTGCG	AATGAAGATC	ATCAAGAATG	ACTTCCCGAT	CCACCTCTT	2040
	TACCTGGAGG	GGGCGCTCAC	CAGGAGCACC	CATTACCAGC	AATACCAACC	GGTTGTCAAC	2100
	CTGCAGAGG	GCTACACCAT	CCACTGGGAC	CAGACGGGCC	CCGCCGAAC	CGCCATCTGG	2160
20	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGCTACCC	GCGAGGACCC	2220
	ACATCTCTCA	TCTCTCGGGA	TGTTCACAAT	CGCCTGCTGA	AGCAAACTGC	CAAGACGGGC	2280
	GTCTTCGTGA	GAGCCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTGGG	CAGGAGCCAC	2340
	TACTACTGGG	ACGAGGACTC	AGGGCTGTGG	TTCTTGAAGC	TGAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
25	CCAAAGAACG	CAGGCGTCAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
	GCTGTGCTAG	AGGTGCCGAT	GCCCAAGAG	CTCTTTGGTT	CTCAGCTGAA	AACAAAGGAC	2580
	CATTCTTTGG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAACGAC	2640
	TTGCTTACA	TTGAAGTGA	TGGGAAGAG	TACCCAGTT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACCTCAAT	2760
30	CTGCAAGGCA	TACCATGGCA	GCTTTTCAAC	TATGTGGGGA	CCATCCCTGA	CAATTCCATA	2820
	GTGCTTATGG	CATCAAAAGG	AAGATACGTC	TCCAGAGGCC	CATGGACAGG	AGTGTGGGAA	2880
	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAGAGCAAAA	TGGCATTCTG	TGGCTTCAAA	2940
	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCAAAAAGC	CAAAATCTTC	3000
	CAAGTTGTC	CCATCCCTGT	GGTGAAGAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
35	GCCACCTCGT	GGTAGACTAT	GACGGTGACT	CTTGGCAGCA	GACCACTGGG	GGATGGCTGG	3120
	GTCCCCAGC	CCCTGCCAGC	AGCTGCTGCG	GAAGGCCGCT	TTTCAGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TCAGAGACCC	TGGTGCTGCC	ACCTGCCCT	ACTCAAGTGT	CTACCTGGAG	3240
	CCCTGGGGGC	GGTGCTGGCC	AATGCTGGAA	ACATTCACIT	TCTGCGACCC	TCTTGGGTGC	3300
	TTCTCTCTTA	TCGTGCTCTC	TTGAGTGGGG	GTTTGGGGAC	CATATCAGGA	GACCTGGGTT	3360
40	GTGCTGACAG	CAAAAGATCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAGTCTGGA	3420
	GGGCTGGTCA	TTCAAGATGC	CCCATGGTCT	TCAGCAGACA	AGTAGGGGTG	GTAAATGTAG	3480
	GAGAAGGAGC	CTTGGGCTTA	AGGAAATCTT	TACTCTGTGA	AGCAAGAGCC	AACCTCACAG	3540
	GATTAGGAGC	TGGGGTAGAA	CTGGCTATCC	TTGGGGAAGA	GGCAAGCCCT	GCCTCTGGCC	3600
	GTGTCCACCT	TTGAGGAGAC	TTTGAAGTGG	AGGTTTGGAC	TTGGACTAGA	TGACTCTCAA	3660
45	AGGOCCTTTT	AGTTCTTGAGA	TTCCAGAAAT	CTGCTGCATT	TCACATGGTA	CCTGGAAACC	3720
	AACAGTTTAT	GGATATCCAC	TGATATCCAT	GATGCTGGGT	GCCCCAGCGC	ACACGGGATG	3780
	GAGAGGAGCA	AACTAATGCC	TAGCTTGAGG	GGTCTGCAGT	CCAGTAGGGC	AGGCAGTCAG	3840
	GTCCATGTGC	ACTGCAATGC	CAGGTGGAGA	AATCACAGAG	AGGTAAATG	GAGGCCAGTG	3900
	CCATTTCAGA	GGGGAGGCTC	AGGAAGGCTT	CTTGCTTACA	GGAAATGAAG	CTGGGGGCAT	3960
50	TTTGTGAGGG	GGAGATGAGG	CAGCCTCTGG	AATGGCTCAG	GGATTACAGC	CTCCCTGCCG	4020
	CTGCGCTGCT	AAGCTGGTGA	CTACGGGGTC	GCCCTTTGCT	CAGCTCTCTC	TGGGCCACTC	4080
	ATGATAGAGC	CTGTGGGTGA	GAGGGGAGCA	ATGGGCTTTG	CTGCTTATGA	GCAACAGGGA	4140
	ATTCACTCCC	CAGGCAGCCC	TGCCCTCTGAC	TCCAAGAGGG	TGAAGTCCAC	AGAACTGAGC	4200
	TCTCGCTTAA	GGGCCTCATT	TGCTCTTCAT	CCAGGGAACT	GAGCACAGGG	GGCCTCCAGG	4260
55	AGACCTTAGA	TGTGCTTGTA	CTCCCTGGGC	CTGGGATTTC	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA	TTTTAAACAG	TGGGGAAAGT	GAGCCCCCAA	GATGGGAAAG	4380
	AAACCACAGC	CTAAGGGAGG	GCCTGGGGAG	CCCCACCTTA	GCCTTGTCTG	CCACACCAAC	4440
	TTGCTCAAC	AACCGGCCCC	AGAGTGCCCA	GGCACTCCTG	AGGTAGCTTC	TGGAAATGGG	4500
	GACAAGTCCC	CTGGAAGGAA	AGGAAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
60	CCCTCTGTCT	CCAGCGCAC	ACAAACCCGC	CCTCCCTTGG	GTGTTGGCGG	TCCCTGTGGC	4620
	CTTCACTTTG	TTCACTACCT	GTGACGCCAG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCAT	4680
	TGGTGCTACC	TGGCTCTCCT	GTCTCTGCAG	CTCTACAGGT	GAGGCCAGC	AGAGGGAGTA	4740
	GGGCTGCGCA	TGTTTCTGGT	GAGCCAATTT	GGGTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTC	AGCTGCTGCT	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
65	ATAGAGAGCC	CAAGAGAGCT	CTGTAAGAGG	GAGAAGCTTA	TCTGTGGTTT	ATAATCTTGC	4920
	ACGAGGACCC	AGAGTCTCCC	TGGGTCTTGT	GATGAATCAC	ATTATATCCC	TTTCTGCCCC	4980
	CAACCCACAA	CTCTTTCCCT	CAAGAGGGGC	CTGCCCTGGT	CCCTCCACCC	AACTGCACCC	5040
	ATGAGACTCG	GTCCAAGAGT	CCATTCCCCA	GGTGGGAGCC	AACTGTCAAG	GAGGTCTTTC	5100
	CCACCAACAA	TCTTTCAGCT	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
70	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTATGGAG	5220
	AGGAGAGTTA	AAATGACCTC	ATGTCCTTCT	TGTCAACGGT	TTTGTGTAGT	TTTCACTCTT	5280
	CTAATGCAAG	GGTCTCACAC	TGTGAACCCAC	TTAGGATGTG	ATCACTTTCA	GGTGGCCAGG	5340
	AATGTTGAAT	GTCTTTGGCT	CAGTTCAATT	AAAAAAGATA	TCTATTGTAA	AGTTCCTAGA	5400
	GTGTATACAT	TGTTTCACAG	TACAGGATCT	GTACATAAAA	GTTTCTTTCC	TAAACCATTC	5460
75	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
	TGTGCTCCTT	TGTATTCTCT	GTGTGAAGA	CTTAAGTGAG	TTAGGTCTTT	AAGGAAAGGA	5580
	AGCTCTCTCT	GAATGCTCTG	TCITTTTCTT	GTGCGGAAA	TAGCTGGTCC	TTTTTCGGGA	5640
	GTTAGATGTA	TAGAGTGTGT	GTATGTAAAC	ATTTCTTGTA	GGCATCACCA	TGAACAAAGA	5700
	TATATTTTCT	ATTTATTTAT	TATATGTGCA	CTTCAAGAAG	TCACTGTCTG	AGAAATAAAG	5760
80	AATGTCTCTA	AATGTCAAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	5808

Seq ID NO: C39 DNA Sequence  
Nucleic Acid Accession #: NM\_014373  
Coding sequence: 322.1338

```

1      11      21      31      41      51
|      |      |      |      |      |
5  GTGGCCTCGA GGTGGTGGCA GGGCCGCCCC CTGCAGTCGG GAGACGAACG CACGGACCCG 60
   GCCTCCGGAG GCAGGTTGGG CTGGAAGGAA CCGCTCTCGC TTGCTCCTAC ACTTGCACAA 120
   ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
   AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
   GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGGTCT 300
   TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAAGTCTCT TTTTCAGTAC 360
   CAGTTACGTC AAATAAACCA GCCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420
10  GGGAAATAT TATTAAATAT CCTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAT 480
   TTTATGGAAT ATTTTGTGAT TTCACTAGCA TTCGTTGATC TTTTACTTTT GGTAAACATT 540
   TCCATTATAT TGTATTTCAG GGATTTTGTA CTTTAAAGCA TTAGGTTTCC TAAATACCAC 600
   ATCTGCCTAT TTAATCAAAAT TATTTCCTTT ACTTATGGCT TTTTGCAATTA TCCAGTTTTC 660
   CTGACAGCTT GTATAGATTA TTGCCCTGAAT TTCTCTAAAA CAACCAAGCT TTCATTAAAG 720
15  TGTCAAATAT TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTTCAGT CCTTGTCTAT 780
   GTTTTGGGAG ACCCAAGCCAT CTACCAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840
   TGTCTTTTCT ATGTACAGAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA 900
   TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
   ACTTCCATTA TGAATGAACA TATCTTATAT TTTCTTTTTC CATCCCACTC CAGTTATACT 1020
20  GTGAGATCTA AAAAAATATT CTTATCCAAG CTCATGTCCT GTTTTCTCAG TACCTGGTTA 1080
   CCATTTGTAC TACTTCAGGT AATCATTGTT TTAATTAAG TTCAGATTCC AGCATATATT 1140
   GAGATGAATA TCCCTGGTAT ATACTTTGTC AATAGTTTTT TCATTGCTAC AGTGATTGG 1200
   TTTAATTGTC ACAGCTTAA TTTAAAGAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260
   TGGAGGTGCT GCTTCAATCC ACTTACAATT CCTAATCTTG AGCAAAATGA AAAGCCTATA 1320
25  TCAATAATGA TTTGTTAATA TTATTAAATA AAAGTTACAG CTGTCAATAG ATCATAATTT 1380
   TATGAACAGA AAGAAGCTCAG GACATATTA AAAAAAAT GAACTAAAAA AACTTTTGCC 1440
   CCTGACTGA TAGCATTTC GAATGTGCT TTTGAAGGCG TATACCAGTT ATTAATAGT 1500
   GTTTTATTTT AAAAAAATAA TAATTCCAAG AAGTTTTTAT AGTTATTTCAG GGACACTATA 1560
   TTACAAATAT TGTATTGTTA TTAACACAAA AAGTGATAAG AGTTAAACATT TGGCTATACT 1620
30  GATGTTTGTG TTAATCAAAA AAAGTACTG ATGCAAACTG TTATGTAAT CTGAGATTTC 1680
   ACTGCAACT TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAAT GTAAGCAAGA 1740
   AAAAAAAAAA

```

Seq ID NO: C40 DNA Sequence  
Nucleic Acid Accession #: BC012089  
Coding sequence: 1..2571

```

1      11      21      31      41      51
|      |      |      |      |      |
40  ATGGCCCTCG TACTCGGCTC CCTGTTGCTG CTGGGGCTGT GCGGGAATC CTTTTCAGGA 60
   GGGCAGCCTT CATCCACAGA TGCTCCTAAG GCTTGAATT ATGAATTGCC TGCAACAAT 120
   TATGAGACCC AAGACTCCCA TAAAGCTGGA CCCATTGSCA TTCTCTTTGA ACTAGTGCAT 180
   ATCTTTCTCT ATGTGGTACA GCCGCGTGAT TTCCCAGAAG ATACTTTGAG AAAATTTCTTA 240
   CAGAAGGCAT ATGATCCCAA AATTGATTAT GACAAGATTG TCTACTATGA AGCAGGGATT 300
45  ATTCTATGCT GTGCTCTGGG GCTGCTGTTT ATTATTCTGA TGCTCTGGT GGGGTATTTC 360
   TTTTGTATGT GTGCTTGCTG TAACAAATGT GGTGGAGAAA TGCACCAGCG ACAGAAGGAA 420
   AATGGGCCCT TCCTGAGGAA ATGCTTTGCA ATCTCCCTGT TGGTGATTGG TATAATAATA 480
   AGCATTGGCA TCTTCTATGG TTTTGTGGCA AATCACCAGG TAAGAACCAG GATCAAAAGG 540
   AGTGGGAAC TGCGAGATAG CAATTCCAAG GACTTGGGAA CTCTCTTGAA TGAAACTCCA 600
50  GAGCAATCA AATATATATT GGCCAGTAC AACACTACCA AGGACAAGGC GTTCAAGATC 660
   CTGAACAGTA TCAATTTCAGT GCTAGGAGGC GGAATTTCTG ACCGACTGAG ACCCAACATC 720
   ATCCCTGTTT TTGATGAGAT TAAGTCCATG GCAACAGCGA TCAAGGAGAC CAAAGAGGCG 780
   TTGAGAACCA TGAACAGCAC CTGGAAGAGC TTGCACCAAC AAAGTACACA GCTTAGCAGC 840
   AGCTGACCA AGTCAAAAAA TAGCCTGGCG TCACTCTCTA ATGACCCCTC GTGCTTGGTG 900
55  CATCCATCAA GTGAAACCTG CAACAGCATC AGATTGTCTC TAAGCCAGCT GAATAGCAAC 960
   CCTGAATGGA GGCAGCTTCC ACCCGTGGAT GCAGAACTTG ACAACGTTAA TAAOGTTCTT 1020
   AGGACAGATT TGGATGGCCT GGTCCAACAG GGCATCAAT CCCTTAATGA TATACCTGAC 1080
   AGAGTACAAC GCCAAACCCAG GACTGTGCTA GCAGGATATCA AAAGGCTCTT GAATTCCATT 1140
   GGTTCAGATA TCGAATATGT AACTCAGCGT CTTCCTATTG AGGATATACT CTCAGCATTG 1200
60  TCTGTTTATG TTAATAACAC TGAAGTTTAC ATCCACAGAA ATTTACCTAC ATTGGAAGAG 1260
   TATGATTCAT ACTGTTGGCT GGTGGCCTG GTCATCTGCT CTCTGCTGAC CCTCATCGTG 1320
   ATTTTATTTT ACCTGGGCTT ACTGTGTGGC GTGTGCGGCT ATGACAGGCA TGCCACCCCG 1380
   ACCACCCGAG GCTGTGCTCT CAACACCGGA GCGCTCTTCC TCATGGTTGG AGTTGGATT 1440
   AGTTTCCCTT TTTGCTGGAT ATTGATGATC ATTGTTGGTT TTACCTTTGT CTTTGGTGCA 1500
65  AATGTGGAAG AACTGATCTG TGAACCTTAC ACGAGCAAGG AATTATTCCG GGTTTTGGAT 1560
   ACACCCCTCT TACTAAATGA AGACTGGGAA TACTATCTCT CTGGGAAGCT ATTTAATAAA 1620
   TCAAAAATGA AGCTCACTTT TGAACAAGTT TACAGTGACT GCAAAAAAAA TAGAGGCACT 1680
   TACGGCACTC TTCACCTGCA GAACAGCTTC AATATCAGTG AACATCTCAA CATTATGAG 1740
70  CATACTGGAA GCATAAGCAG TGAATTGGAA AGTCTGAAGG TAAATCTTAA TATCTTTCTG 1800
   TTGGGTGCAG CAGGAAGAAA AAACCTTCAG GATTTTGCTG CTTTGGGAAT AGACAGAATG 1860
   AATTATGACA GCTACTTGGC TCAGACTGGT AAATCCCCCG CAGGAGTGAA TCTTTTATCA 1920
   TTTGCATATG ATCTAGAAGC AAAAGCAAAC AGTTTGCCCC CAGGAATTTT GAGGAATCC 1980
   CTGAAAGAG AGTCACAAAC TATTAAACAA ATTCACCAGC AACGAGTCTT TCCTATAGAA 2040
   CAATCACTGA GCACTCTATA CCAAGCGTC AAGATACTTC AACGCACAGG GAATGGATTG 2100
75  TTGGAGAGAG TAACTAGGAT TCTAGCTTCT CTGGATTTTG CTCAGAATTT CATCAAAAC 2160
   AATGATTCCT CTGTATTAT TGAAGAACT AAGAAGTATG GGAGAACAAT AATAGGATAT 2220
   TTTGAACATT ATCTGCAGTG GATCGAGTTC TCTATCAGTG AGAAAGTGGC ATCGTGCAAA 2280
   CCTGTGGCCA CCGCTCTAGA TACTGTGTTT GATGTCTTTC TGTGTAGCTA CATTATCGAC 2340
   CCTTGAATT TGTTTTGGTT TGGCATAGGA AAAGCTACTG TATTTTACT TCGGGCTCTA 2400
80  ATTTTGGCGG TAAAGCTGGC TAAGTACTAT CGTGAATGG ATTCGGAGGA CGGTGACGAT 2460
   GATGTTGAAA CTATACCAT GAAAAATATG GAAAAATGTA ATAATGGTTA TCATAAAGAT 2520
   CATGTATATG GTATTCACAA TCTGTTTATG ACAAGCCCAT CACAACATTG A 2571

```

Seq ID NO: C41 DNA Sequence

Nucleic Acid Accession #: NM\_033049  
Coding sequence: 28..1566

```

5      1      11      21      31      41      51
|      |      |      |      |      |
CCACGCGTCC GAGCAAGAAC AGCTAAATG AAAGCCATCA TTCATCTTAC TCTTCTTGCT 60
CTCCTTTCCTG TAAACACAGC CACCAACCAA GGCAACTCAG CTGATGCTGT AACCAACCACA 120
GAAACTGCGA CTAGTGGTCC TACAGTAGCT GCAGCTGATA CCACTGAAAC TAATTTCCCT 180
GAAACTGCTA GCACCACAGC AAATACACCT TCTTTCCCAA CAGCTACTTC ACCTGCTCCC 240
10    CCCATAATTA GTACACATAG TTCCTCCACA ATTCCTACAC CTGCTCCCCC CATAATTAGT 300
ACACATAGTT CCTCCACAAT TCCTATACCT ACTGCTGCAG ACAGTGAGTC AACCACAAAT 360
GTAAATTCAT TAGCTACCTC TGACATAATC ACCGCTTCAT CTCCAAATGA TGGATTAAATC 420
ACAATGGTCT CTCTGAAAC ACAAGTAAC AATGAAATGT CCCCCACCAC AGAAGACAAT 480
CAATCATCAG GGCCTCCAC TGGCACCGCT TTATTGGAGA CCAGCACCTT AAACAGCACA 540
15    GGTCCACGCA ATCCTTGCCA AGATGATCCC TGTGCAGATA ATTCGTTATG TGTTAAGCTG 600
CATAATACAA GTTTTTCCTG GTGTTTAGAA GGGTATTACT ACAACTCTTC TACATGTAAG 660
AAAGGAAGAG TATTCCCTGG GAAGATTTCG GTGACAGTAT CAGAAACATT TGACCCAGAA 720
GAGAAACATT CCATGGCCTA TCAAGACTTG CATAGTGAAA TTACTAGCTT GTTTAAAGAT 780
GTATTTGCCA CATCTGTTTA TGGACAGACT GTAATCTTGA CTGTAAGCAC ATCTCTGTCA 840
20    CCAAGATCTG AATGCGTGC TGATGACAAG TTTGTTAATG TAACAATAGT AACAAATTTG 900
GCAGAAACCA CAAGTGACAA TGAGAAGACT GTGACTGAGA AAATTAATAA AGCAATTAGA 960
AGTAGCTCAA GCAACTTTCT AAACATATGAT TTGACCCCTC GGTGTGATTA TTATGGCTGT 1020
AACCAGACTG CGAGTACTG CCTCAATGGT TTAGCATGCG ATTGCAAATC TGACCTGCAA 1080
AGGCTTAAGC CACAGAGCCC TTTCTGCGTT GCTTCCAGTC TCAAGTGTC TGATGCTGCG 1140
25    AACGCACAGC ACAAGCAATG CTTAATAAAG AAGAGTGGTG GGGCCCTGTA GTGTGCTGTC 1200
GTGCCCGGCT ACCAGGAAGA TGCTAATGGG AACTGCCAAA AGTGTGCAAT TGGCTACAGT 1260
GGACTCGACT GTAAAGACAA ATTTCACTG ATCCTCACTA TTGTGGGCAC CATCGCTGGC 1320
ATTGTCACTC TCAGCATGAT AATTGCATTG ATTTGCACAG CAAGATCAAA TAAACAAAAGC 1380
AAGCATATTG AAGAAGAGAA CTTGATTGAC GAAGACTTTC AAAATCTAAA ACTGCGGTGC 1440
30    ACAGGCTTCA CCAATCTTGG AGCAGAAGGG AGCGTCTTTC CTAAGGTGAG GATAACGGCC 1500
TCCAGAGACA GCCAGATGCA AAATCCCTAT TCAAGACACA GCAGCATGCC CGGCCCTGAC 1560
TATTAGAATC ATAAGAATGT GGAACCCGCC ATGGCCCCCA ACCAATGTAT AAGCTATTAT 1620
TTAGAGTGTG TAGAAGAGCT GATGGAGAAG TGAGCACCAG TAAAGATCTG GCCTCOGGGG 1680
TTTTCTTCCC ATCTGACATC TGCCAGCCTC TCTGAATGGA AGTTGTGAAT GTTTGCAACG 1740
35    AATCCAGCTC ACTTGCTAAA TAAGAATCTA TGACATTAAA TGTAGTAGAT GCTATTAGCG 1800
CTTGTCAGAG AGGTGGTTTT CTTCATCAG TACAAAGTAC TGAGACAATG GTTAGGGTTG 1860
TTTTCTTAAT TCTTTTCTG GTAGGGCAAC AAGAACCATT TCCATCTAG AGGAAGCTC 1920
CCCAGCATTG CTGCTCCTG GGCAAACATT GCTCTTGAGT TAAGTGACCT AATTTCCCTG 1980
GGAGCATGAC GACTCAACTG TGGAGGTCCG AGGGGATGAG AAGGGATACC CACCACCTT 2040
40    CAAGGTGTCAG AAGCTCACTC TCTGACAGT CAGAATAGGG ACACTGCTTC TATCCCTCCA 2100
ATGGAGAGAT TCTGGCAACC TTTGAACAGC CCAGAGCTTG CAACCTAGCC TCACCCAAGA 2160
AGACTGGAAA GAGACATATC TCTCAGCTTT TTCAGGAGGC GTGCTGGGA ATCCAGGAAC 2220
TTTTTGATGC TAAATAGAAG GCCTGGACTA AAAATGTCCA CTATGGGGTG CACTCTACAG 2280
TTTTTGAAT ATCTGAGAGC AGAAGGGGCA GAGAGTAAAA AACATGACCT GGTAGAAGGA 2340
45    AGAGAGGCAA AGGAAATCTG GTGGGGAGGA TCAATTAGAG AGGAGGCACC TGGATCCAC 2400
CTTCTTCTCT AGGTCCCTCC CTCCATCAGC AAAGGAGCAC TTCTTAATC ATGCCCTCCC 2460
GAAGACTGGG TGGGAGAAGG TTTAAAAACA AAAAATCCAG GAGTAAGAGC CTTAGTTCAG 2520
TTTGAAATG GAGACAACT GTCTGGCAAA GGGTGCGAGA GGGAGCTTGT GCTCAGGAGT 2580
CCAGCGCTCC AGCTCTCGGG TGTAGTTTC TGAGGTGTGC CATTGGGGCC TCAGCCTTCT 2640
50    CTGGTGACAG AGGCTCAGCT GTGGCCACCA ACACACAACC ACACACACAC AACACACAC 2700
ACAAATGGGG GCAACCATC CCAGTACAAG CTTTACAAA TGTATTAGT GTCCTTTTTT 2760
ATTTCTAATG CCTGTCTCTC TTAAGAGTTA TTTTATTGT TATTATTAT TGTCTTGAC 2820
TGTTAATTGT GAATGGTAAT GCAATAAAGT GCCTTTGTTA GATGGTGAAG AAAAAAAAAA 2880
AAAAAA

```

Seq ID NO: C42 DNA Sequence  
Nucleic Acid Accession #: NM\_001432.1  
Coding sequence: 167..676

```

60      1      11      21      31      41      51
|      |      |      |      |      |
TCACITGCCT GATATTTCCA GTGTCAGAGG GACACAGCCA ACGTGGGGTC CTTCTAGGC 60
TGACAGCGCG TCTCCAGCCA CTGCCCGAG CCGCTCTGCT CCGCCCTGTC CCGTGCACTC 120
TCCGAGCGCG CCTCCGCCA AGCCCCAGCG CCGCTCCCA TCGCCGATGA CCGCGGGGAG 180
65    GAGGATGAGG ATGCTCTGTG CCGGCAGGGT CCTGCGCTG CTGCTCTGCC TGGGTTTCCA 240
TCTTCTACAG GCAGTCTTCA GTACAATGT GATTCCATCA TGTATCCAG GAGAGTCCAG 300
TGATAACTGC ACAGCTTTAG TTCAGACAGA AGACAATCCA CGTGTGGCTC AAGTGTCAAT 360
AACAAAGTGT AGCTCTGACA TGAATGGCTA TTGTTGCAAT GACAGATGCA TCTATCTGCT 420
GGACATGAGT CAAAATCTACT GCAGGTGTGA AGTGGGTAT ACTGGTGTCC GATGTGAACA 480
70    CTTCTTTTTA ACGTCCACC AACCTTAAAG CAAAGAGTAT GTGGCTTTGA CCGTGATTCT 540
TATTATTTTG TTTCTTATCA CAGTCTGTCG TTCCACATAT TATTTCTGCA GATGGTACAG 600
AAATGGAAGA AGTAAGAAAC CAAAGAAGGA ATATGAGAGA GTTACCTCAG GGGATCCAGA 660
GTTGCCGCAA GTCTGAATAT GAGAGAGTTA CCTCAGGGGA TCCAGAGTTG CCGCAAGTCT 720
GAATGGGCCC ATCAACCTTA TGGGCAGGGA TAACAGTGTG CTTGGTTAAT ATTAATATTC 780
75    CATTTTATTA ATAAATATTA TGTGGGTCA AGTGTAGGT CAATAACACT GTATTTTAA 840
GTACTTGAAA AATGTTTTTA TTTTGTGTTT ATTTTGTACA GACTATTGTC TAATGTATAA 900
TGTGCAGAAA ATATTTAATA TCAAAAGAAA ATTGATATTT TTATACAAGT AATTTCCTGA 960
GCTAAATGCT TCATTGAAGC CTTCAAAGTT TATATGCCTG GTGCACAGTG CTTAGAAGTA 1020
AGCAATTCCT ATCAACTAGC TCAAGAAATG TTAGCAATG ACAGATTCT GTAGCCTAT 1080
80    ATATATAGTC AATCGATTT AGTAAGTATG TTTTATATG TCCTCAAATC AGTGATAATT 1140
GGTTTGACTG TACCATGTTT TGATATGTAG TTGGCACCAT GGTATCATAT ATTAACAAA 1200
TAATGCAATT AGAATTTGGG AGAAGCAAA ATAGTCTCTG TGTAAACAC TACACATTTG 1260
AAACAAGCTA ACCCTGGGGA GTCTATGGTC TCTTCACTCA GGTCTCAGCT ATAATTCTGT 1320
TATATGAGGG GCAGTGGACA GTTCCCTATG CCAACTCAGC ACTCTACAG GTACTAGTCA 1380

```

	CTCATCTACC	AGATTCTGCC	TATGTAAAAT	GAATTGAAAA	ACAAATTTCT	GTAATCTTTT	1440
	ATTTAAGTAG	TGGGCATTTT	ATAGCTTCAC	AATGTTCCCT	TTTTGTATAT	TACAAACATT	1500
	ATGTGAGGTA	ATTATTTGCTC	AACAGACAAT	TAGAAAAAAG	TCCACACTTG	AAGCCTAAAT	1560
5	TTGTGCTTTT	TAAGAATATT	TTTAGACTAT	TTCTTTTAT	AGGGGCTTTG	CTGAATTCTA	1620
	ACATTAAATC	ACAGCCCAAA	ATTGTATGGA	CTAATTATTA	TTTTAAAAAT	TATGAAGACA	1680
	ATAATTCTAC	ATGTGTGCTT	AAGATGGAAA	TACAGTTATT	TCACTTTTAA	TTCAAGGAAG	1740
	TTTTAACTTT	AATACAGCTC	AGTAAATGGC	TTCTTCTAGA	ATGTAAGATT	ATGTATTATA	1800
	AGTTGTATCT	TGACACAGGA	AATGGGAAAA	AACTTAAAAA	TTAATATGGT	GTATTTTTTC	1860
10	AAATGAAAAA	TCCTCAATTGA	AAGCTTTTAA	AATGTAGAAA	CTTAAACACA	CCTTCCCTGT	1920
	GAGGCTGAGA	TGAAACTAG	GGCTCATTTT	CCTGACATTT	GTTTATTTTT	TGGAAGAGAC	1980
	AAAGATTCTT	TCTGCACTCT	GAGCCCATAG	GTCTCAGAGA	GTTAATAGGA	GTATTTTTGG	2040
	GCTATTGCAAT	AAGGAGCCAC	TGCTGCCACC	ACTTTTGGAT	TTTATGGGAG	GCTCCTTCAT	2100
	CGAATGCTAA	ACCTTTGAGT	AGAGTCTCCC	TGGATCATAT	ACCAGGTCAG	GGAGGATCTG	2160
15	TTCTTCTCT	ACGTTTATCC	TGGCATGTGC	TAGGTAACAC	GAAGGCATAA	TAAGCCATGG	2220
	CTGACCTCTG	GAGCACCAGG	TGCCAGGACT	TGTCTCCATG	TGTATCCATG	CATTATATAC	2280
	CCTGGTGTCT	TCCAGCATCT	GTCTCTAAA	GTCTGCCCC	TGGCCCTTAC	TATTAGGAAA	2340
	ATAAACAGAC	AAAAACAAGT	AAATATATAT	GGTCTTATAC	ATATTGTATA	TATATTCTATA	2400
	TACAAACATG	TATGTATACA	TGACCTTAAT	GGATCATAGA	ATTGCAGTCA	TTTGGTGTCT	2460
20	TGCTAACCAT	TTATATAAAA	CTTAAAAACA	AGAGAAAAAG	AAAAATCAAT	AGATCTAAAC	2520
	AGTTATTTCT	GTTCCTTATT	TAATATAGCT	GAAGTCAAAA	TATGTAGAAA	CACATTTTAA	2580
	ATACTCTACT	TCTGCACTCT	CCTCTGTGGT	TAGTTCCACA	TCTGTGATT	CAACCAACCA	2640
	AGGACGGAAA	ATGCTTAAAA	AATAATACAA	CAACACAAA	AAATACATTA	TAACAACTAT	2700
	TTACTTTTTT	TTTTTCTTT	TTGAGATGGA	GTCTCGCTCT	GTGCCCCAGG	TTGAGATGCA	2760
25	GTGGCAGCAT	CTCGGCTCAC	TGCAACCTCA	CCTCCCGGGT	TCAAGAGATC	CTCCTGCCTC	2820
	AGCCTCCTGA	GCAGCTGGGA	CTACAGGCGC	ATGCCACCAT	GCCCCAGCTAA	TTTTTGTATT	2880
	TTTAGTAGAG	GCGGGTTTTC	ACCATGTTGG	CCAGGATGGT	CTCAATCTCC	TAACCTTGAG	2940
	ATCCACCTTC	CACAGCTCCC	CAAACTGCTG	GGATTACAGG	CGTGAGCCAC	CGCAGTAGC	3000
	ATTTACATTA	GGTATTACAA	GTAAATGTAA	GATGATTTAA	GTATACAGGA	GGATGTGAAT	3060
30	AGGTATATG	CAAGCACTAT	GCCCTTTTAT	ATAAGTGACT	TGAACATCTG	TGCCCGATT	3120
	TAGTATGTGC	AGGGGGGCGA	TCTGGGAATC	AGTCCCCCTG	GGATACCAAG	GTACAACTGT	3180
	ATTTATTAACT	GCTTACTAGA	TGTGAGGAGA	GTCTGAATAT	TTTCAGTGAT	CTTGGCTGTT	3240
	TCAAAAAAAT	CTATTGACTT	TTCAATAAAT	CAGCTGCAAT	CCATTATTAT	CATTTACAAA	3300
	AGATTATATG	TAAGCCCTCT	AATCTTGGTT	TTTCAGTTGA	TCTTAAGCAT	GTCAATTTCAT	3360
35	AAAAACAAGT	CATTTTGTGA	TTTTTCATCT	TTAAGAAATG	TTAAAAAAGC	TAATCCCTAA	3420
	AATAGTTAGA	TCTTTGTAAA	TGCATATTAA	ATAATAAAGT	ATGACCCACA	TTACTTTTAA	3480
	TGGGTGAAAA	TAGACAAAAA	ATAATAGTTT	TAGTGAGGAT	GGTGCTGAGT	AAACATAAAA	3540
	ACTGATTGTC	TCTCAGCTGA	TGTGTCTGCT	ACACAGTGGG	AAGATTTTAG	TTACACTTAA	3600
	GTCTAATCTC	CCCATTTTAC	AGATTCTTCA	CTATATATAT	TTCTAGAAGG	GGCTATGCAT	3660
40	ATTTCAATGA	TTGAGAACCA	AAGCAACCCAC	AAATGCATAA	ATGCATAATT	TATGGTCTTC	3720
	AACCAAGGCC	ACATAATAAC	CCAGTTAACT	TACTCTTTAA	CCAGGAATAT	TAAGTTCTAT	3780
	AACTAGTAAC	CAAGGTTTAA	CCTTAAATTT	AAGATTTCCT	TAACCTTAAC	CTTAAATTTG	3840
	ATATTATATT	AAACATACAT	AATACAAATG	AACCTCACTG	TTCTCCTGAA	TATTTTTTGC	3900
	TCTAATCTCT	CTGCGGAAGG	TCARAAGTAT	GGGAGAATTG	GTATACTGGT	ATGACTACGT	3960
45	CTTAAGTCAG	ATTTTTATTT	ATGAGTCTTT	GAGACTAAAT	TCAATCAGCA	CCAGGTATCA	4020
	AATCAACTTT	TATGCAGCAA	ATATATGATT	CTAGTGTCTG	ACTTTTGTGA	AAATTCAGTAA	4080
	TGCAGTTTTT	AAAAACCTGT	ATCTGACCCA	CTTTGTAAAT	TTTGTCTCAA	TATCCATTCT	4140
	GTAGACTTTT	GAATAAAAAA	TTTTTAATTT	GATGCCCAAT	ATATTCTGAC	CGTTAAAAAA	4200
	TTCTTGTCTA	TATGGGAGAA	GGGGGAGTAA	TGACTGTATC	AAACAGTATT	TCTGGTGTAT	4260
50	ATTTTAATGA	TTTTTAAAAA	AGTAATTTCA	TTTAAATATC	TGTTATTCAA	ATTGTATGAT	4320
	GTAAATGTGA	ATATAATGTA	TTTTCTTTTT	ATTTTGCACT	CTGTAATTGC	ACTTTTAAAG	4380
	TTTGAAGAGC	CATTTTGGTA	AACGGTTTTT	ATTAAAGATG	CTATGGAACA	TAAAGTTGTA	4440
	TTGCATGCAA	TTTAAAGTAA	CTTATTGGAC	TATGAATATT	ATCGGATTAC	TGAATTGTAT	4500
	CAATTGTGTT	GTGTTCAATA	TCAGCTTTGA	TAATTGTGTA	CCTTAAGATA	TTGAAGGAGA	4560
55	AAATAGATAA	TTTACAGAGT	ATTATTAATT	TTTATTATT	TTTCTTGGGA	ATTGAAAAAA	4620
	ATTGAATAAA	ATAAAAATGC	ATTGAACATC	TTGCATTCAA	AATCTTCACT	GAC	4673

Seq ID NO: C43 DNA Sequence  
Nucleic Acid Accession #: AF011468.1  
Coding sequence: 257..1468

	1	11	21	31	41	51	
	GGAAGACTTG	GGTCTTGGG	TGCGAGGTGG	GAGCCGACGG	GTGGGTAGAC	CGTGGGGGAT	60
65	ATCTCAGTGG	CGGACGAGGA	CGGCGGGGAC	AAGGGGCGGC	TGGTCCGAGT	GGCGGAGCGT	120
	CAAGTCCCTT	GTCCGTTCCT	CGTCCCTGGA	GTGTCTTGG	GGTCCCTTGG	TGCCCGCCCA	180
	GCGCCTTTGC	ATCCGCTCCT	GGGCAACGAG	GCGCCCTGTA	GGATAGTCTG	TGTTACTTTAT	240
	TACAGCTAGA	GGCATCATGG	ACCGATCTAA	AGAAAACTGC	ATTTTCAGGAC	CTGTTAAGGC	300
70	TACAGCTCCA	GTTCGAGGTC	CAAAACGCTG	TCTCGTGACT	CAGCAAAATC	CTTGTGAGAA	360
	TCCATTACCT	GTAAATAGTG	GCCAGGCTCA	GCGGGTCTTG	TGTCCTTCAA	ATTCTTCCCA	420
	GCGGTTCTCT	TTGCAAGCAC	AAAAGCTTGT	CTCCAGTCAC	AAGCCGGTTC	AGAATCAGAA	480
	GCAGAAGCAA	TTGCAGGCAA	CCAGGTGTACC	TCATCTCTGT	TCCAGGCCAC	TGAATAACAC	540
	CCAAAGAGAG	AAGCAGCCCC	TGCCATCGGC	ACCTGAAAT	AATCCTGAGG	AGGAACCTGGC	600
75	ATCAAAACAG	AAAAATGAAG	AATCAAAAAA	GAGGCAGTGG	GCTTTGGAAG	ACTTTGAAAT	660
	TGGTCCGCCCT	CTGGGTAAAG	GAAAGTTTGG	TAATGTTTAT	TTGGCAAGAG	AAAAGCAAAG	720
	CAAGTTTAT	CTGGCTCTTA	AAGTGTATT	TAAAGCTCAG	CTGGAGAAAG	CCGGAGTGGG	780
	GCATCAGCTC	AGAAGAGAA	TAGAAATACA	GTCCCACTTT	CGGCATCCTA	ATATTCTTAG	840
	ACTGTATGGT	TATTTCCATG	ATGCTACCAG	AGTCTACCTA	ATTCTGGAAT	ATGCACCATC	900
80	TGGAAACAGT	TATAGAGAA	TTCAAAACT	TTCAAAGTTT	GATGAGCAGA	GAACTGCTAC	960
	TTATATAACA	GAATTGGCAA	ATGCCCTGTC	TTACTGTCTAT	TGGAAGAGAG	TTATTCTATG	1020
	AGACATTAA	CCAGAGAACT	TACTTCTTGG	ATCAGCTGGA	GAGCTTAAAA	TTGCAGATT	1080
	TGGGTGGTCA	GTACATGCTC	CATCTTCCAG	GAGGACCACT	CTCTGTGGCA	CCCTGGACTA	1140
	CCTGCCCTCT	GAAATGATTG	AAGGTCCGAT	GCATGATGAG	AAGGTGGATC	TCTGGAGCCT	1200
	TGGAGTTCTT	TGCTATGAAT	TTTTAGTTGG	GAAGCCTCCT	TTTGAGGCAA	ACACATACCA	1260

	AGAGACCTAC	AAAAAATAT	CACGGGTGA	ATTCACATTC	CCTGACTTTG	TAACAGAGGG	1320
	AGCCAGGAC	CTCATTTC	GAATCTTGA	GCATAATCCC	AGCCAGAGGC	CAATGCTCAG	1380
	AGAAGTACT	GAACCCCT	GGATCACAGC	AAATTCATCA	AAACCATCAA	ATTGCCAAAA	1440
5	CAAAGAATCA	GCTAGCAAC	AGTCTTAGGA	ATCGTGCAGG	GGGAGAAATC	CTTGAGCCAG	1500
	GGCTGCCATA	TAACCTGACA	GGAAATGCT	ACTGAAGTTT	ATTTTACCAT	TGACTGCTGC	1560
	CCTCAATCTA	GAACGCTACA	CAAGAAATAT	TTGTTTTACT	CAGCAGGTGT	GCCTTAACCT	1620
	CCCTATTCCG	AAAGCTCCAC	ATCAATAAAC	ATGACACTCT	GAAGTGAAAG	TAGCCACGAG	1680
	AATTGTGCTA	CTTACTCTGG	TTTATAATCT	GGAGGCAAGG	TTGAGCTGCA	GGCCGCCCGT	1740
10	CAGCCTGTGC	TAGGCATGGT	GTCTTACAG	GAGGCAATC	CAGAGCCTGG	CTGTGGGGAA	1800
	AGTGACCACT	CTGCCCTGAC	CCGATCAGT	TAAGGAGCTG	TGCAATAACC	TTCTAGTAC	1860
	CTGAGTGAGT	GTGTAACCTA	TTGGGTGGC	GAAGCCTGGT	AAAGCTGTTG	GAATGAGTAT	1920
	GTGATTCCTT	TTAAGTATGA	AAATAAAGAT	ATATGTACAG	ACTTGATATT	TTTCTCTGGT	1980
	GGCATTCCCT	TAGGAATGCT	GTGTCTCTGT	CCGGCAGCCC	GGTAGGCTTG	ATTGGGTTTC	2040
15	TAGTCTCTCT	TAACCACTTA	TCTCCCATAT	GAGAGTGTA	AAAATAGGAA	CACGTGCTCT	2100
	ACCTCCATTT	AGGGATTGTC	TTGGGATACA	GAAGAGGCCA	TGTGTCTCAG	AGCTGTTAAG	2160
	GGCTTATTTT	TTTAAACAT	TGGAGTCATA	GCATGTGTGT	AAACTTTAAA	TATGCAATAA	2220
	AAATAAGTATC	TATGTCTAAA	AAAAAATAAA	AAA			2253
20	Seq ID NO: C44 DNA Sequence Nucleic Acid Accession #: NM_013372 Coding sequence: 63..617						
	1	11	21	31	41	51	
25	GCGGCGCCAC	TCAGCGCCAC	GCGTCGAAAG	CGCAGGCCCC	GAGGACCCGC	CGCACTGACA	60
	GTATGAGCCG	CACAGCCTAC	ACGGTGGGAG	CCCTGCTTCT	CCTCTTGGGG	ACCCTGCTGC	120
	CGGCTGCTGA	AGGGAATAAG	AAAGGGTCCC	AAGGTGCCAT	CCCCCGCCCA	GACAAGGCC	180
	AGCACATGA	CTCAGAGCAG	ACTCAGTGGC	CCGAGCAGCC	TGGCTCCAGG	AACCGGGGGC	240
30	GGGCGCAAGG	GCGGCGCACT	GCCATGCCCC	GCGAGGAGGT	GCTGGAGTCC	AGCCCAAGAGG	300
	CCCTGATGTT	GACGGAGCGC	AAATACCTGA	AGCGAGACTG	GTGCAAAACC	CAGCCGCTTA	360
	AGCAGACCAT	CCACGAGGAA	GGCTGCAACA	GTCCGACCAT	CATCAACCGC	TTCTGTTACG	420
	GCCAGTGCAA	CTCTTTCTAC	ATCCCCAGGC	ACATCCGGAA	GGAGGAAGGT	TCCTTTCAGT	480
	CCCTGCTCCT	CTGCAAGCCC	AAGAAATTC	CTACCATGAT	GGTCACACTC	AACTGCCCTG	540
35	AACTACAGCC	ACCTCAACAG	AAGAAGAGAG	TCACACGTGT	GAAGCAGTGT	CGTTCATAT	600
	CCATCGATTT	GGATTAAAGC	AAATCCAGGT	GCACCCAGCA	TGCTCTAGGA	ATGCAGCCCC	660
	AGGAAGTCCC	AGACCTAAAA	CAACCAGATT	CTTACTTGGC	TTAAACCTAG	AGGCCAGAAG	720
	AACCCCCAGC	TGCCTCTGG	CAGGAGCCTG	CTTGTGCGTA	GTTCTGTGTC	ATGAGTGTGG	780
	ATGGGTGCCT	GTGGGTGTTT	TTAGACACCA	GAGAAAAAC	AGTCTCTGCT	AGAGAGCACT	840
40	CCCTATTGTT	TGCGCATATC	TGCTTTAATG	GGGATGTACC	AGAAACCCAC	CTCACCCCGG	900
	CTCACATCTA	AAGGGGCGGG	GCGTGTGCT	GGTCTGACT	TTGTGTTTTT	GTGCCCTCCT	960
	GGGGACCGCA	ATCTCCTTTC	GGAATGAATG	TTATGGAAG	AGGCTCCTCT	GAGGSCAAGA	1020
	GACCTGTTTT	AGTGTGTCAT	TGACATGGA	AAAGTCTTTT	TAACCTGTGC	TTGCATCTCT	1080
	CTTCTCTCCT	CCTCTCACA	ATCCATCTCT	TCTTAAGTTG	ATAGTGACTA	TGTCACTCTA	1140
45	ATCTCTGTGT	TGCGCAAGGT	CCTAAATTA	TTCACTTAAC	CATGATGCAA	ATGTTTTTCA	1200
	TTTTGTGAAG	ACCTCCAGA	CTCTGGGAGA	GGCTGGTGTG	GGCAAGGACA	AGCAGGATAG	1260
	TGGAGTGAGA	AAGGGAGGGT	GGAGGGTGAG	GCCAAATCAG	GTCCAGCAAA	AGTCAGTAGG	1320
	GACATTGCGA	AAGCTTGAAA	GGCCAAATACC	AGAACACAGG	CTGATGCTTC	TGAGAAAGTC	1380
	TTTTCTAGT	ATTTAAACAGA	ACCCAAGTGA	ACAGAGGAGA	AATGAGATTG	CCAGAAAGTG	1440
50	ATTAACCTTG	TGCGGTGCAA	TCTGCTCAAA	CCTAACACCA	AACTGAAAAC	ATAAATACTG	1500
	ACCACTCCTA	TGTTGGGACC	CAAGCAAGTT	AGCTAAACCA	AACTAACTCC	TCTGCTTTGT	1560
	CCCTCAGGTG	GAAAGAGAG	GTAGTTTGA	ACTCTCTGCA	TAGGGGTGGG	AATTAATCAA	1620
	AAACCKCAGA	GGCTGARAAT	CCTAATACCT	TTCTTTATC	GTGGTTATAG	TCAGCTCAT	1680
	TCATTTCCAC	TATTTCCCAT	AATGCTTCTG	AGAGCCACTA	ACTTGATTGA	TAAAGATCCT	1740
55	GCCTCTGCTG	AGTGTACCTG	ACAGTAAGTC	TAAAGATGAR	AGAGTTTAGG	GACTACTCTG	1800
	TTTTAGCAAG	ARATATTKTG	GGGGTCTTTT	TGTTTTAACT	ATTGTACAGA	GATTGGGCTA	1860
	RAGAGAAGAC	GACGAGAGTA	AGGAAATAAA	GGGATTGCCC	TCTGGCTAGA	GAGTAAGTTA	1920
	GGTGTTAATA	CCTGTAGAAA	ATGTAAGGGA	TATGACCTCC	CTTTCTTTAT	GTGCTCACTG	1980
	AGGATCTGAG	GGGACCTGTT	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCACTGC	2040
60	CTACTGTGTTG	GATGAGACATA	ACTATTGTAA	CTATTCACTA	TTTACTTGTA	GGCACTGTCC	2100
	TCTGATTAATA	CTTGGCCTAC	TGGCAATGGC	TACTTAGGAT	TGATCTAAGG	GCCAAAGTGC	2160
	AGGGTGGGTG	AACCTTTATTG	TACTTTGGAT	TTGGTTAACC	TGTTTTCTTC	AAGCCTGAGG	2220
	TTTTATATAC	AAACTCCCTG	AATACTCTTT	TTGCTTGTGA	TCCTCTCAGC	CTCCTAGCCA	2280
	AGTCTATGTT	AATATGGAAA	ACAAACACTG	CAGACTTGAG	ATTCACTGTC	CGATCAAGGC	2340
65	TCTGGCATTC	AGAGAACCTC	TGCAACTCGA	GAAGCTGTTT	TTATTTCTGT	TTTGTTTTGA	2400
	TCAGTGTCTC	TCCATCTAA	CAACTAAACA	GGAGCCATT	CAAGGCGGGA	GATATTTTAA	2460
	ACACCCAAAA	TGTTGGGTCT	GATTTTCAAA	CTTTTAAACT	CACACTGAT	GATTTCTCAG	2520
	CTAGGCGAAT	TTGTCCAAAC	ACATAGTGTG	TGTGTTTTGT	ATACACTGTA	TGACCCACC	2580
	CCAAATCTTT	GTATGTGCA	CATTCTCCAA	CAATAAGCA	CAGAGTGGAT	TTAATTAAAG	2640
70	ACACAAATGC	TAAGGCAGAA	TTTTGAGGGT	GGGAGAGAAG	AAAAGGGAAA	GAAGCTGAAA	2700
	ATGTAATAAC	ACACCAAGGA	GGAAATGA	CATTCAAGAC	CAGCAAAAC	TGAATTTCTC	2760
	TGTTGTGTTT	ACTCTGCA	CAAGAAATGA	ATTTGTGTA	TGGAGATGAC	TTAAGTTGGC	2820
	AGCAGTAATC	TTCTTTTAGG	AGCTTGTACC	ACAGTCTTGC	ACATAAGTGC	AGATTGGCT	2880
	CAAGTAAAGA	GAATTTCTCT	AACACTAATC	TCACTGGGAT	AATCAGCAGC	GTAATACCC	2940
75	TAAAGCATTA	TCACTAGCCA	AAGAGGGAAA	TATCTGTTCT	TCTTACTGTG	CCTATATTAA	3000
	GACTAGTACA	AATGTGGTGT	GTCTTCCAAC	TTTCATTGAA	AATGCCATAT	CTATACCATA	3060
	TTTTATTGCA	GTCACTGATG	ATGTAATGAT	ATATTTTTTC	ATTATTATAG	TAGAATATTT	3120
	TTATGGCAAG	ATATTTGTGG	TCTTGATCAT	ACCTATTAAA	ATAATGCCAA	ACACCAATA	3180
	TGAATTTTAT	GATGTACACT	TTGTGCTTGG	CATTAAAGAA	AAAAACACA	CATCCTGGAA	3240
80	GTCTGTAAAT	TGTTTTTTGT	TACTGTAGGT	CTTCAAGATT	AAGAGTGTA	GTGAAAAATC	3300
	TGGAGGAGAG	GATAATTTCC	ACTGTGTGGA	ATGTAATAG	TTAAATGAAA	AGTTATGGTT	3360
	ATTTAATGTA	ATTAATCTTT	CAATCCTTT	GGTCACTGTG	ATTTCAGCA	TGTTTTCTTT	3420
	TTCTCCTTTA	TATGACTTTT	TCTGAGTTGG	GCAAGAAGA	AGCTGACACA	CCGTATGTTG	3480
	TTAGAGTCTT	TTATCTGGTC	AGGGGAAACA	AAATCTTGAC	CCAGCTGAAC	ATGTTCTCCT	3540
	GAGTCAGTGC	CTGAATCTTT	ATTTTTTAAA	TTGATGTTTC	CTTAAAGGTT	AACATTTCTA	3600

5 AAGCAATATT AAGAAAGACT TTAATGTTA TTTTGAAGA CTTACGATGC ATGTATACAA 3660  
 ACGAATAGCA GATAATGATG ACTAGTTCAC ACATAAAGTC CTTTAAAGGA GAAATCTAA 3720  
 AATGAAAGT GGATAAACAG AACATTATA AGTGATCAGT TAATGCTTAA GAGTGAAAGT 3780  
 AGTTCTATTG ACATTCTCTCA AGATATTAA TATCAACTGC ATTATGTATT ATGTCTGCTT 3840  
 AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG 3900  
 ATGAAAGGGG AGTTGATAGT CTCATAAAAC TAATTTGGCT TCAAGTTTCA TGAATCTGTA 3960  
 ACTAGAAATT AATTTTCACC CCAATATGT TCTATATAGC CTTTGCTAAA GAGCAACTAA 4020  
 TAAATTAAC CTATTCCTTC AAAAAAAA 4049

10 Seq ID NO: C45 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 200..2932

15 1 11 21 31 41 51  
 ATTGCTGATG GATCAGTGAG CCTGTGTTCA TGCCAGTGAG CTGCTGTGSC TCAGATACTG 60  
 ATACTTTCTT TCCAAACAGC ATAAGAAGTG ATTGAGCCAC AAGTATACTG AAGGAAGGGC 120  
 TCCCTCGAGT TCTGGTGTGA AGAGATAAAT CACCAGTCAC AGACTATGCA CCGGACTGCT 180  
 GCTGTTCACT CCAGGGAAAA TGAAAGTTGG AGTGCTGTGG CTCATTCTT TCTTCACTT 240  
 20 CACTGACGGC CACGGTGGCT TCCTGGGGAA AAATGATGGC ATCAAACAA AAAAAAGACT 300  
 CATGTGAAT AAGAAAAAAC ATCTAGGCC AGTCGAAGAA TATCAGCTGC TGCTTCAGT 360  
 GACCTATAGA GATTCCAAGG AGAAAAGAGA TTTGAGAAAT TTTCTGAAGC TCTTGAAGCC 420  
 TCCATTATTA TGTGCATG GGCTAATTAG AATTATCAGA GCAAAGGCTA CCACAGACTG 480  
 CAACAGCCTG AATGGAGTCC TGCAGTGTAC CTGTGAAGAC AGCTACACCT GGTTCCTCC 540  
 25 CTCATGCCCT GATCCCCAGA ACTGTACCT TCACACGGCT GGAGCACTCC CAAGCTGTGA 600  
 ATGTATCTC AACCACTCTA GCCAGAGTGT CAATTTCTGT GAGAGAACA AGATTGGGG 660  
 CACTTTCAAA ATTAATGAAA GGTTTACAAA TGACCTTTG AATTCATCTT CTGCTATATA 720  
 CTCCAAATAT GCAATGGAA TTGAAATTC ACTTAAAAA GCATATGAAA GAATTCAGAG 780  
 TTTTGAAGT GCTCAGTCA CCAATTTG AAATGGAAGC ATCGTTGCTG GGTATGAAGT 840  
 30 TGTGAGCTCC AGCAGTGCAT CTGAAGTCT GTACGCCATT GAACATGTTG CCGAGAAGGC 900  
 TAAGACAGCC CTTCACAAGC TGTTCCTATT AGAAGACGGC TCTTCAGAG TGTTCGAAA 960  
 AGCCCACTGT AATGACATTG TCTTTGGATT TGGGTCCAAG GATGATGAAT ATACCTTGCC 1020  
 CTGCAAGCAGT GGCTACAGGG GAACATCAC AGCCAAGTGT GAGTCTCTG GGTGGCAGGT 1080  
 CATCAGGGAG ACTTGTGTGC TCTCTGTCT TGAAGAAGT AACAAGAATT TCAGATGATG 1140  
 35 TGTAGGCAAT GCCACTGAGG CAGCTGTGTC ATCCTTCGTG CAAATCTTT CTGTCTCAT 1200  
 TCGGCAAAAC CCATCAACCA CAGTGGGGAA TCTGGCTCG GTGGTGTGCA TCTGTAGCAA 1260  
 TATTTCTAT CTGTCACTGG CCAGCCATT CAGGGTGTCC AATTCACAA TGGAGGATGT 1320  
 CATCAGTATA GCTGACAATA TCCTTAATTC AGCCTCAGTA ACCAAGTGA CAGTCTTACT 1380  
 40 GCGGGAAGAA AAGTATGCCA GCTCAGGTT ACTAGAGACA TTAGAAAACA TCAGCACTCT 1440  
 GGTGCTCCG ACAGCTCTTC CTCTGAATTT TTCTCGGAAA TTCAATTGACT GGAAGGGAT 1500  
 TOCAGTGAAC AAAAGCCAC TCAAAGGGG TTACAGCTAT CAGATTAAAA TGTGTCCCA 1560  
 AAATACATCT ATTCCCATCA GAGGCGTGT GTTAATTGGG TCAGACCAAT TCCAGAGATC 1620  
 CCTTCCAGAA ACTATTATCA GCATGGCCCT GTTGACTCTG GGAACATTC TACCCGTTTC 1680  
 45 CAAAAATGA AATGCTCAGG TCAATGGACC TGTGATATCC ACGGTTATTC AAAACTATTC 1740  
 CATAAATGAA GTTTTCTCTT TTTTTCCAA GATAGAGTCA AACCTGAGCC AGCCTCATG 1800  
 TGTGTTTTGG GATTTCAGTC ATTTGCAGTG GAACGATGCA GGCTGCCACC TAGTGAATGA 1860  
 AACTCAAGAC ATCGTGAGCT GCCAATGTAC TCACCTGACC TCCTTCTCCA TATTGATGTC 1920  
 ACCTTTGTG CCTCTACAA TCTTCCCGT TGTAAATGG ATCACTATG TGGGACTGGG 1980  
 50 TATCTCCATT GGAAGTCTCA TTTATGCCT GATCATCGAG GCTTTGTTTT GGAAGCAGAT 2040  
 TAAAAAAGC CAACTCTC ACACAGTCTG TATTGTCATG GTGAACATAG CCCTGTCCCT 2100  
 CTGATTGCT GATGTCTGGT TTATTGTTGG TGCCACAGTG GACACCAGG TGAACCTTC 2160  
 TGGAGTCTGC ACAGCTGCTG TGTCTTTAC ACATCTCTC TACCTCTCTT TGTCTCTCTG 2220  
 GATGCTCATG CTGGGCATCC TGCTGGCTTA CCGGATCATC CTGCTGTCC ATCATATGTC 2280  
 55 CAGCATTG ATGAGTGGCT TTGGATTG CCGGCTTAT GGGTGGCCCT TCATTATATC 2340  
 TGTCAATACC ATGTCTGTCA CGCAACCTAG CAATACCTAC AAAAGGAAAG ATGTGTGTTG 2400  
 GCTTAACTGG TCCAAATGGA GCAAACTACT CCTGGCTTT GTTGTCCCTG CACTGGCTAT 2460  
 TGTGGCTGTG AACTTCTGTT TGGTGTGCT AGTTCTCACA AAGCTCTGGA GGCGGACTGT 2520  
 TGGGGAAGCA CTGAGTCGGG ATGACAAGGC CACCATCATC CGCTGGGGGA AGAGCCTCCT 2580  
 60 CATTCTGACC CCTCTGCTAG GGCTCACCTG GGGCTTTGGA ATAGGAACAA TAGTGGACAG 2640  
 CCAGAATCTG GCTTGGCATG TTATTTTTC TTTACTCAAT GCATTCCAGG GATTTTTAT 2700  
 CTTATGCTTT GGAATACTCT TGGACAGTAA GCTGGACAA CTTCTGTTCA ACAAGTTGTC 2760  
 TGCCTTAAGT TCTTGAAGC AAACAGAAAA GCAAACTCA TCAGATTAT CTGCCAAACC 2820  
 CAAATCTCA AAGCCTTCA ACCCACTGCA AAACAAAGGC CATTATGCAT TTTCTCATAC 2880  
 65 TGGAGATTCC TCCGACAACA TCATGCTAAC TCAGTTTGTG TCAATGAAT AAGGCAAGGA 2940  
 ATCATAAAT CAAGAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA 3000  
 AGAAATTATG CTCAGTATTC GATCGGTTT TCTGATTAG GGGTCTGGGA ATAAACAG 3060  
 AATGTCTCAG TGGCTTCA 3078

70 Seq ID NO: C46 DNA Sequence  
 Nucleic Acid Accession #: NM\_000584.1  
 Coding sequence: 75..374

75 1 11 21 31 41 51  
 AGCAGAGCAC ACAAGCTTCT AGGACAAGAG CCAGGAAGAA ACCACCGGAA GGAACCATCT 60  
 CACTGTGTGT AAACATGACT TCCAAAGCTGG CCGTGGCTCT CTTGGCAGCC TTCCTGATT 120  
 CTGCAGCTCT GTGTGAAGGT GCAGTTTTCG CAGGAGTGC TAAAGAAGCT AGATGTCAGT 180  
 GCATAAGAC ATACTCCAAA CCTTTCACCC CCAATTTTAT CAAAGAAGCT AGAGTGATTG 240  
 80 AGAGTGGACC ACATCTGGCC AACACAGAAA TTATTGTAAA GCTTTCTGAT GGAAGAGAGC 300  
 TCTGTCTGGA CCCCAAGGAA AACTGGGTGC AGAGGGTTGT GGAGAAGTTT TTGAAGAGGG 360  
 CTGAGAATTC ATAAAAAAT TCATTCTCTG TGTATCCAA GAATCAGTGA AGATGCCAGT 420  
 GAAACTTCAA GCAATCTAC TTCAACACT CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480  
 CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTCA GTAAACAATG AATAGTTTTT 540  
 CATTGTACCA TGAATATCC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA 600



5  
10  
15  
20

```

CAAAAAACAA CAAATAATTT TTAATATATA GGATTTTCCT AGATATTGCA CGGGAGAATA 660
TACAAATAGC AAAATTGAGC CAAGGGCCAA GAGAATATCC GAACCTTAAT TTCAGGAATT 720
GAATGGGTTT GCTAGAATGT GATATTTGAA GCATCACATA AAAATGATGG GACAATAAAT 780
TTTGCCATAA AGTCAAAATTT AGCTGGAAAT CCTGGATTTT TTCTGTAA ATCTGGCAAC 840
CCTAGTCTGC TAGCCAGGAT CCACAAGTCC TTGTTCCACT GTGCCTTGGT TTCTCCTTA 900
TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTTACCTCAC AGTGATGTTG TGAGGACATG 960
TGGAAGCACT TTAAGTTTTT TCATCATAAC ATAAATTATT TTCAGTGTA ACTTATTAAC 1020
CTATTATTA TTTATGTATT TATTTAAGCA TCAAAATATT GTGCAAGAAT TTGGAAAAAT 1080
AGAAGATGAA TCATTGATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTA 1140
GATATTAATG GATGTTTTAT TAGATAAATT TCAATCAGGG TTTTATAGAT AAACAAGAA 1200
ACAAATGGGT ACCCAGTTAA ATTTTCATTT CAGATAAACA ACAAATAATT TTTTAGTATA 1260
AGTACATTAT TGTATTATCG AAAGTTTTAA TTGAACATAA AATCCTAGTT TGATACTCCC 1320
AGTCTTGTC TAAGCAGCTG TGTGTGTAGT GCTGTGTGA ATTACGGAAT AATGAGTTAG 1380
AACTATTAAA ACAGCCAAAA CTCACAGTC AATATTAGTA ATTTCTGCT GGTGAAACT 1440
TGTTATTAT GTACAAATAG ATTCTTATA TATTATTAA ATGACTGCAT TTTTAAATAC 1500
AAGGCTTATT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTACTGT 1560
TTCTGATTGT ATGGAATAT AAAAGTAAAT ATGAAACATT TAAATATATA TTTGTTGTCA 1620
AAGTAAAAAA AAAAAAAA 1639

```

Seq ID NO: C47 DNA Sequence  
Nucleic Acid Accession #: NM\_005603.1  
Coding sequence: 1..3756

25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ATGAGTACAG AAAGAGACTC AGAAACGACA TTTGACGAGG ATTCTCAGCC TAATGAGGAA 60
GTGGTTCCTC ACAGTGATGA TGAACAGAAA GATGAACCTG ATGACCAGGG GTCTGCTGTT 120
GAACACGAAC AAACCCGAGT CAACAGGGAA GCAGAGGAGA ACCGGGAGCC ATTCAGAAAA 180
GAATGTACAT GGCAGTCAA AGCAACGAT CGCAAGTACC ACGAACAAAC TCACTTTATG 240
AACACAAAT TCTTGTGTAT TAAGGAGAGT AAATATGCGA ATAATGCAAT TAAACATAC 300
AAGTACAACG CATTTACCTT TATACCAATG AATCTGTTTG AGCAGTTTAA GAGAGCAGCC 360
AATTTATATT TCCTGGCTCT TCTTATCTTA CAGGCAGTTC CTCAAATCTC TACCCTGGCT 420
TGGTACACCA CACTAGTGCC CCTGCTTGTG GTGCTGGGCG TCACTGCAAT CAAAGACCTG 480
GTGGACGATG TGCTCGCCA TAAATGGAT AAGGAAATCA ACAATAGGAC GTGTGAAGTC 540
ATTAAGGATG CGAGGTTCAA AGTGTCTAAG TGGAAAGAAA TTCAGTTGG AGACGTCAAT 600
CGTCTGAAA AAAATGATTT TGTTCAGCT GACATTCTCC TGCTGTCTAG CTCTGAGCCT 660
AACAGCCTCT GCTATGTGGA AACAGCAGAA CTGACGAGG AAACCAATTT AAAATTTAAG 720
ATGTCACTTG AATTCACAGA CCAGTACCTC CAAAGAGAAG ATACATTGGC TACATTGAT 780
GGTTTATATG AATGTGAAGA ACCCAATAAC CGACTAGATA AGTTTACAGG AACACTATTT 840
TGGAGAAACA CAAGTTTCCC TTTGGATGCT GATAAAATTT TGTACGTGG CTGTGTAATT 900
AGGAACACCG ATTTCTGCCA CGGCTTAGTC ATTTTTCAG GTGCTGACAC TAAATAAATG 960
AAGAATAGTG GGAHAACCGA ATTTAAAAAG ACTAAATTTG ATTACTTGAT GAACACTAGT 1020
GTTTACACGA CTTTGTGTGT TCTTATCTG CTTTCTGCTG GTCTTGCCAT CGGCGATGCT 1080
TATTTGGGAG CACAGTGGG CAATTCCTCT TGTACCTCT ATGATGGAGA AGACGATACA 1140
CCCTCTTACC GTGGATTCTT CATTTCTGG GGCTATATCA TTGTTCTCAA CACCATGGTA 1200
CCCATCTCTC TCTATGTCTG AGTGAAGTGT ATTCTCTTG GACAGAGTCA CTTCTATCAC 1260
TGGGACCTGC AAATGTACTA TGCTGAGAAG GACACACCG CAAAGCTAG AACCAACACA 1320
CTCAATGAAC AGCTCGGCGA GATCCATTAT ATCTTCTCTG ATAAGACGGG GACACTCACA 1380
CAAAATATCA TGACCTTTAA AAGTGCTGT ATCAACGGGC AGATATATGG GGACCATCGG 1440
GATGCTCTC AACACAACA CAACAAATA GAGCAAGTTG ATTTAGCTG GAATACATAT 1500
GCTGATGGGA AGCTTGCAAT TTATGACCAC TATCTTATG AGCAAATCCA GTCAGGGAAA 1560
GAGCCAGAAG TAOCACAGTT CTCTCTCTG CTCGCAGTTT GCCACACAGT CATGGTGGAT 1620
AGGACTGATG GTCACTGCAA CTACAGGCGA GCCTCTCCCG ATGAAGGTGC CCGTGTAAAC 1680
GCTGCCAGGA ACTTGGCTT TGCCCTCTC GCCAGGACCC AGAACACCAT CACCATCAGT 1740
GAACCTGGCA CTGAAGGCAT TTACAATGTT CTTGCCATT TGGACTTCAA CAGTGACCGG 1800
AAGCGAATGT CTATCATTTG AAGAACCCCA GAAGGCAATA TCAAGCTTTA CTGTAAAGGT 1860
GCTGACACTG TTATTTATGA ACGTTTACAT CGAATGAATC CTACTAAGCA AGAAACACAG 1920
GATGCCCTGG ATATCTTTGC AAATGAAACT CTTAGAACCC TATGCCCTTG CTACAGGAA 1980
ATTGAAGAAA AAGAATTTAC AGAATGGAAT AAAAAGTTTA TGGCTGCCAG TGTGGCCTCC 2040
ACCAACCGGG ACGAAGCTCT GGATAAAGTA TATGAGGAGA TTGAAAAGA CTTAATTCTC 2100
CTGGGAGCTA CAGCTATTGA AGACAAGCTA CAGGATGGAG TTCCAGAAAC CATTTCAAAA 2160
CTTGCAAAAG CTGACATTAA GATCTGGGTG CTTACTGGAG ACAAAGGGA AACTGCTGAA 2220
AATATAGGAT TGTCTGTGA ACTTCTGACT GAAGACACCA CCATCTGCTA TGGGGAGGAT 2280
ATTAATTTCT TCTTCTATGC AAGGATGGAA AACAGAGGA ATAGAGGTGG GGTCTACGCA 2340
AAGTTTGCAC CTCTCTGCA GGAATCTTTT TTTCACCCG GTGAAACCG TGCCTTAATC 2400
ATCACTGTTT CTGTGTTGAA TGAATTTCTT CTCGAGAAA AGACCAAGAG AAATAAGATT 2460
CTGAAGCTGA AGTTCCCAAG AACAGAAGAA GAAAGACGGA TGGGACCCA AAGTAAAGG 2520
AGGCTAGAAG CTAAGAAAGA GCAGCGGCAG AAAAATTTTG TGGACCTGGC CTGCGAGTGC 2580
AGCGCAGTCA TCTGCTCGCG CGTCAACCCC AAGCAGAAGG CCATGGTGGT GGACCTGGTG 2640
AAGAGGTGCA AGAAGCCAT CACGCTGGCC ATCGGAGATG GGGCAATGA CGTGAACATG 2700
ATCAAACTG CCCACATTGG CGTTGGAATA AGTGGACAAG AAGGAATGCA AGCTGTGATG 2760
TGAGTGACT ATTCCTTTGC TCAGTTCCGA TATCTGCAGA GGCTACTGCT GGTGCATGCG 2820
CGATGGTCTT TCATAGAGAT GTGCAAGTTC CTACGATACT TCTTTTACAA AAACCTTTGCC 2880
TTTACTTTGG TTCAATTTCTG GTACTCTCTC TTCAATGGCT ACTCTGCGCA GACTGCATAG 2940
GAGGATTGGT TCATCACCTT CTACAACTG CTGTACACCA GCCTGCGCTG GCTCCTCATG 3000
GGGCTGCTCG ACCAGGATGT GAGTGACAAA CTGAGCCTCC GATTCCTGCG GTTATACATA 3060
GTGGGACAAA GAGACTTACT ATTCAACTAT AAGAGATTCT TTGAAGCTT GTTGCATGGG 3120
GTCCTAATCT CGATGAPCTT CTCTTCATA CCTCTTGGAG CTTATCTGCA AACCGTAGGG 3180
CAGGATGGAG AGGCACTCTC CGACTACCAG TCTTTTGGCG TCACCAATGC CTCTGCTCTT 3240
GTAATAACAG CCAATTTCCA GATTGGCTTG GATACTTCTT ATTGGAATTT TGTGAATGCT 3300
TTTCAATTT TTGGAAGCAT TGCATTTTAT TTTGGCATCA TGTTTGACTT TCATAGTGCT 3360
GGAATACATG TTCTCTTTCC ATCTGCATTT CAATTTACAG GCACAGCTTC AAACGCTCTG 3420
AGACAGCCAT ACATTTGGTT AACTATCATC CTGACTGTTG CTGTGTGCTT ACTACCGCTC 3480

```

5 GTTGCCATTG GATTCTGTG AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG 3540  
 CATCGCAAGC GGTGGAAGGC GGAGGAGCAG TGGCAGCGAC GGCAGCAGGT GTTCCGCCGG 3600  
 GGCCTGTCAA CGCGGCGCTC GGCCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC 3660  
 ATCTCTCCG GGCAGCAT CCGCAAGAAG CGCTCGCCGC TTGATGCCAT CGTGGCGGAT 3720  
 GGCACCGCG AGTACAGGCG CACCGGGGAC AGCTGA 3756

Seq ID NO: C48 DNA Sequence  
 Nucleic Acid Accession #: XM\_044533  
 Coding sequence: 238..2751

10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 GCTCTGCCA AGCCGAGGCT GCGGGGCGG CGCCGGCGGG AGGACTGCGG TGCCCCGCGG 60  
 AGGGGCTGAG TTTGCCAGGG CCCACTTGAC CCTGTTTCCC ACCTCCCGCC CCCCAGGTCC 120  
 GGAGGCGGGG GCCCGCGGGG CGACTCGGGG GCGGACCGCG GGGCGAGCT GCGCGCCGTG 180  
 AGTCGGGCGG AGCCACCTGA GCCCGAGCCG CGGGACACCG TCGCTCTGSC TCTCGSAATG 240  
 CTGCGCACCG CGATGGGCGT GAGGAGCTGG CTGCGCGCCC CATGGGGGCG GCTGCGCGCT 300  
 CGGCCACCGC TGCTGCTGCT CCTGCTGCTG CTGCTCTGCG TGACGCGGCC GCCTCCGACC 360  
 TGGGCGCTCA GCCCCGCGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCG ATTCTCAGA 420  
 TTGGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC 480  
 CTGTACGTGG GTGCTCGAGA GGCCTCTTT GCACTCAGTA GCAACCTCAG CTTCTGCGCA 540  
 GGGCGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCG AGAAGAAACA GCAGTGACAG 600  
 TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAAACTACA TCAAGATCCT CCGTCCGCTC 660  
 AGCGGCACTC ACCTGTTTCA CTGTGGCACA GCAGCCTTCA GCCCATGTG TACCTACATC 720  
 AACATGGAGA ACTTACCCCT GGCAGGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780  
 AAGGGCGGTT GTCCCTTGA CCGAATTTC AAGTCCACTG CCTGGTGGT TGATGGCGAG 840  
 CTCTACACTG GAACAGTCAG CAGCTTCCAA GGGAAATGACC CGGCCATCTC GCGGAGCCAA 900  
 AGCCTTCGCC CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG 960  
 GCCTCAGCCT ACATTCTCTG GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020  
 TTTTCTTCA GCGAGACTGG CCAGGAATTT GAGTCTTTTG AGAACACCAT TGTGTCCCGC 1080  
 ATTGCCCGCA TTTGCAAGGG CGATGAGGGT GGAGAGCGGG TGTACAGCA GCGCTGGACC 1140  
 TCCTTCTCTA AGGCCAGCT GCTGTGCTCA CGGCCCGACG ATGGCTTCCC CTTCAACGTG 1200  
 CTGCAGGATG TCTTCAAGCT GAGCCCCAGC CCCCAGGACT GCGGTGACAC CTTTCTTAT 1260  
 GGGGTCTTCA CTTCCTAGTG GCACAGGGGA ACTACAGAAG GCTCTGCGGT CTGTGTCTTC 1320  
 ACAATGAAG ATGTGACAG AGTCTTACG GGCCTCTACA AGGAGGTGAA CCGTGAGACA 1380  
 CAGCAGTGGT ACACCGTGAC CCACCCGCTG CCCACACCCC GGCCTGGAGC GTGCATCACC 1440  
 AACAGTGCCT GGGAAAGGAA GATCAACTCA TCCCTGCAGC TCCCAGACCG CGTGTGAAC 1500  
 TTCTCAAGG ACCACTTCTT GATGGACGGG CAGGTTCGAA GCGCATGCT GCTGTGACG 1560  
 CCCCAGGCTC GATACAGGAG CGTGGCTGTA CACCGGCTCC CTGGCTGCA CCACACTTAC 1620  
 GATGTCTCTT TCCTGGGAC TGGTGACGGC CGCTTCCACA AGGCAGTGAG CGTGGGCCCC 1680  
 CCGGTGACCA CAITTAGGA GCTGCAGATC TTCTCATCGG GACAGCCGCT GCAGATCTG 1740  
 CTCCTGGACA CCCACAGGG GCTGTGTAT GCGGCTTAC ACTCGGGCGT AGTCCAGGTG 1800  
 CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGACT GCCTCTCTGC CCGGAGACCC 1860  
 TACTGTGCTT GATGGGCTC CAGCTGCAAG CAGCTCAGCC TCTACAGCC TCGCTGGCC 1920  
 ACCAGGCGGT GGATCCAGGA CATCGAGGGA GCCAGGCCCA AGGACCTTTG CAGCGGTCT 1980  
 TCGGTGTGT CCCTGCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040  
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCTCT CCAACCTGGC GACCCGACTC 2100  
 TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCTCTCT GCCACGTGCT ACCCACTGGG 2160  
 GACCTGCTGC TGGTGGGAC CCAACAGCTG GGGGAGTTC AGTGTGGTTC ACTAGAGGAG 2220  
 GGCCTTCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280  
 CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGACCA 2340  
 GCTGTGTGCA AGGCCAGCTG GGTGTCAGAC AGGTCTTACT GGAAGGAGTT CCTGGTGATG 2400  
 TGCACGCTCT TGTGCTGGC CGTGTGCTC CAGTCTTAT TCTGTCTTA CCGGCACCGG 2460  
 AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA GCGTGACACC CAAGAOTGCT 2520  
 CCTGTGTGTC TGCCCTCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCC TAGCACCCCG 2580  
 CTGATACAC GAGGGTACCA GTCCCTGTCA GACAGCCCC CGGGTCCCG AGTCTTCACT 2640  
 GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTG TGGAGGTATC CCCAGTGTGC 2700  
 CCCCAGCCCC GGGTCCGCTT TGGCTCGGAG ATCCGTGACT CTGTGTGTG AGAGCTGACT 2760  
 TCCAGAGGAC GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820  
 TCCCCTCCGC TCTGCTCTTC GTGGAACAGC ACCGTGGTGC CCGGCCCTTG GAGCCTTGG 2880  
 GGCAGCTGG CTTGCTGCTC TCCAGTCAAG TAGCGAAGCT CTAACCAACC AGACCCCAA 2940  
 ACAGCCGTGG CCCCAGAGGT CCGGCCCAA TATGGGGGCC TGCCTAGGTT GGTGGAACAG 3000  
 TGCTCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAAGTGAAT 3060  
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCCAGTTCA TGGCTCCCA 3120  
 GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAC 3180  
 TGGCTCTTC ACCTTCCACA TTATCCGCT GCCACGGCT GCCCTGTCTC ACTGCAGATT 3240  
 CAGGACACAG TTGGGCTGCG TGCGTCTGTC CTTGCCAGTC AGCCGAGGAT GTAGTTGTTG 3300  
 CTGCGTGTG CCCACCACT CAGGAGCCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360  
 GGTCTGGGC TCGGACCCAA CTCTGGACC TTTCAGGCT GTATCAGGCT GTGGCCACAC 3420  
 GAGAGGACAG CGCGAGCTCA GGAGAGATT CTGTACAATG TACGCCCTTC CCTCAGAAAT 3480  
 CAGGGAAGAG ACTGTGCGCT GCCTTCTCC GTTGTGCGT GAGAACCCTG GTGCCCCCTC 3540  
 CCACCATATC CACCTCGCT CCATCTTTGA ACTCAACAC GAGGAACATA CTGCACCTG 3600  
 GTCTCTCCC CAGTCCCCAG TTCACCTCC ATCCCTCAC TTCTCCACT CTAAGGGATA 3660  
 TCAACACTGC CCAGCACAGG GGCCTGAAT TTATGTGGT TTTATACATT TTTTAATAAG 3720  
 ATGCACCTTA TGTCATTTT TAATAAAGTC TGAAGAATTA CTGTTT 3766

Seq ID NO: C49 DNA Sequence  
 Nucleic Acid Accession #: NM\_007019.1  
 Coding sequence: 41..580

1 11 21 31 41 51  
 GGCACGAGCG AGTCTCTGTC TCTCTGCCAA CGCCGCCCGG ATGGCTTCCC AAAACCGCGA 60

	CCCAGCCGCC	ACTAGCGTCG	CCGCCGCCCG	TAAAGGAGCT	GAGCCGAGCG	GGGGGGCCCG	120
	CCGGGGTCCG	GTGGGCAAAA	GGCTACAGCA	GGAGCTGATG	ACCTCATGA	TGCTCGGCGA	180
	TAAAGGATT	TCTGCCTTCC	CTGAATCAGA	CAACCTTTTC	AAATGGGTAG	GGACCATCCA	240
5	TGGAGCAGCT	GGAAACAGTAT	ATGAAGACCT	GAGGTATAAG	CTCTCGCTAG	AGTTCCCCAG	300
	TGGCTACCTT	TACAATGCGC	CCACAGTGAA	GTTCCCTCAG	CCCTGCTATC	ACCCCAACGT	360
	GGACACCCAG	GGTAACATAT	GCCTGGACAT	CCTGAAGGAA	AAGTGGTCTG	CCCTGTATGA	420
	TGTCAGGACC	ATTCTGCTCT	CCATCCAGAG	CCTTCTAGGA	GAACCCAAAC	TGTATAGTCC	480
	CTTGAACACA	CATGCTGCGG	AGCTCTGGAA	AAACCCCAAC	GCTTTTAAGA	AGTACCTGCA	540
10	AGAAACCTAC	TCAAAGCAGG	TCACCAGCCA	GGAGCCCTGA	CCCAGGCTGC	CCAGCCTGTC	600
	CTTGTGTGCT	CTTTTAAATT	TTTCCTTAGA	TGGTCTGTCC	TTTTTGTGAT	TTCTGTATAG	660
	GACTCTTTAT	CTTGAGCTGT	GGTATTTTGT	TTTTGTTTTT	GTCTTTTAAA	TAAAGCCTCG	720
	GTGAGCCCT	TGTATATTAA	ATAAATGCAT	TTTGTCTCTT	TTTTAAAAAA	AAAAAAAAAA	780
	AAA						783
15	Seq ID NO: C50 DNA Sequence Nucleic Acid Accession #: NM_014584.1 Coding sequence: 227..1633						
20	1	11	21	31	41	51	
	GCACGAGCCC	CGGGCTGCCG	GCGCGGGCGC	CGCGGCACGT	CCACAGGCTG	GGTCCGAGAG	60
	TGGCGATGCG	TGAGAGGCGAG	GAGGGCCGAG	GCGGGCCCTGG	GAGGCGGCCC	GGAGGTGGGG	120
	CGCGGCTGGG	GCGGGCCCGC	ACGGGCTTCA	TCTGAGGGCG	CACGGCCCGC	GACCGAGCGT	180
25	GCGGACTGGC	CTCCCAAGCG	TGGGGCGACA	AGCTGCCGGA	GCTGCAATGG	GCCGCGGCTG	240
	GGGATTTCTG	TTTGCGCTCC	TGGGCGCGGT	GTGGCTGCTC	AGCTCGGGCC	ACGGAGAGGA	300
	GCAGCCCCCG	GAGACAGCGG	CACAGAGGTG	CTTCTGCCAG	GTTAGTGGTT	ACTTGGATGA	360
	TTGTACTCTG	GATGTTGAAA	CCATTGATAG	ATTTAATAAC	TACAGGCTTT	TCCCAAGACT	420
	ACAAAACCTT	CTTGAAAGTG	ACTACTTTAG	GTATTACAAG	GTAACCTGTA	AGAGGCGGTG	480
30	TCCTTTCTGG	AATGACATCA	GCCAGTGTGG	AAGAAGGGAC	TGTGCTGTCA	AACCATGTCA	540
	ATCTGATGAA	GTTCCTGATG	GAATTAAATC	TGCGAGCTAC	AAGTATTCTG	AAGAAGCCAA	600
	TAATCTCATT	GAAGAATGTG	AACAAGCTGA	ACGACTTGGG	GCAGTGGATG	AATCTCTGAG	660
	TGAGGAAACA	CAGAAGGCTG	TTCTTCAGTG	GACCAAGCAT	GATGATTCTT	CAGATAACTT	720
	CTGTGAAGCT	GATGACATTC	AGTCCCTGGA	AGCTGAATAT	GTAGATTTCG	TTCTTAATCC	780
35	TGAGCGCTAC	ACTGGTTACA	AGGGACCAGA	TGCTTGGAAA	ATATGGAATG	TCATCTACGA	840
	AGAAAACTGT	TTTAAGCCAC	AGACAATTAA	AAGACCTTTA	AATCCTTTGG	CTTCTGGTCA	900
	AGGGACAAGT	GAAGAGAACA	CTTTTACAG	TGGCTAGAAA	GGTCTCTGTG	TAGAAAAAAG	960
	AGCATTCTAC	CACTTATAT	CTGGCCTACA	TGCAAGCATT	AATGTGCATT	TGAGTGCAAG	1020
	ATATCTTTTA	CAGAGAACCT	GTTAGAAAA	GAAATGGGGA	CACAACATTA	CAGAATTTC	1080
40	ACAGCGATTT	GATGGAATTT	TGACTGAAGG	AGAAGGTCCA	AGAAGGCTTA	AGAAGCTTGA	1140
	TTTTCTCTAC	TTAATAGAAC	TAAAGGCTTT	ATCCAAAGTG	TTACCATCT	TCGAGCGCCC	1200
	AGATTTCTAA	CTCTTTACTG	GAAATAAAAT	TCAGGATGAG	GAAACAAAA	TGTTACTTCT	1260
	GGAAATACCT	CATGAATACA	AGTCATTTC	TTTGCAATTT	GATGAGAATT	CATTTTTTGC	1320
	TGGGATAAAT	AAAGAAGCAT	ACAAACTAAA	GGAGGACTTT	CGACTGCATT	TTAGAAATAT	1380
45	TTCAAGAAAT	ATGGATTGTG	TTGGTTGTTT	TAAATGTCGT	CTGTGGGGAA	AGCTTCAGAC	1440
	TCAGGGTTTG	GGCACTGCTC	TGAAGATCTT	ATTTCTTGAG	AAATTGATAG	CAAAATATGCC	1500
	AGAAAGTGGA	CCTAGTTATG	AATTCCATCT	AACCAGACAA	GAAATAGTAT	CATTATTCAA	1560
	CGCATTTGGA	AGAAATTTCT	CAAGTGTGAA	AGAATTAGAA	AACCTCAGGA	ACTTGTTCAC	1620
	GAATATTCTA	TAAAGAAAAC	AAGCTGATAT	GTGCTGTGTT	CTGGACAATG	GAGGCGAAGG	1680
50	AGTGAATTTT	CATTCAAAGG	CATAATAGCA	ATGACAGTCT	TAAGCCAAAC	ATTTTATATA	1740
	AAGTGTCTTT	TGTAAGAGAG	AATTATATTG	TTTTAAGTAA	ACACATTTT	AAAAATTTGT	1800
	TTAAGTCTAT	GTAAATTAAT	ACTGTGAGTA	AAAGTAATAC	TTTAATAATG	TGTTACAAAT	1860
	TTTAAAGTTT	AATATTGAAT	AAAAGGAGGA	TTATCAAATT	CATATATGAT	AAAAGTGAAT	1920
	GTTCTAAGTC	TCTCAACTAC	GCGTTTATG	TAATAATATG	TAATATAAAT	AAAACATATG	1980
55	TAAATGTGAC	AAGCATTTAA	TAGGAAAATG	CTAAGGAGGC	CTCATAAATG	ACCCATAATT	2040
	ACCAACGTAG	AATTTTTCAG	TACATTTAGG	GTGTCTGGAT	TTAGCAAAAT	AAAAATAAGA	2100
	TTGCCAGTGT	AGATTGGAAT	TTCAAGATAA	CAATTAGTTT	TTTAATATT	TACATGGAAT	2160
	ATTTGGAAAA	TACTTATACT	AAAAAATTAT	TTGTTTGAAA	TTCAATTTA	ACTGGGAGTC	2220
	TTGTATTTTA	CTCGCAATAC	CTAAAATACA	TTGGTATGAA	ACAAATCACT	TTTAGAAGTA	2280
60	TATTGCTATT	TTGATTGGGT	TGTTTTTGTG	TGTAGAAACG	TACAATAACA	ACTCAAGGC	2340
	ACAGGAGATT	TCTAAACATT	GTGAAAAGTT	GAATAGATTA	TATATTATT	CTCATAATAC	2400
	TTTCACTAAT	ACTAAATAAA	ATTTGGGGAA	CACCTTTTAT	TTTTATATA	TTTCCAATTT	2460
	ACAGAAAAGT	TTCAAAATA	GTACAAAGAG	CTCTCTTACC	CAGATTCAC	AATTGTTTCA	2520
	AGTGCTTTA	CTTTCTATGC	TTTCTCTGTA	CACACACACA	CACACACAAA	TTTTTCTTCA	2580
65	ATCATTTGAA	AGTCAGTTAT	AGGCATCATG	CCCCTTAAAC	CCTAAATACT	TCAGTGTGTA	2640
	ATACTGAATA	ATTACTAAAA	ATGATTTTCT	CAGAAAAAAA	AACCTCCACA	ATTCTGGAAC	2700
	TATAATACTG	TAAAGCTTAG	AATAAATAAT	ACTTTCAAGT	TCCAATCTAA	AGTTCTTTTT	2760
	GAGTTTGTG	GCCCGTTTAA	TGCTTGATGT	GTATAGTAAT	AGGGTAGGCT	ATTTATTTTA	2820
	TAAAAATTTT	TTTTAGAGAC	AAGGTTTTGC	TGTGTTGCCC	AAGCTGGAAC	TTGAACGACT	2880
70	GGGCTGAAGT	GATCTTCCCA	CCTCAGCCTC	CCAAGTAGCT	GGGAATACAG	GTGCTGCGCA	2940
	CCATACCCAG	TTTCATTTT	GTTTTTTATA	CCGAAGTTTC	ATTTCTTTTG	TCTCCCTAAA	3000
	ACTGAACCTG	AATTTTGGGA	GGTTTTTCAT	AGTGGGAAGCT	CTTCATTTAT	AAAGCTATTT	3060
	GAGGGGGTTT	AGGAATTTAT	ATCAGATGTT	AATTGTAGAG	AAAAAGAGGC	TATATACCTC	3120
	AAAACTGTGC	CCTCTTTTCA	TATGCTTTAT	CAGGTATAAC	ATGTTGAAAT	GTACATTAG	3180
75	TAGTAAAGTG	GGGTTTATTT	ATATAGTGGT	TAAGAAATGT	CAGTTTACAC	TGCTGTATAC	3240
	TTCTTCTTCT	GTGTCCTTAA	GGCCTGGTAC	AGTGCCAAGC	ACATACTTGG	TATCCAATAA	3300
	ATATTGTGTT	GATGAAAAAA	AAAAAAAAAA	AAAA			3334
80	Seq ID NO: C51 DNA Sequence Nucleic Acid Accession #: NM_002888.1 Coding sequence: 37..723						
	1	11	21	31	41	51	

5  
 10  
 15

```

CCACGCTCCGG GGTGCGGAGC CAACTTTCCT GCGTCCATGC AGCCCCGCG GCAACGGCTG 60
CCCCCTCCCT GGTGCGGGCC CAGGGGCCCG CGCCCCACCG CCCCGCTGCT CGCGCTGCTG 120
CTGTTGCTCG CCCCGGTGGC GCGCGCCGCG GGTTCGCGGG GCCCGGACGA CCCTGGGCAG 180
CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGGCGCGCGC GCGGCTTCAC 240
TTCTTCAACT TCGGTCGCG CTGCGCCAGC GCGCTGCGAG TGCTGGCGGA GGTGCAGGAG 300
GGCCGCGCGT GGATTAATCC AAAAGAGGGA TGTAAAGTTC ACGTGGTCTT CAGCACAGAG 360
CGCTACAACC CAGAGTCTTT ACTTCAGGAA GGTGAGGGAC GTTTGGGGAA ATGTTCTGCT 420
CGAGTGTITT TCAAGAATCA GAAACCCAGA CCAACCATCA ATGTAACCTG TACACGGCTC 480
ATCGAGAAAA AGAAAAGACA ACAAGAGGAT TACCTGCTTT ACAAGCAAT GAAGCAACTG 540
AAAAACCCCT TGGAAATAGT CAGCATACCT GATAATCATG GACATATTGA TCCCTCTCTG 600
AGACTCATCT GGGATTGGC TTTCCTTGA AGCTCTTACG TGATGTGGGA AATGACAACA 660
CAGGTGTGAC ACTACTACT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC 720
TGAAAATTAA CTGTGCCAC AAGAGTTACA ATCAAAGTGG TCTCCTTAGA CTGAATTCAT 780
GTGAATCTCT AATTTCATAT CAAGAGTTGT AATCACAATT ATTTCAATAA ATATGTGAGT 840
TCTCTG 846
  
```

Seq ID NO: C52 DNA Sequence  
 Nucleic Acid Accession #: NM\_005409.3  
 Coding sequence: 94..378

20  
 25  
 30  
 35  
 40  
 45

```

1 11 21 31 41 51
| | | | |
TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
TTGGCTGTGA TATGTGTGTC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
TGCTTTTGCA TAGGCCCTCG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
ATAATGTACC CAGATTAACA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAAT 300
AAGGACAAC GAGTCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAGAGG GCATCTGAAA 420
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
AGACTTTTCT ATGCTTTTGT GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCOA 600
CTGCCCAAG GAGTCCAGCA ATTAAATGGA TTCTAGGAAA AAGCTACCTT AAGAAAGGCT 660
GGTTACCATC GAGGTTTACA AAGTGCTTTC ACGTCTTAC TTGTGTATT ATACATTTCAT 720
GCATTCTTAG GCTAGAGAAC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
GAGAACATT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
CATCTATGTC TGTAAAGCA TTCTCAAAAC ATTTTTCAT GCAAAATACAC ACTTCTTCC 960
CCAAATATCA TGTAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTTGTTTGT 1020
TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATAGCTA 1080
TGGGATCTGT GCAACAGTGC ACATATTICA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140
GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
TGACTTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTTGAAA 1260
TACAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320
AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
TTGTTATGTC CTATATACTG TAAAATTAG GTATACTCAA GACTAGTTTA AAGAATCRAA 1440
GTCATTTTTT TCTTAATAA ACTACCACAA CCTTCTTTT TTAACAAAAA AAA 1493
  
```

50  
 Seq ID NO: C53 DNA Sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..609

55  
 60  
 65

```

1 11 21 31 41 51
| | | | |
ATGCTGCGGC AGGTGCTTCG CAGAGGGCTC CAGTCGTTCT GCCACAGGCT GGGTTTGTGC 60
GTGAGCGGCG ACCCGGTCTT TTCTCTCACC GTGCCGCGAG TCCTGACAAAT CACCTTCGCG 120
CTCAGCGCGC TCAACCGCTT CCAGCCCGAG GCGACCTGG AGCGCTCTGT CGCTCCGAGC 180
CACAGCGCTG CCAAGATCGA GCGCAGCCTG GCCAGCAGCC TTTTCCCGCT GGACCACTCC 240
AAAAGCCAGC TCTATTCCGA CTTACACACC CCGGGAGGT ATGGCAGGCT GATCCTCCTC 300
TCCCCAACCG GGGACAATAT TTGTCTCCAG GCTGAGGGGA TCCTGCAGAC CCACCGAGCC 360
GTGCTGGAAG TGAAGGTGAA CCACAAGGCG TATAATTATA CTTTTTCCCA TCTGTGTGTG 420
TTGAGAAATC AGGATAAGAA ATGCGTGTCT GATGATATTA TTTCAGTGTCT AGAGGATCTC 480
AGGCAGGCTG CCGTCTCCAA TAAGACAACA GCCAGGGTGC AAGTGAGGTA TCCCAACACT 540
AAATTAAGG TATGCTCCTT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCATTTT 600
TTGCCCTAA 609
  
```

70  
 Seq ID NO: C54 DNA Sequence  
 Nucleic Acid Accession #: NM\_002438.1  
 Coding sequence: 104..4474

75  
 80

```

1 11 21 31 41 51
| | | | |
GGGAACTTGG ATTAGGTGGA GAGGCAGTTG GGGGGGCTCG TTGTTTGGG TCTTAGTTCC 60
GCCCTCCTGT CCATCAGGAG AAGGAAAGGA TAAACCTCG GCCATGAGGC TACCCCTGCT 120
CCTGGTTTTT GCCTCTGTCA TTCCGGGTGC TGTTCTCTA CTGGACACCA GGCAATTTTT 180
AATCTATAAT GAAGATCACA AGCGCTGCGT GGTGCAAGT AGTCCAGTG CCGTCCAAAC 240
CGCAGCTTGC AACCAGGATG CCGAATCACA GAAATCCGA TGGGTGTCCG AATCTCAGAT 300
TATAGTGTGT GCATTGAAAT TATGCTGGG AGTGCCATCA AAAACAGACT GGGTTGCTAT 360
CACTCTCTAT GCCTGTGACT CAAAAAGTGA ATTTCAAGAA TGGGAGTGCA AAAATGACAC 420
ACTTTTGGGG ATCAAGAGGAG AAGATTATT TTTTAACTAC GGCAACAGAC AAGAAAAGAA 480
TATTATGCTC TACAAGGGAT CGGTTTATG GAGCAGGTGG AAGATCTATG GAACCAAGA 540
CAATCTGTGC TCCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC 600
AACCTGGGCA TTCCCGTTCA AGTTTGAAGA CAAGTGTGAC GCAGATTGCA CGAGTGCTGG 660
GCGGTGCGAT GGATGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT 720
  
```

5	TGGATATTGT	CCATTGAAAT	TTGAGGGCAG	TGAAAGCTTA	TGGAATAAAG	ACCCGCTGAC	780
	CAGCGTTTCC	TACCAGATAA	ACTCCAAATC	CGCTTTAAAG	TGGCACCAG	CGAGGAAAG	840
	CTGCCAACA	CAGAACGCTG	AGCTCCTGAG	CATCACAGAG	ATACATGAGC	AAACATACT	900
	GACAGGATTA	ACCAGTTCCT	TGACCTCAGG	ACTCTGGATT	GGACTTAACA	GTCTGAGCTT	960
	CAACAGCGGT	TGGCAGTGA	GTGACCCGAG	TCCTTTCCGA	TATTTGAACT	GGTTACCAGG	1020
	AAGTCCATCA	GCTGAACCTG	GAAAAAGCTG	TGTGTCACTA	AATCCTGGAA	AAAATGCTAA	1080
	ATGGGAAAT	CTGGAATGTG	TTCAAGAACT	GGCTATATT	TGCAAAAAGG	GCAACACCAC	1140
	TTTAAATTCT	TTTGTATTTC	CCTCAGAAAG	TGATGTGCCT	ACTCACTGTC	CTAGTCAGTG	1200
10	GTGGCCGTAT	GCCGGTCACT	GTTACAAGAT	TCACAGAGAT	GAGAAAAAAA	TCCAGAGGGA	1260
	TGCTCTGACC	ACCTGACAGG	AGGAAGGCGG	TGACCTCACA	AGTATCCACA	CCATCGAGGA	1320
	ATTGGACTTT	ATTATCTCCC	AGCTAGGATA	TGAGCCAAAT	GACGAATTGT	GGATCGGCTT	1380
	AAATGACATT	AAGATTCAAA	TGTACTTTGA	GTGGAGTGAT	GGGACCCCTG	TAACGTTTAC	1440
	CAAATGGCTT	CGTGGAGAAC	CAAGCCATGA	AAACAACAGA	CAGGAGGATT	GTGTGGTGAT	1500
15	GAAAGGCAAG	GATGGGTACT	GGGCAGATCG	GGGCTGTGAG	TGGCCTCTTG	GCTACATCTG	1560
	CAAGATGAAA	TGCAGAGGCC	AAGGTCCAGA	AATAGTGGAA	GTGAAAAAAG	GCTGCAGGAA	1620
	AGGCTCGAGG	GGCTATCTGG	TTTACTGCTA	TATGATTGGA	CATACGCTTT	CAACATTTCG	1680
	AGAAGCAAA	CAAACCTGTA	ATAATGAGAA	TGCTTATTTA	ACAACATTAT	AAGACAGATA	1740
	TGAACAAGCC	TTCTGACTA	GTTTCGTTGG	CTTAAGGCCT	GAAAAATATT	TCTGGACAGG	1800
20	ACTTTCAGAT	ATACAACCTA	AAGGGACTTT	TCAGTGGACC	ATCGAGGAAG	AGGTTGGGTT	1860
	CACCCACTGG	AATTACAGATA	TGCCAGGGCG	AAAGCCAGGG	TGTGTGCCA	TGAGAACCGG	1920
	GATTGCAGGG	GGCTATCTGG	ATGTTTTGAA	ATGTGATGAA	AAGGCCAAAT	TGTGTGCA	1980
	GCCTGGGCA	GAAGGAGTAA	CCCAACCCAC	GAAGCCACG	ACGACTCCCG	AACCCAAATG	2040
	TCCGGAGGAT	TGGCGGCCCA	GCAGTAGAAC	AAGCTTGTGT	TTCAAGCTGT	ATGCAAAAGG	2100
25	AAAACATGAG	AAAAAAGCT	GGTTTGAATC	TCGAGATTTT	TGTCGAGCTC	TGGGTGGAGA	2160
	CTTAGCTAGC	ATCAATAACA	AAGAGGAACA	GCAACAATA	TGCGGATTAA	TAACAGCTAG	2220
	TGGAAGCTAC	CACAACTGT	TTTGGTTGGG	ATTGACATAT	GGAAGCCCTT	CAGAAGGTTT	2280
	TACTTGGAGT	GATGTTCTCT	CTGTTTCATA	TGAAAACCTG	GCTTATGGAG	AACCTAATAA	2340
	TTATCAAAAT	GTTGAATACT	GTGTTGAGCT	GAAAGGTGAC	CCTACTATGT	CTTGGAAATGA	2400
30	TATTAATTGT	GAAACCTTAA	ACAACCTGAT	TTGCCAGATA	CAAAAAGGAC	AAACACCAAA	2460
	ACCTGAGCCA	ACACAGCTC	CTCAAGACAA	TCCACAGTT	ACTGAAGATG	GGTGGGTTAT	2520
	TTACAAAGAC	TACCACTATT	ATTTCAGCAA	AGAGAAGGAA	ACCATGGACA	ATGCGGAGAC	2580
	GTTTTGCAAG	AGGAATTTTG	GTGATCTTGT	TTCTATTCAA	AGTGAAGATG	AAAAGAAGTT	2640
	TCTATGAAA	TATGTAAACA	GAATGATGTC	ACAGTCTGCA	TATTTTATTG	GTTTATTGAT	2700
35	CAGCTTGGAT	AAAAAGTTTG	CTTGGATGGA	TGGAAGCAAA	GTGGATTACG	TGCTTGGGC	2760
	CACAGGTGAA	CCCAATTTTG	CAATGAAGA	TGAAAACCTG	GTGACCATGT	ATTCAAATTC	2820
	AGGGTTTTGG	AATGACATTA	ACTGTGGCTA	TCCAAACGCC	TTCAATTGCC	AGCGACATAA	2880
	CAGTAGTATC	AATGTACCA	CAGTTATGCC	TACCATGCC	TCCGTCCCAT	CAGGGTGCAA	2940
	OGAAGGTTGG	AATTTCTACA	GCAACAGTG	TTTCAAAATC	TTTGGATTGA	TGGAAGAAGA	3000
40	AAGAAAAAAT	TGGCAGAGG	CACGAAAAGC	TTGTATAGGC	TTTGGAGGGA	ATCTGTTCTC	3060
	CATACAAAT	GAAAAAGAGC	AAGCAATTCT	TACCTATCAC	ATGAAGGACT	CCACTTTCAG	3120
	TGCCTGGAAT	GGCTGAAATG	ATGTCAATTC	AGAACACACG	TTCTTTGGA	CGGATGGAGC	3180
	AGGAGTCCAT	TACCAAACT	GGGGAAAGG	TTACCTGGT	GGAAGAAGAA	GCAGTCTTTC	3240
	TTATGAAGAT	GCTGACTGTG	TTGTTATTAT	TGGAGGTGCA	TCAATGAAG	CAGGAAATG	3300
45	GATGGATGAT	AACTCGCACA	GTAACGAGG	CTACATATGC	CAGACACGAT	CCGACCTTTC	3360
	CTTGACTAAT	CCTCCAGCAA	CGATTCAAAC	AGATGGCTTT	GTTAAATATG	GCAAAAGCAG	3420
	CTATTCACTC	ATAGACACAA	AATTTCAATG	GCATGAAGCG	GAGACATACT	GCAAGCTTCA	3480
	CAATTCCCTT	ATAGCCAGCA	TTCTGGATCC	CTACAGTAAT	GCATTTCGCT	GGCTGCAGAT	3540
	GGAAACATCT	AATGAACGTG	TGTGGATCGC	CCTGAACAGT	AACCTGACGT	ATAATCAATA	3600
50	CACITGGACT	GATAAGTGA	GGGTGAGGTA	CACATACTGG	GCTGCTGATG	AGCCCAAAAT	3660
	GAAATCAGCA	TGTGTTTATC	TGGATCTTGA	TGGCTACTGG	AAGACAGCAC	ATTGCAATGA	3720
	AAGTTTATAC	TTTCTCTGTA	AAAGATCAGA	TGAAATCCCT	GCTACTGAAC	CCCCACAATC	3780
	GCCTGGCAGA	TGCCCGAGT	CAGATCACAC	AGCATGGATT	CCTTTCATG	GTCACTGTTA	3840
	CTATATTGAG	TCCTCATATA	CAAGAAACTG	GGGCCAAGCT	TCTCTGGAAT	GTCTTCGAAT	3900
55	GGGTTCCTCT	TGGTTTCCA	TTGAAAGTGC	TGCAGAAATC	AGTTTCTCTG	CATATCGGGT	3960
	TGAGCCACTT	AAAAGTAAAA	CCAATTTTGG	GATAGGATTG	TTCAAGAAATG	TTGAAGGGAG	4020
	TGGCTGTGG	ATAAATAACA	GTCCGGTCTC	CTTTGTCAAC	TGGAACACAG	GAGATCCCTC	4080
	TGGTGAACGG	AATGATTGTG	TAGCTTTACA	TGCGTCTTCT	GGGTTTGGGA	GTAATATTCA	4140
	CTGTTCTTCC	TACAAGGAT	ATATTTGTAA	AAGACCAAAA	ATTATTGATG	CTAAACCTAC	4200
60	TCATGAATTA	CTTACACCAA	AAGCTGACAC	AAGGAAGATG	GACCTTCTTA	AACCGTCTTC	4260
	CAACGTGGCC	GGAGTAGTCA	TCAATTGTGAT	CCTCCTGATT	TTAACGGGTG	CTGGCCTTGC	4320
	CGCCTATTTC	TTTTATAAGA	AAAGACGTGT	GCACCTACCT	CAAGAGGGCG	CCTTTGAAAA	4380
	CACCTCTGAT	TTTAACAGTC	AGTCAAGCCC	AGGAACAGT	GATATGAAG	ATCTCGTGGG	4440
	CAATATTGAA	CAGAATGAAC	ACTCGGTCAT	CTAGTACCTC	AATGCGATTG	TGAGATATTT	4500
65	GAATTTCTATA	AAATTTGAAC	TGAAATTTAA	AAATTTTAGT	TCAATGTGAT	TGTTTCTTTT	4560
	AAAATGAGTA	CTGAATTTGA	CTGGTCTGTC	CTTTTTCTCT	TTGCTTAATT	GAAGAAATAA	4620
	TTGCTTGTTT	TCTAGCTCGG	CAAGATATTT	TCATAAAAGA	GGGATAACAA	TGCTGATTAC	4680
	TACCTTTTAA	AATATTTTAG	ATAAATGCAC	AGCACACAG	CACCACTCT	AAGCATTAGT	4740
	GATGGGTAGC	TGATGTCAGC	TTTATGTGGA	TTTAAAGCAC	TCTAGAAACA	ATGAAGCTTC	4800
70	TTGGCATATT	TTAAGGAGCT	CCCAAAATGT	GTTACCTATT	AAATTTGAAC	TCAGCAAGTA	4860
	GAAGACCAAT	TGAAAGTCA	GGTACAAAT	TCCTCAAGTG	GCATAAAAT	GTAGTCAGTT	4920
	TTCTCTTTTA	CCAGTTTFTA	TTTCCACTCC	AATTAATTAG	AACITTTATT	GTACATGTGC	4980
	AGAAGAATAA	GGCAGCTGAG	AATCTTGTTC	CCCCAAGAG	AGTTTTCAG	GCTGAGTGT	5040
	GCAAAATGTG	TCTTTGTCTT	GTTATATGTA	TATCAGGAAT	ACAAGGATGT	GAAATAAAAC	5100
75	TGTAATTTTG	CATAACTGGA	TGTACTTAGA	TAATGTGAAA	TAAACATTAA	AGACAAGGTC	5160
	TATTTTTAAT	AAAAAANA	AAAA				5185

Seq ID NO: C55 DNA Sequence  
Nucleic Acid Accession #: NM\_024574.2  
Coding sequence: 424..2130

1	11	21	31	41	51	
AGTGGGACTA	GCGGCGGCGG	GCGAAGCCCG	CGCCAGCCCC	GCGGGTCCGT	GCGGCATCCT	60
CCCGCCGCC	AGCCCCGCA	CGCTCCCTGC	AGTTTAAAG	GACCTCCCGC	CGCTTCTCGG	120

	CGCTGCCCCG	GGATTCCCCA	GCCCCGCGCG	GCTCCCTACT	CCACTTCGCA	GCAACTTCGG	180
	CGACCGCGCG	CCGCCCCGCC	TCGCCCCGCT	TTGAAGTTTG	CTGTGCCGAC	CGCAAAGTTG	240
	GGACACTTCA	GCGGATTGAA	TTTTCTCTTT	TTATCTGCCT	CCGTCCCCGC	CCTCCAGGCT	300
5	TCCTGTTCTC	GGATATTGGT	GCITTAGCATC	TTGGCAGGGT	CCGCGGACGT	GGACTATTTT	360
	GCACACCACA	CCACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAC	AGATCTTTTT	420
	AAGGATGGTG	CTGCTCCACT	GGTGCCTGCT	GTGGCTCCTG	TTTCCACTCA	GCTCAAGGAC	480
	CCAGAAATTA	CCCACCCGGG	ATGAGGAAC	TTTTCAGATG	CAGATCCGGG	ACAAAGGCATT	540
	TTTTCATGAT	TCGTCAGTAA	TTCCAGATGG	AGCTGAAATT	AGCAGTTATC	TCTTTAGAGA	600
10	TACACCTAAA	AGGTATTTC	TTGTGTTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
	GAGCCCTGT	GATGCGCCTT	TGGAGTGGAA	GCTGAGCCTC	CAGGAGCTGC	CAGAGGACAG	720
	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTAA	780
	TGAGGAAGGC	ACTGAGTTAT	TCTCTACAA	AGGCAATGAT	GTTGAGTATT	TTATATCGTC	840
	TAGTTCCCA	TCCGGTTTAT	ATCAGTTGGA	TCTTCTTTCA	ACAGAGAAAG	ACACACATTT	900
15	CAAAGTATAT	GCCACCACAA	CTCCAGAATC	TGATCAGCCA	TACCTTGAGT	TACCCTATGA	960
	CCCAAGAGTA	GATGTGACCT	CATCGGGCG	CACCACGGTC	ACTTTGGCCT	GGAAACCAAG	1020
	CCCACTGCC	TCTTTGCTGA	AACAACCCAT	TCAGTACTGT	GTGGTCATCA	ACAAAGAGCA	1080
	CAATTTCAA	AGTCTCTGTG	CAGTGGAAAG	AAAACCTGAGT	GCAGATGATG	CTTTTATGAT	1140
	GGCACCGAAA	CCGCTGCTGG	ACTTCAGCCC	CTTTGACTTT	GCCCACTTTG	GATTTCTTTC	1200
20	TGATAATTC	GGTAAAGAAC	GCAGTTTCCA	GGCAAAGCCT	TCTCCAAAAC	TGGGGCGTCA	1260
	TGTCTACTCC	AGGCCCAAGG	TTGATATTCA	GAAATATCTG	ATAGGAAACA	AGAACATCTT	1320
	CACCGTCTCT	GATCTGAAAC	CCGACACGCA	GTACTACTTT	GACGTATTTG	TGGTCAACAT	1380
	CAACAGCAAC	ATGAGCACCG	CTTATGTAGG	TACCTTTGCC	AGGACCAAGG	AAGAAGCCAA	1440
	ACAGAAGACA	TCGAGCTCA	AAGATGGGAA	GATAACAGAT	GTATTTGTTA	AAAGGAAGGG	1500
25	AGCAAAGTTT	CTACGGTTTG	CTCCAGTCTC	TTCTCACCAA	AAAGTCACCT	TCTTTATTCA	1560
	CTCTTGTCTG	GATGCTGTCC	AAATCCAAAGT	GAGAAGAGAT	GGGAAACTTC	TTCTGTCTCA	1620
	GAATGTGGAA	GGCATTTCAG	AGTTTCAGCT	TAGAGGAAAA	CCTAAAGCTA	AATACCTCGT	1680
	TCGACTGAAA	GGAAACAAGA	AAGGAGCATC	TATGTTGAAA	ATTCTAGCTA	CCCAAGGCC	1740
	TACTAAGCAG	TCAITTCCTCT	CTCTTCTCTG	AGACACAAGA	ATCAAAGCCT	TTGACAAGCT	1800
30	CCGTACCTGT	TCTTCGCGCA	CCGTGGCTTG	GCTAGGCACT	CAGGAAAGGA	ACAAGTTTGT	1860
	CATCTACAAA	AAAGAAGTGG	ATGATACTA	CAATGAAGAC	CAGAAGAAAA	GAGAGCAAAA	1920
	CCAAATGTCTA	GGACACAGATA	TAAGGAAGAA	GTGAGAAAAG	GTCTCTCTGA	AATATTTC	1980
	CAGTCAAAAC	CTGCAGAAAG	CAGTGACCAC	AGAAACAATT	AAAGGTCTTC	AGCCTGGCAA	2040
	ATCTTACCTG	CTGATGTTT	ATGTCATAGG	ACATGGGGGG	CACCTGTGTA	AGTATCAGAG	2100
35	TAAGGTTGTG	AAAAC TAGAA	AGTTCTGTTA	GTTACCTTCT	TATAGAGATA	TATTATGTAG	2160
	AACTCCAGGA	GGGACATTAA	ATCACTTTAA	GTATAAACTG	ACTACTCCCA	CAGTTGAGAG	2220
	AAGTTGTGAC	CTGTACTTGT	ACTATGGAAG	GAAGGATATC	AACGTGTGTA	TATTGATGTT	2280
	TATATAAGTA	ACTCTGAAG	GAGACTTGT	CTAGCGTGCC	CCATGGTACC	TAGTGTGTGT	2340
	CTGATGCGCG	TTGTTAAGTT	AGATAGAGGG	CTTCTGAAG	GAACITGCCA	TTCTTGTCTT	2400
40	TGACCACTGC	ATGAACCTGCT	TCTAAATTAT	TTTATTACCT	AAAAATTAA	AATATGCCAT	2460
	TCATTGCACA	CACCCACAAA	TGCAAAATCAT	TCTCTCTAT	AGATGCTAGG	ATATATATAA	2520
	ATTATTATAT	GAATCTTGT	TTTAAATGTC	AGTGTCTCTA	TGATTGTAAA	CTATTAAATT	2580
	CTTTCTCTAT	TAAAGTACAG	ATCTAATCTA	AGTATTATTA	AGTTGATAGC	CCTCTAGTCA	2640
	GTTATATTGC	TATTGTAAT	TCTTGTGTGT	TGAGTAAAT	GTTTAAATAC	TATATGTATC	2700
45	TCATGTACAA	AGTTGACATA	CATTATATTC	ATGTACATAA	AATTAAGAG	ATTAGATTAT	2760
	ATACTGTTAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	2808

Seq ID NO: C56 DNA Sequence

Nucleic Acid Accession #: BC034229.1

Coding sequence: 373..1422

50							
	1	11	21	31	41	51	
55	ATCCGGCGGT	GGTGACGCGA	GAGGCTGGGG	TCCTCAGGAC	CAACTCCTCT	TCATCTTCGT	60
	CTTCTCAGC	CTGCTCAATG	TGAAGCCCTT	GATCATGATT	CACCTTCCAT	TAATAAATAA	120
	AGTGTTTTCA	AATCAGAAATA	ACTTTTAGAC	AATATTAAAG	TGGTAATCAT	GAACAGAAAA	180
	GATTTTGTAG	TTCTTCCATG	GGGAAACCTT	GGAAATCTGT	TAAAGCTAAA	ATATAGCAAT	240
	GAATAATTA	AAACAAAAGT	CTAAGATTG	AAGAGATAAT	TTGCTTCAGG	ATTTTGATGG	300
60	AAGGCAATG	CTAAGTTTAA	AAACCAGATT	TCGGAGAAGT	ACAAAAGAAA	TAGAAATGCT	360
	CAAGAAGTGC	GAATGGAGAA	AGTACAGTTA	GAGTTTGAGA	ACCAAGAGAT	GGAGAGAGAA	420
	CTGCAAGAA	TCCGATCCAC	AAGAAACAAA	GAAAAGGAAG	ATAGAGAGTG	AAGCGAGTAT	480
	TACTGGAAT	CTGGAAGAGT	GGGCAAAATG	GTCAATCAAT	CATATATGAT	GTCAACAAAT	540
	AAAGGAAAT	TTGTTAAGTT	TTCTGCTGGA	AAAGTGAAAT	TAAAATTGCT	GAAGGAACAG	600
65	ATTCAAGAGC	CAGTGAAACC	AACAGTTAAT	TATAAAATGG	CAAAATCTTC	AGAATGTGAA	660
	AAACCAAGAA	TAAATGGGAA	AGTTTGTGGA	CAGTGTGAGA	ACAAAGCTGC	TCTACTGGTA	720
	TGCCTTGAAT	GTGGAGAAGA	TTATTGTTCA	GGATGCTTTG	CTAATGTTCA	CCAGAAAGGG	780
	GCACTAAAGC	TCCACAGAAC	AACTCTTTTG	CAGGCAAGAT	CTCAATATTT	ATTCAATGTA	840
	TTGGATGTTG	CCCATCAGTT	TATAAAGGAT	GTTAATCCAG	ATGAACCCAA	AGAGGAGAA	900
70	AATTCTACAA	AGGAAACCCG	TAAAATTCRA	CATAAACCCA	AATCTGTACT	TCTCCAGAGG	960
	AGCAGCTCTG	AGGTAGAAAT	TACAACGATG	AAAAGAGCAC	AACGTACAAA	ACCAAGAAAG	1020
	AGTCTGTTTG	GTGAAGGGTC	ATTGATGAAA	GAAAGCTTCT	CACAGTCTTT	TCAGGAAGTG	1080
	TTAAGTCAAT	GGAGAACCGG	AAATCATGAT	GACAACAAGA	AACAGAAATT	ACATGCAGCA	1140
	GTAAGAAGCT	CATTGGAAGA	ATGCGAAGTA	CAGACTAATC	TGAAAATTTG	GAGAGAACCA	1200
75	CTTAATATTG	AACTTAAAGA	AGACATTCTA	TCCTATATGG	AAAAATTATG	GCTTAAAAAA	1260
	CACAGGAGAA	CTCCACAAGA	GCAACTTTTT	AAATGCTACC	AGATACGTTT	CCACATCCAC	1320
	ATGAACACAC	TGGTGGATCA	CAGTGTCTCT	AAATGAAAAA	CGATGAAGAT	AGTGATGGTG	1380
	AGGAGACCAA	AGTACAAAC	ACAGCTCTTT	TATTGCCAGT	AGAAACATTA	AACATAGAGA	1440
	GACCTGAAC	ATCTCTGAAG	ATAGTGAAC	TGGATGATAC	TTATGAAGAG	GAATTTGAAG	1500
80	AAGCAGAAAA	TATTGTGCCT	TACAAAGTTA	AATTAGCTGA	TGCAGACAGT	CAACGAAGTT	1560
	GTGCTTTCTG	TGATTGTGAG	AAGAATAGCT	TTCCATATGA	AAATGGGATC	CATCAACATC	1620
	ATGTTTTCTG	TAAAGGGAAG	AGAGACTTCT	TAAATCTTTG	TCTGAGAAAC	AGCTCTACTT	1680
	ATTATAAAGA	TAAATCAAAA	GGAGAAACTT	CAAAACAGAA	TTTTGACAAC	ATCGTGGATC	1740
	CTGATGTGTA	TTCTTCTGAC	ATTGAAAAAA	TTGAGGAAAG	CACCTCCTTT	GAAAGAAATT	1800
	TAAAGGAGAA	AAATATAGTT	TTAGAAAGTA	ATCAAAAGTC	TGATGATTCC	TGTGTATCAC	1860

5  
10  
15

```

TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCAT T GAGGAGAAAT 1920
TATCTCAAGA CATCAAGAA TCCTTGGAA T TGAGCAATCT GTATAAGAGG CCAAGCTTTG 1980
AAGAATCAAA AACTACAAAG TCATCACTGT TGTACAAAGA AATAGCCTGC AGAAGTAAGC 2040
CTATAACAAA ACATATATCA GGACTTGAGA GATTCTTTAT TTTTGATACA AATGAAAGAC 2100
TCAACTTACT TCCTTCTCAT CGTTTAGAAT GCAACAATTC CAGTACTAGG ATTCACTTG 2160
CAGGTGAGAA ATCAGACAGA CCTTCAACAG CAAATTTTCC ACTTTCCAAC TCTGTTAAAG 2220
AAAGCTCCAG TTGCTTTTCA TCCTCTCATC CTCGATCAAG AAGTGCAGCT GCTCAATCAT 2280
CATCTAGAGC TGCTTCTGAA ATTTAGAAA TTGAATATAT TGATATTACT GACCAGAAATG 2340
AGCTTTCTCT AGATGACACT ACTGATCAAC ATACTTTAGA CAATTTGGAA AAAGAATTAC 2400
AAGTGTCTGAG ATCTCTTGCA GATACTTCAG AAAAGCTTTA CAGCTTAAAC TCAGAAGAGT 2460
TCCCGATTAT CAGCAGCCAA TCACTGAATA TAAGTCAGAT TTCCACAGAT TTCCTTAAGA 2520
CCTCAGATGT GAGGGGTCCT TGTGGAGTTG AGGAATTGAG CTGTTCTGGA AGAGATACCA 2580
AAATTGAGTC TTTGCTGTCA CTTTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC 2640
TCAACAGCA ACATGTCATC AACTACCGT GGTCAAAGAG TACTTAAAGA TTATTGTTC 2700
ATTACTGTTT CCATTTTGTA CCCAGAGTAA AGCAAAACAG TGAGAAAAGT AACCAAGTGA 2760
TTACTATCC AAGTGTCTGA GATTTTGATT ACTAATGTCT TTGATGTTT AAGGCTACAA 2820
ACTAATAAAA GTAAATTAT AAGTTCAAAA AAATTTTAA AAAAAAAAT AAAAAA 2876

```

20 Seq ID NO: C57 DNA Sequence  
Nucleic Acid Accession #: NM\_024687.1  
Coding sequence: 138..1706

25  
30  
35  
40  
45  
50  
55

```

1 11 21 31 41 51
| | | | |
AAAAACATGA TGACAACAAG AAACAGAATT TACATGCAGC AGTAAAAGAC TCATTGGAAG 60
AATGCGAAGT ACAGACTAAT CTGAAAATTT GGAGAGAACCT ACTTAATATT GAACCTTAAAG 120
AAGACATTTCT ATCCTATATG GAAAAATTAT GGCTTAAAAA ACACAGGAGA ACTCCACAAG 180
AGCAACTTTT TAAATGCTA TCAGATACGT TCCACATCC ACATGAAACC ACTGGTGATG 240
CACAGTGTTC TCAAAATGAA AACGATGAAG ATAGTGATGG TGAGGAGACC AAAGTACAAC 300
ACACAGCTCT TTTATTGCCA GTAGAAACAT TAAACATAGA GAGACCTGAA CCATCTCTGA 360
AGATAGTCCA ACTGGATGAT ACTTATGAAG AGGAATTTGA AGAAGCAGAA AATATTGTGC 420
CTTACAAAGT TAAATTAGCT GATGCAGACA GTCAACGAAG TTGTGCTTTT CATGATTGTC 480
AGAAGATAG CTTTCCATAT GAAAATGGCA TCCATCAACA TCATGTTTTC GATAAGGGAA 540
AGAGAGACTT CTTAAATCTT TGTCTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA 600
AAGGAGAAAC TTCAAACACA GATTTTGACA ACATCGTGGG TCCTGATGTG TATTCTTCTG 660
ACATTGAAAA AATTGAGGAA AGCACCTCCT TTGAAAGAAA TTTAAAGGAG AAAAATATAG 720
GTTTAGAAG ATGCAAAAGT TCTGATGATT CCTGTGTATC ACTTGAAGGC AAGGACACTT 780
TGCTAGGTAG AGATTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAAG 840
AATCCTTGA ATTGAGCAAT CTGTATAAGA GGCCAAGCTT TGAAGAATCA AAAACTACAA 900
AGTCATCACT GTTGTACAA GAAATAGCCT GCAGAAGTAA GCCTATAACA AAACAATATC 960
AAGGACTTGA GAGATTCTTT ATTTTGTATA CAATGAAAG ACTCAACTTA CTCTCTCTC 1020
ATCGTTTAGA ATGCAACAAT TCCAGTACTA GGATTACACT TGCAGAAGAC AGAGAATGGA 1080
TTCCAGACCA TAGCTTAAGT GAAATGCTG ATAATGCAAT TGTCTTGGGT GTTCTGCAGG 1140
GTGCTCAGAG TCCATCATCA AGTAGAAAAC AGCAAAAGAT GGGTCAGAAA TCACAGAGAC 1200
CTTCAACAGC AAATTTTCCA CTTTCCAACCT CTGTTAAAGA AAGCTCCAGT TGCCTTTTCT 1260
CCTCTCATCC TCGATCAAGA AGTGCAGCTG CTCAATCATC ATCTAGAGCT GCTTCTGAAA 1320
TTTCAGAAAT TGAATATATT GATATTACTG ACCAGAATGA GCTTTCCTTA GATGACACTA 1380
CTGATCAACA TACTTTAGAC AATTTGGAAG AAGAATTACA AGTGTGAGA TCTCTTGCA 1440
ATACTTCAGA AAAGCTTTAC AGCTTAACCT CAGAAGAGTT CCCAGATTTC AGCAGCCAT 1500
CACTGAATAT AAGTCAGATT TCCACAGATT TCCTTAAGAC CTCACATGTG AGGGGTCCCT 1560
GTGGAGTTGA GGAATTGAGC TGTCTCGAA GAGATACCAA AATTCAGTCT TTGCTGTAC 1620
TTTCTGAGAG CAGTACAGAT GAGGAGGAGG AAGATTTTCT CAACAAGCAA CATGTCATCA 1680
CACTACCGTG GTCAAGAGAT ACTTAAAGAT TATTGTGTCA TTACTGTTTC CATTTGTAC 1740
CCAGAGTAAA GCAAAACACT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGTGGAG 1800
ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAG TAAATATATA 1860
AGTTCAAAAA AAAAAA AAAA 1884

```

60 Seq ID NO: C58 DNA Sequence  
Nucleic Acid Accession #: NM\_005408.1  
Coding sequence: 76..372

65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
AAAAGGCGCG CGGAACAGCC AGAGGAGCAG AGAGGCAAG AAACATTGTG AAATCTCCAA 60
CTCTTAACCT TCAACATGAA AGTCTCTGCA GTGCTTCTGT GCCTGCTGCT CATGACAGCA 120
GCTTTCAACC CCCAGGACT TGCTCAGCCA GATGCATCA AGTCCCATC TACTTGCTGC 180
TTCACATTTA GCAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC 240
AGCAGGTGTC CCCAGAAGGC TGTCTCTTC AGAACCACAC TGGGCAAGGA GATCTGTGCT 300
GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCCGGA AGCTCACACC 360
CTGAAGACTT GAATCTGCT ACCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420
TCCATTCTCC TCTGGCTCC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480
AGGATGCATT CGGTTTGTG ATTCAAAATG TACTATGTGT TAAGTAATAT TGGCTATTAT 540
TTGACTGTGT GCTGGTTTG AGTTTATTG AGTATTGCTG ATCTTTCTA AAGCAAGGCC 600
TTGAGCAAGT AGGTTGCTGT CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660
GGGTTGTAT TCGGTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG 720
GATGCTGCAA TGTAAGGAGG AGAGCTCTTT GTGAATGTGA GGTGTGCTA AATATGTTAT 780
TGTGAAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATTT 840
AAAATCTCCA AAAAAA 860

```

Seq ID NO: C59 DNA Sequence  
Nucleic Acid Accession #: AK097746.1  
Coding sequence: 185..2224

1 11 21 31 41 51  
5 CTTTCATGAC AGTAACAAAT CCAAGATTTT GGAAAAGCGC CTACGATATT TAAATGACCA 60  
CTTCACATAC AACTTATATT GTAATATATG CCGATCACTA TTTGAGAAGG ACAAGCTGTT 120  
ATTTTCCTTT TTATTATGTG CCAATCTTCT TCTGGCAAGG AAAGAGATTG AATACCAAGG 180  
ACTGATGTTT CTTTAACTG GAGGAGTAAG TCTTAAAGT GCTGAGAAA ATCTGATCC 240  
AACTTGGCTA CAGGACAAAA GCTGGGAGGA AATCTGTGG GCAAGTGAAT TTCCTGCCTT 300  
CAGAGGACTC AGSCAACATT TTTGTGAACA TATATATGAA TGGCGAGAAA TCTATGACAG 360  
TAAAGAGCCA CATATGCTA AATTTCCAGC ACCAATGGAT AAGAACCTAA ATGAACCTACA 420  
GAAAATAATA ATTCTTCGGT GTTAAAGACC TGATAAGATA ACCCCAGCTA TAACAACTA 480  
TGTAACCTGAC AAACAGGGA AAAAGTTTGT AGAGCCTCCA CCATTTGATT TGACAAAGAG 540  
TTACTTGGAT TCAATTGCA CCATTCCTTT AATTTTGTG CTATCTCCAG GAGCAGATCC 600  
TATGGCCAGC CTGCTGAAAT TTGCAAAATG TAAATCTATG TCTGGAATA AGTTTCAAGC 660  
TATTTCACTG GAGCAGGAGC AAGGACCGAT TGCAGCAAAA ATGATTAAG CAGCAATTGA 720  
AGAAGGAATC TGGGTGTGCC TACAGAAATT CCATCTTGCA GTGTCTGGA GCCCATGTT 780  
GGAAAAATA TGTGAAGATT TTACCTCTGA AACCTGTAAC TCATCTTTA GGCTTTGGCT 840  
GACAAGCTAT CCATCTTCAA AATTCCTAGT AACAACTCTA CAGAATGGAG TAAAAATGAC 900  
TAATGAACCT CCCACGGGTC TTGGGCTGAA TCTCCTTCAA TCATATCTCA CTGATCCAGT 960  
TTCGTATCCT GAGTTTTTCA AGGGATGCCG TGGAAAAGGAA CTGTTATTTA TCAATGAATA 1020  
TGATACAATT CCATTTGAAG CTATATCTTA CCGTACTGGG GAGTGTAAAT ATGGAGGAAG 1080  
AGTGACAGAC GATTGGGACA GAGCTCTTCT ATTAACCATG CTGGCTGACT TTTATAATCT 1140  
GTACATAGTT GAAAACCTC ATTATAAGTT TTTCCCTAGT GGAACTATT TTGCACTTCC 1200  
TAAAGGCACT TATGAGGACT ACATTGAATT CATTAAGAAA CTTCCTTTA CTCACACCCC 1260  
TGAGATATTT GGATTACATG AAAACGTTGA CATCTCCAAG GATCTTCAAC AAACAAAAAC 1320  
CCTCTTTGAG TCGTGTGCTC TCACCCAGGG AGGCTTCAAA CAGACAGGAG CCTCAGGAAG 1380  
TACTGATCAG ATTCTGTTAG AAATTACCAA AGATATCCTC AACAGCTCC CTAGTGATT 1440  
CGACATTGAA ATGGCACTAC GGAAGTATCC TGTGAGATAT GAAGAAAGCA TGAATACTGT 1500  
GTTAGTACAA GAAATGGAAA GATTAAACAA TTTAATTATA ACTATACGTA ACACCTACG 1560  
GGACCTTGAA AAAGCTATTA AGGGTGTGGT TGTGATGGAT TCTGCTATGG AGGCACTCTC 1620  
CAGTAGCTTA CTGTTTGGAA AGGTTCCAGA AATATGGGCC AAACGTTTAT ACCCAAGCT 1680  
TAAGCCCTTG GGAAGTTACA TCACAGATTT CTTAGCCCGG TTGAACCTTT TACAGGACTG 1740  
GTATAATTCA GGAACCTTT GTGTGTTTTG GCTGTCAAGT TTTCTTTTCA CTCAGGCTTT 1800  
TTTAACTGGA GCTATGCAGA ATTATGCCAG AAAATATACC ACCCTATTG ATTTGCTAGG 1860  
ATATGAATTT GAGGTATATC CATCTGATAC ATCTGACACA TCACCAGAAG ATGGTGTFTA 1920  
TATCCACGGA CTGTATCTCG ATGGCGCACG CTGGGACCGA GAAAGTGGAT TGCTTGCTGA 1980  
ACAATATCCC AAATCTCTGT TTGACCTGAT GCCCATATA TGGATAAAAC CAACTCAAAA 2040  
ATCTCGGATT ATAAAGTCGG ATGCCATATG CTGTCCCCTC TACAAGACAA GTGAACGTAA 2100  
AGGAACCTTT TCACTACGG GACATTTCTAC TAACTTTGTC ATTGCAATGT TGTAAAAAC 2160  
AGACCACTCT ACTCGGCACT GGATCAAGCG CGGGGTGCTT TTGCTTTGTC AGTTGGATGA 2220  
CTAAATTGGA CAAATTATA AAACATCCAA AAGTTT 2256

Seq ID NO: C60 DNA Sequence  
Nucleic Acid Accession #: J02761.1  
Coding sequence: 14..1159

1 11 21 31 41 51  
50 GAATTCGGGT GCCATGGCTG AGTCACACCT GCTGCAGTGG CTGTGCTGTC TGCTGCCAC 60  
GCTCTGTGGC CCAGGCACTG CTGCTGAGC CACCTCATCC TTGGCCTGTG CCCAGGGCCC 120  
TGAGTTCTGG TGCCAAAGCC TGGAGCAAGC ATTGCAGTGC AGAGCCCTAG GGCATTGCCT 180  
ACAGGAAGTC TGGGACATG TGGGAGCCGA TGACCTATGC CAAGAGTGTG AGGACATCGT 240  
CCACATCCTT AACAGATGG CCAAGGAGGC CATTTTCCAG GACACGATGA GGAAGTTCTT 300  
GGAGCAGGAG TGCAACGTCC TCCCTTGAA GCTGCTCATG CCCAGTGCA ACCAAGTGCT 360  
TGACGACTAC TTCCCTCTGG TCATCGACTA CTTCAGAAC CAGACTGACT CAACCGGCAT 420  
CTGTATGCAC CTGGGCTGTG GCAAACTCCG GCAGCCAGAG CCAGAGCAGG AGCCAGGGAT 480  
GTACAGCCCC CTGCCAAAC CTCTGCGGGA CCTCTGCCA GACCTCTGC TGGACAGCT 540  
CGTCTCCCT GTCTGCCCCG GGGCCCTCCA GGGAGGCTT GGGCTTACA CACAGGATCT 600  
CTCCGAGCAG CAATTCCTCA TTCTCTCCC CTATTGCTGG CTCTGCAGG CTCTGATCAA 660  
GGGATCCAA GCCATGATTC CCAAGGCTGC GCTAGCTGTG CAGTGGGCC AGGTGTGCCG 720  
CGTGTACTCT CTGGTGGGCG GCGCATCTG CCAGTGCTGG GCTGAGGCT ACTCCGTCAT 780  
CCTGCTCGAG AGCTGTCTGG GCGCATGCT GCCCAGCTG GTCTGCCGCT TCGTCTCCG 840  
GTGCTCCATG GATGACAGCG CTGGCCCAAG GTGCGGACA GGAGAATGGC TGCGCGAGA 900  
CTCTGAGTGC CACCTCTGCA TGTCCGTGAC CACCCAGGCC GGGAACAGCA GCGAGCAGG 960  
CATACACAG GCAATGTCTC AGGCTGTGTG TGGCTCTGG CTGACAGGG AAAAGTGCAA 1020  
GCAATTTGGT GAGCAGACA CGCCCCAGCT GCTGACCTG GTGCCAGGG GCTGGGATGC 1080  
CCACACCACT TGCCAGGCC TGGGGTGTG TGGGACCATG TCCAGCCCTC TCCAGTGTAT 1140  
CCACAGCCCC GACCTTTGAT GAGAATCTAG CTGTCCAGCT GCAAGGAAA AGCCAAGTGA 1200  
GACGGGCTCT GGGACCATGG TGACCAAGCT CTTCCCTGCT TCCCTGGCCC TCGCCAGCTG 1260  
CCAGGCTGAA AAGAAGCCTC AGCTCCACA CCGCCCTCT CACCTCCCTT CCTCGGCAGT 1320  
CACTTCCACT GGTGGACAC GGGCCCCAG CCGTGTGCG GCCTTGTCTG TCTCAGTCA 1380  
ACCACAGTCT GACACAGAG CCCACTTCCA TCCTCTCTGG TGTGAGGCAC AGCGAGGGCA 1440  
GCATCTGGAG GAGCTCTGCA GCTTCCACAC CTACCAAGAC CTCACAGGGC TGGGCTCAGG 1500  
AAAAACCAAG CACTGCTTTA CAGGACAGGG GGTGAAGCT GAGCCCCGCC TCACCCAC 1560  
CCCCATGCAC TCAAGATTG GTTTTACAG CTACTTGCAA TTCAAAATTC AGAAGAATAA 1620  
AAAAATGGAA CATACAGAAC TCTAAAAGAT AGACATCAGA AATTGTTAAG TTAAGCTTTT 1680  
TCAAAAAATC AGCAATTTCC CAGCGTAGTC AAGGGTGGAC ACTGCAGCT CTGGCATGAT 1740  
GGGATGGCGA CCGGGCAAGC TTTCTTCTC GAGATGCTCT GCTGCTTGG AGCTATTGCT 1800  
TTGTTAAGAT ATAAAAAGGG GTTCTTTTT GTCTTCTGT AAGGTGGACT TCCAGATTTT 1860  
GATTGAAGT CCTAGGGTGA TTCTATTCT GCTGTGATT ATCTGCTGAA AGCTCAGCTG 1920  
GGGTGTGCA AGCTAGGGAC CCATCTCTGT GTAATACAA GTCTGCACCA ATGCTAATAA 1980  
AGTCTTATTC TCTTTTAAAA AAAAAAAGG GAATTC 2026

Seq ID NO: C61 DNA Sequence



Nucleic Acid Accession #: NM\_139172.1  
Coding sequence: 19..552

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGGGCTCTGGG GAGGTGACAT GTTGGGCTGT GGGATCCCAG CGCTGGGCGT GCTCCTGTCTG 60
      CTGACAGGCT CGGCAGACGG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG 120
      GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180
10     TGCCCTGCGTC TCGGTGCTG CTACCGCAAT GGGGTCTGCT ACCACCACGG TCCAGACGAA 240
      AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGACGT GCAGCGGCTT CCTCTCTCTG 300
      AGCTGCGCA TCTGCTTGT CTGGTGGGCC AAGCGCCGGG ACGTGTCTGA TATGCCCGGT 360
      TTCTTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCA GCACCGAGGG 420
      ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCACTCGCCC TGTCCTAAGA GTCCAGGGAT 480
      GTGGAGGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA 540
15     GAGGAGGATT AGGGGAGTCC CCGGGGGACT GCTCAATACA GATACGGTGG ACG 593

```

Seq ID NO: C62 DNA Sequence  
Nucleic Acid Accession #: NM\_054023.2  
Coding sequence: 98..379

```

20     1      11      21      31      41      51
      |      |      |      |      |      |
      GGGGACACTT TGTATGGCAA GTGGAACCAC TGGCTTGGTG GATTTTGCTA GATTTTCTG 60
      ATTTTAAAC TCCTGAAAAA TATCCCAGAT AACTGTCAAT AAGCTGGTAA CTATCTTCCT 120
      GCTGGTGACC ATCAGCCTTT GTAGTTACTT TGCTACTGCC TTCTCATCA ACAAAGTGCC 180
      CCTTCTGTT GACAGATTGG CACCTTTACC TCTGGACAAC ATTCTTCCTT TATGGATCC 240
      ATTAAAGCTT CTCTGAAAAA CTCTGGGCAT TTCTGTGAG CACCTTGGG AGGGGCTAAG 300
      GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAAC TGCTGGAGGC 360
      GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGAAGATGA 420
      TGCTCTATTC CTCCCTGCTT GAAACCTGTT CTACCAATTA TAGATCAAT GCCCTAAAT 480
      GTAGTGACCC GTGAAAAGGA CAAATAAAGC AATGAATACT AAAAAAAAAA AAAAAAAAAA 540
      AAAAAAAAAA 550

```

Seq ID NO: C63 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2874

```

35     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCCTGT CCTATGCCTA TAAAAACGCT GAGACCCCTAG CAGGCAGACA CACAAGCAGC 60
      TGGATGTGGA GAGGAGCATA TCAGCGGAGG AACACACGGG CAGCTGGAGC TCCAGAGGAA 120
      TGCACTGACA GAAACTGGCA TGCTGGCAGA ACAGGTGGAA TTGGCTGGG GCAGTTGGAG 180
      GAGAGATGTT CAGATGTGTT CGGAGTTTCT TTCTTCTGTT GGGTTCGTGG TCTCGCTGGC 240
      TCAGGAGCGA AGCTGCAGAC CTTCAACGCC GCCCAGGAAG GGGCTCCAC AGTGACGCGG 300
      CAGGCTGAAG CGCTCTCAA GTGCCGCCAG AGTGGCGCTC CAGGCAGAGG AGGCGCCGAG 360
      AGCAGGCGAG CGAGGATGCG CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC 420
      CCAACGTCTT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACCGAAAT TGCTCACAAG 480
      AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCCCTCCTT 540
      GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTAC CATTCTTGT GACTCATTG 600
      TACTTTCTGG GGGTGTGAC CACTGGGATG GAACAACAG ATTTTGAAAC AGGACCAAC 660
      ATATTTGATT TGCAAGTTTA TGTGAAGGAT GAGGTTGGTG TCACAGACCT GCAAGTCTG 720
      ACTGTCCAGG TAAACAGATG GAAACGAGCA CCTCAGTTTC AAGGCAACTT GGCAGAAGAT 780
      CATCTCGGTG CAGACCAGCC ACATTTCAAT GCTCATAGTC ACACGTACGT GAGGGTAGTG 840
      GCTACTGCAT TGGCCAGGCA CAGGCTTAGA TCTAGCATTG GTTCCCTCTT CCTGGGCACC 900
      TTCTGTGTG TGGTGGGCGT CAGATATTTT CTGATTTCTC CCCCAGAGAG CTTTCAAGAT 960
      TCTGCTAATG GCACCTCTT TCCACAACA GAATGGAGT TTGAAGCAG ACACAGAAGT 1020
      TTCCATCTCA TGTGGGAGGT GAGGACAGT GGAGGCTCA AAGCTCCAC AGAGCTCCAG 1080
      GTGAACATCG TGAACCTCAA CGACGAAGTC CCTGCTTTA CCAGCCCGAC ACGAGTGTAC 1140
      ACAGTCTCTG AGGAACTGAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1200
      GATGATGAAG GTTTTCCAG CCACCTCTCT TACAGCATTA CCACTGTTAG CAAATATTT 1260
      ATGATAATC AGTTGACTGG TACAATCCAA GTGGCCCAAA GGATAGACCG AGATGCAGGT 1320
      GAATTTAGAC AAAATCCCAT CATTTCCCTG GAAGTTCTAG TGAAGGACAG ACCATATGGG 1380
      GGTACGAGGA ATCGCATCCA GATAACCTTC ATGTGGAAG ACGTCAACGA CAATCCTGCC 1440
      ACATGCCAAA AGTTCACTT CAGATCCAGT CTCACCCCTG CTCTGTGCTC CAAGACGCTG 1500
      ACCTGGATGG ATACCGTATT AGACTGTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1560
      GGGCGATTTA CAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1620
      CTCACAATCA TGGCAGAAGG CAAGGAGGAG CAAGTCACAT CTTACATGGA TGGCAGCAGG 1680
      CAAAGAGATA GAGCTTGTGT AGGGAACCTC CTCCTTATAA AGCCATCAGA TCTCATGAGA 1740
      CTTAGTCACT ATCAGGAGAA CAACTCAGGA AAGACTTGCC CCCATGATTC CATTCTCTCC 1800
      TACCAAGTCC CTCCCAACAC ATGTAGGAAT TCAAGAATCC AGGCCACCAA CAAGGAAGAC 1860
      ACAAGCTCTG TCACTGTGAC TGTGAACATC CTTGAAGAAA ATGATGAAAA GCCAATTTGT 1920
      ACTCCAAACT CTTATTTCTT GGCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATTCTAG 1980
      AATTTCAAGC TGACATGTAC CGACCTTGAT TCCAGCCCA GATCTTTCCG TTATTCCATT 2040
      GGCCAGGTA ACGTCAACAA TCATTTACCC TTCTCTCCCA ATGCTGGTTC CAATGTACA 2100
      CGCTGCTGCT TTACATCTCG CTTTGACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC 2160
      AAGCTACTTG TCTAGCTAAC TGATGACAA TGTAGTCTG ACAGGAAGAA AGCGAGGCT 2220
      CTGTTGAGA CAGGAACAGT GACTGAGT ATTAAGTCA TTCCCAACC AACCACTATC 2280
      ATCACCAGCA CCCCCAGGCC CAGGTCACC TATCAGTCC TGAGGAAGAA CGTTTACTCT 2340
      CCATCTGCAT GGTACGTGCC GTTTGTATC ACTTTGGGCT CCATATTGCT TCTGGGTCTC 2400
      CTCGTGTACC TGGTCTGCTT ATTGGCCAA GCCATCCACA GACTGCCC CTGCAAGACT 2460
      GGGAGAACA AGGAACCTCT GACAAAGAAA GGAGAAACGA AGACTGCAGA GAGAGACGTC 2520
      GTGGTGGAAA CTATCCAGAT GAACACTATC TTGATGGAG AAGCCATAGA TCCAGAGCCT 2580
      GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCAGCT GCTGGACCC TAGTCCAGTA 2640
      ACCCTAAGAA AGGTCCAGGT GTGTGGGAG AGTGAAGAGA COGTCAGTG TTCCGGCCAC 2700

```

ATCACACTTC CCGGCAAGAT TCCAGTCGAT GACCCAAGGA AACAGGAAAC AGGCCTGCAG 2760  
 GGTGATTTCG AGGTCTGGAC TCTATGCCCC GCTGTGAAGG TGGTTGTAGG CAGCCCTCAA 2820  
 GCTGAACGGT GCATTGCAATT GGTCTCAGT CTGAAAAAGT ACAGTTCTGA TTAA 2874

5 Seq ID NO: C64 DNA Sequence  
 Nucleic Acid Accession #: XM\_168571.1  
 Coding sequence: 155..988

10 1 11 21 31 41 51  
 TACACAGTCC TGGAGGAACT GAGTCCAGGA ACCATCGTGG CCAATATCAC AGCGGAGGAT 60  
 CCTGATGATG AAGGTTTTTC CAGCCACCTC CTCTACAGCA TTACCACTGT TAGCAAAATAT 120  
 TTCATGATAA ATCAGTTGAC TGGTACAATC CAAGTGGCCC AAAGGATAGA CCGAGATGCA 180  
 15 GGTGAATTGA GACAAAATCC CACCAATTCC CTGGAAGTTC TAGTGAAGGA CAGACCATAT 240  
 GGGGGTCAGG AGAATCGCAT CCAGATAACC TTCATTGTGG AAGACGTCAA CGACAATCCT 300  
 GCCACATGTC AAAAGTTTCA CTTCAGCATT ATGGTGCCGG AAAGAACAGC CAAGGGGAOC 360  
 TTGCTTCTTG ACCTAAACAA GTTCTGCTTT GATGATGACA GTGAGGCACC AAACAACAGA 420  
 TTCAACTTCA CCATGCCATC TGGAGTGGGG AGCGGCAGCA GATTTTACA GGATCCAGCT 480  
 20 GGCTCTGGGA AGATTGTGCT GATTGGTGAT CTAGACTACG AAAATCCAAG TAACCTAGCA 540  
 GCGGGCAATA AATATACGGT GATAATCCAG GTGCAGGATG TGGCCCCCCC TFACTATAAA 600  
 AATAAGCTCT ACGTTTATAT CCTAACAGC CCAGAAAATG AGTTTCTCT CATTTTGTAT 660  
 AGGCCATCCT ATGTATTGGA TGTGTGAGAA AGAAGGCCCG CCCAGGGTCA CCTATCAGT 720  
 CCTGAGGAAA AAGCTTTACT CTCCATCTGC ATGGTACGTG CCGTTTGTCA TCACTTTGGG 780  
 25 CTCCATATTG CTCTGGGTC TCCTCGTGTG CCTGGTCTGC CTATTGGCCA AAGCCATCCA 840  
 CAGACACTGC CCCTGCAAGA CTGGGAAGAA CAAGGAACCT CTGACAAAGA AAGGAGAAAC 900  
 GAAGACTGCA GAGAGAGAGC TCGTGGTGGG AACTATCCAG ATGAACACTA TCTTTGATGG 960  
 AGAAGCCATA GATCCAGTGA CCGGGGAAAC ATATGAATTC AACTCAAAA CTGGAGCCAG 1020  
 AAGTGGAAA GATCCACTAA CCCAAATGCC AAAATGGAAA GAGTCCAGCC ACCAGGGAGC 1080  
 30 TGCCCCACGC AGAGTCACTG CTGGGAAGG GATGGGGTCA CTGAGAAGTG CCAACTGGGA 1140  
 AGAAGATGAG CTGAGTGGCA AAGGTGGGG TGAGGATGCT GGTCTGGGTT CCAGAAATGA 1200  
 GGGTGGCAAG CTGGGCAACC CAAAGAACAG AAATCCAGCC TTCATGAACA GGGCTTACCC 1260  
 CAACACACAC CCAGGAAAGT AAACGGGGTC TAAGGAGGGG CCTGTCAATC ACTGAGATGC 1320  
 TGCTCAACC TAAATCTCAT GGGGATGGTG TGGCATGTG GTAGGGGGA AAATGTGGGC 1380  
 35 TGAGGGGATT CAGACATCCA GGGTCAACA TGGGATGTTT GACAAATTTT TAAACAATA 1440  
 GAAAGGGGTT TGATCACATA GTTGCCTGTT CTGAAATGAT ACAGGAACAT TTCTATCAG 1500  
 ATTTGAGAAC TACCTGTGCT TCTGATAAGC AAGACTGTTA ACTTTGGGTT GTGGAATTGT 1560  
 TGTGTTCTTT CTTTGCAATT ACTGCTAGGA AGCTCTATTC TGTTCACCAT AGAAAGTTTG 1620  
 TAGGAATTTT TGACATAAAT AGTGAAGACT ATCCTTACAT CTGGTTTCCA CCTATTITTC 1680  
 40 CTGCCCTCGT TTTAACATCA CCCAGATTTC TTCAGTTATA AATATGCCAT ACACCTTTGT 1740  
 AAGTCACCTC AAATCTTCTT CAAAGAAGC AGAAGCAGTA AAAAAACAGA TGAGTAAGTT 1800  
 AAGAGTTGTT CATCTGGAAG GAAGAAACT CAGTAGGCAC CTCTTTTGT TTTTCTTGT 1860  
 GGTGTCCGGA TCAGCATCCT GCATGTGAGA TTATCCACG TTGTCTGTGC TAGCAGTAGT 1920  
 TCAGTTCTCT TCATGCTTAT GTCTGGTTTC ATTCTATGAT TATATCACA TTTATCTATT 1980  
 45 CTACACTTGG GTGCGAGCTG CTTCAGATTT TTTACTTTTA AAAAAATATC TTTAAAGTGA 2040  
 ACTACAGGCA GGGCATGATG GCTCATGCTT GTAATGCCAG CACTTTGCCA AGGTGGGCAG 2100  
 ATACCTTAAG CTTAGGAGTT CAAGATCAGC CTGGCCTAGA TGGCAAAACC CTGTCTCTAC 2160  
 TAAAAAATCA AAAAATATAG TTGGTGTGGT GGTGGGCACA TGTAATCCCA GCTACTTGGG 2220  
 AGGCTAGGT AGGGAGAACT GCTTAAACCT GAGAGGTGGA GGTTACAGTG AGTTGAGATT 2280  
 50 GTGCCACTGC ACTCTAGCCT GGGTGACAAA GCAAGACTCC ATCTCAGAAA AAAAAAATAA 2340  
 AAGTGAATTA CAACACT 2357

55 Seq ID NO: C65 DNA Sequence  
 Nucleic Acid Accession #: NM\_005266.3  
 Coding sequence: 122..1198

1 11 21 31 41 51  
 GGACAGAGGC CATTTTCAA CAGTCCCTCC TGGGAGAACA CAGACAGGCA GAGGATTACA 60  
 60 ACACAAGGCA GCAGACACTG GGAGACGAAA GTTTTGGCAT CTGTTCCCTG GCTGTGCCAA 120  
 GATGGGCGAT TGGAGCTTCC TGGGAAATTT CCTGGAGGAA GTACACAAGC ACTCGACCGT 180  
 GGTAGGCAAG GTCTGGCTCA CTGTCTCTTT CATATTCGCT ATGCTGTGTC TGGGCACAGC 240  
 TGCTGAGTCT TCTTGGGGGG ATGAGCAGGC TGATTTCCGG TGTGATACGA TTCAGCCTGG 300  
 CTGCCAGAAAT GTCTGTCTAG ACCAGGCTTT CCCATCTCC CACATTCCGT ACTGGGTGCT 360  
 65 GCAGATCATC TTGCTCTCCA CGCCCTCTCT GGTGTACATG GGCCACGCCA TGCACTACTG 420  
 GGGCATGCAG GAGAAGCGCA AGCTACGGGA GGCAGAGAGG GCCAAAGAGG TCCGGGGCTC 480  
 TGGCTCTTAC GAGTACCCGG TGGCAGAGAA GGCAGAACTG TCCTGTCTGG AGGAAGGGAA 540  
 TGGAAAGGATT GCCCTCCAGG GCACTCTGCT CAACACCTAT GTGTGCAGCA TCCTGATCCG 600  
 CACCAACATG GAGGTGGGCT TCATTGTGGG CCAGTACTTC ATCTACGGAA TCTTCTGTAC 660  
 70 CACCTGCTAT GTCTGCGCA GAGTCCCTG TCCCAACCG GTCAACTGTT ACGTATCCCG 720  
 GCCCACAGAG AAGAATGTCT TCATTGTCTT TATGCTGGCT GTGGCTGCAC TGTCCCTCCT 780  
 CCTTAGCCTG GCTGAACACT ACCACCTGGG CTGGAAGAAG ATCAGACAGC GATTGTCTCA 840  
 ACCGCGGCGC CACATGGCTA AGTGCCAGCT TTCTGGCCCC TCTGTGGGCA TAGTCCAGAG 900  
 CTGCACACCA CCCCAGACT TTAATCAGTG CCTGGAGAAT GGCCTGGGG GAAATTTCTT 960  
 75 CAATCCCTTC AGCAATAATA TGGCCTCCCA ACAAACACA GACAACCTGG TCACCGAGCA 1020  
 AGTACAGGAT CAGGAGCAGA CTCTGGGGA AGGTTTCAAT CAGGTTCTGT ATGCCAGAA 1080  
 CCTGAGCTG CCAATGGAG TCTCACAGG TCACCGCCTT CCCCAGGCT ATCATAGTGA 1140  
 CAAGCGAGCT CTTAGTAAGG CCAGCAGCAA GGCAAGGTCA GATGACCTAT CAGTGTGACC 1200  
 CTCTTTATG GGAGGATCAG GACCAGGTGG GAACAAGGA GGCCTCAGGA GGAAGAGCT 1260  
 80 GTCCCTCTG AACTGATGCT TTCTCACTGT CATCACTGCT TGGCTCTTT GAGCCCGGG 1320  
 TCTCAATGAC GTTGTCTATT AATTCTAGAA ACTATAACCA GGGCTCTGG ATAGTAAGAG 1380  
 AGGTGACAA CACCCAGAG TGCAGTTCCC TCCCACCTT CTACCCAGTA TACGAAGCCT 1440  
 TTCAGATTAC TCATGAAACA GGGTAGAGGG AAAGAAGGGA AGCATGGCAA AAGCTGGCCT 1500  
 GGAAGGGATA GCCAGAGGGA TAGAATGACT CTCTCTCTAC ATACCCAGCAG CATACCAAT 1560  
 GCGTCTCTA AGTCTCTACC TCCTTGACCT GATCACCTC CCTCCTCAA GGAAGAGCTC 1620

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

AAAGTTCCCA GCCAATAGAC AGCATGAATC AAGGAACCTG CATTATATGT GCTCTTGAAT 1680  
 CTGTTGTCTC CATGGACCAT TCCTCGGAGT AGTGGTGAGA TGGCCTTGGG TTGCCCTTGG 1740  
 CTCTCTCTCC CTCTACTCAG CTTAAAAAG GGCTTCTTGG AACTTTACCA GCAGCCTCAG 1800  
 CTTTACAAAT GCCTTGGTAT GTACCTCTGG CAAATGCCCT GGTATGTACC TCTGGCAAAT 1860  
 GCCCACCTT GGTGATGTTG CAACCTTTCC TTCTGTCTAGG GTGTACACCT AGCCTGTGCA 1920  
 GGTGTACGCC CTGCTAGGGA GTCACTGTAC ACACAAATC TACTGGAATT CCTGCCAACA 1980  
 TCTGTACACC TGCAGTCTCT TTACAGTTCA ATCCAAATGAT AGAAACCATC CCTTCCCTTT 2040  
 CTCCCTTGGC TGTTACCCA GCCATTCCCT GAAGGCCCTT CCAACAGGAA TATCCAAGAA 2100  
 GCTGTTGTCC TCTCTGAAAC CCTGACCAGA TCATCAGCCA CTGAGGCCAG TGGAAATTCC 2160  
 CCAAGCCTTG TTAACAAAAA AAAAAAAAAA 2190

Seq ID NO: C66 DNA Sequence  
 Nucleic Acid Accession #: NM\_014459.2  
 Coding sequence: 738..3407

1 11 21 31 41 51  
 GTAGATGCAG TCCGCGCGCG CGCTGCCTC AGCCAGCAAT GCAAGATTAG ATCTCTAAAT 60  
 GCAGCAAAAC ACTGCTCTGA AACAGACCGG CCCGCGCAGC AAGCAGACAT TTCACGGTGC 120  
 GCTGGGGAAG CTTCAAAATA TATCTGTGAC TCTGTCTTGG TTGCTCTTCA TCCCATCAAA 180  
 TTTTCATCAG GAGGCGGAGC AGCAAGTAAG AATTTCACCT TGGATCTGCG CTAGAGACAC 240  
 ACCTCCCTGC TCCCTCCCCC ACTCGATGTG AAGAGTATTC CGGAGTCTCC GGGCGGGAGT 300  
 AGATTTGACG CACCTTAGCG GGAGCGAGGA AAACCTACTG ATTCTTAGC TCATTATCAT 360  
 CTCTCCCAAG CGAGATTTCG TTCTTATCGC CTGCTCTATC GCTCAAGTTT GAGCCTCCCG 420  
 AAGTCCGGGG GGGAGAGAGC AAACCCCTGG CTCACCCCCA GCCGCGAGAA GCCACCGCCT 480  
 TGCTCCAAAG CCTGTCAGCT CTGCTGCACC GCAGCTTCTC ACCCAGTCCG GATGCTGTAG 540  
 ATCAACAGGT TCAGGGAACCT TGAGCAGAAAT AAGGAGAGAC CACCGGGTGC CGCAGCTCGG 600  
 GTGCAGAGGG AAAAAGGAGC CCATAGACTT GTGGCTCGCG TCGCGCGCGC ACGCTGCGCC 660  
 AGGGCCCCAG GCTGGCGCGC ACTCCCTCTC TGGCTCTCTC AGTCCGATTG CTCCTGCCCC 720  
 CACCTTACAG GTCTGGGATG TACCTTTCCA TCTGTGTCTG CTTTCTTCTA TGGGCCCTCG 780  
 CCCTCACTCT CAAGAACTCT AACTACTCGG TGCCGAGGA GCAAGGGGCC GGCACGGTGA 840  
 TCGGGAACAT CGGCAGGGAT GCTCGACTGC AGCCTGGGCT TCGCCTGCA GAGCGCGGCG 900  
 GCGGAGGGCG CAGCAGTTCG GGTAGCTACC GGTGCTGGA GAACTCCGCA CGCAGCTGCG 960  
 TGGACGTGGA CGCAGACAGC GGGCTCCTCT ACACCAAGCA CGCATCGAC CGCAGTCCC 1020  
 TGTGCGGCCA CAATGCCAAG TGCCAGCTGT CCTCGAGGT GTTCGCAAC GACAAGGAGA 1080  
 TCTGATGATG CAAGGTAGAG ATCCAGGACA TCAACGACAA CGCGCCCTCG TTCTCTCGG 1140  
 ACCAGATGCA AATGGACATC TCGGAGAACG CTGCTCCGGG CACCGCTTC CCCCTCACA 1200  
 GCGCACATGA CCGCAGCGCC GCGGAGAATG GGCTCGCAC CTACCTGCTC ACGCGGACG 1260  
 ATCAGCGCCT CTTTGGAGTG GACGTTAAGT CCGCGCGCGA CGCACCAAG TTCCAGAAC 1320  
 TGGTATCCA GAAGGCTCTG GACCGCGAGC AACAGAATCA CCATAGCTCT GTGCTGACTG 1380  
 CCCTGGACGG TGGCGAGCCT CCACGTTCCG CCACCGTACA GATCAACGTG AAGGTGATTG 1440  
 ACTCCAACGA CAACAGCCCG GTCTTCGAGG CGCATCTCTA CTTGGTGGAA CTGCCGAGA 1500  
 ACGCTCCCGG GGTATACGTG GTCATCGATC TGAACGCCAC CGACGCGGAT GAAGTCCCA 1560  
 ATGGTGAAGT GCTCTACTCT TTCAGCAGCT ACGTGCCTGA CCGCGTGCAG GAGCTCTTCT 1620  
 CCATCGACCG CAAGACCGGC CTAATCCGTG TGAAGGGCAA TCTGAGTAT GAGGAAAAG 1680  
 GGATGCTCCA GATTGACGTG CAGGCCGAG AGCTGGGGCC TAACCTATC CCAGCCACT 1740  
 GCAGAGTACG GGTGAGCTC ATCGACCGCA ACGACAATGC GCGCTCCATC GGTTCGTCT 1800  
 CGCTGCGCGA GGGGCGCTG AGCGAGGCGG CCGCTCCCGG CACGCTATC GCCTGTGTC 1860  
 GGGTCACTGA CCGGAGCTCT GGCAAGAACG GACAGCTGCA GTGTGCGGTC CTAGGCGGAG 1920  
 GAGGGAAGGG CGCGCGCGGG GGCTGGGGCG GCGCGGGGG TTGCTCCCTC TTCAAGCTTG 1980  
 AGGAGAATCA CGACAACTT TACACGGTGG TGACTGACG CCGCTGGAC GCGAGACAC 2040  
 AAGAGAGATA CAACGTGACC ATCGTGGCGG GGGACGGGGG CTCTCTCTCC CTCAACTCCA 2100  
 CCAAGCTGTT CGCGATCAAG ATTCTAGAGC AGAACGACAA CCGCCTCGG TTCAACAAAG 2160  
 GGCTCTACGT GCTTCAGGTG CACGAGAACA ACATCCCGGG AGAGTACCTG GGCTCTGTGC 2220  
 TGCGCCAGGA TCCCGACCTG GGCCAGAACG GCACCGTATC TACTCTATC CTGCGCTCGC 2280  
 ACATGCTGCA CGTGTCTATG TACACCTATG TGTCTGTGAA TCCACGAAAC GGGGCCATCT 2340  
 ACGCCCTCGG CTCTTTAAAC TTGAGCAGCA CCAAGGCTTT TGAGTTCAAG GTGCTGTGTA 2400  
 AGGACTCGGG GGGCGCCCGG CACTTGGAGA GCAACGCCAC GGTGAGGGTG ACAGTGTCTAG 2460  
 ACGTGAATGA CAACGCGCCA GTGATCGTGC TCCCAAGCTC GCAGAACGAC ACCGCGGAGC 2520  
 TGCAGGTGCC GCGCAACGCT GGCTCGGGCT ATCTGGTGAG CACTGTGCGC GCCCTAGACA 2580  
 GCGACTTCGG CGAGAGCGGG CGTCTCACCT ACGAGATCGT GGAAGGCAAC GACGACCACC 2640  
 TGTGTTGAGT CGACCGCTCC AGCGGCGGAG TCCGCAAGCT GCACCTTTTC TGGGAGGACG 2700  
 TGACGCCCGT GGTGGAGCTG GTGGTGAAGG TGACCGACCA CGGCAAGCCT ACCCTGTCCG 2760  
 CAGTGCCCAA GCTCATCATC CGCTCGGTGA GCGATCCCT TCCGAGGGG GTACCAAGGG 2820  
 TGAATGGCGA GCAGCACCAC TGGGACATGT CGCTGCGGCT CATCGTACT CTGAGCACTA 2880  
 TCTCCATCAT CCTCTAGCG GCGATGATCA CCATCGCGGT CAAGTGCAAG GCGGAGAACA 2940  
 AGGAGATCCG CACTTACAAC TGCGCATCG CCGAGTACAG CCACCGCAG CTGGGTGGGG 3000  
 GCAAGGGCAA GAAGAAGAAG ATCAACAAAA ATGATATCAT GCTGGTGCAG AGCGAAGTGG 3060  
 AGGAGAGGAA CGCATGAAC GTCATGAACG TGGTGAAGC CCGCTCCCTG GCCACCTCCC 3120  
 CCATGTACTT CGACTACCAAG ACCCGCTGCG CCCTCAGCTC GCGCGGTGCG GAGGTGATGT 3180  
 ATCTCAAAAC GGCCTCCAAC AACCTGACTG TCCCTCAGGG GCACGCGGGG TGCCACACCA 3240  
 GCTTCACCGG ACAAGGGACT AATGCAAGCG AGACCCCTGC CACTCGGATG TCCATAATTC 3300  
 AGACAGACAA TTTTCCGCA GAGCCCAATT ACATGGGCGC CAGGCAGCAG TTTGTTCAAA 3360  
 GTATTTCACT AGCTCCACGT TTAAGGACCC AGAAAGAGCC AGCCTGAGAG ACAGTGGGCA 3420  
 CGGGGACAGT GATCAGGCTG ACAGTGACCA AGACACTAAC AAAGGCTCCT GCTGTGACAT 3480  
 GTCTGTAGG GAGGCACTCA AGATGAAAC TACTTCAACT AAAAGCCAAC CACTTGAACA 3540  
 AGAACCCAGG GAGTGTGTTA ATTGCACAGA TGAATGCGGA GTGCTGTGTC ATTCTGACAG 3600  
 GTGCTGTGAT CCACAGTTCC CTGAGGCCAA TCAGGCTGAA AATGCAGATT ACCGCACAAA 3660  
 TCTCTTTGTA CCTACAGTTG AAGCTAATGT TGAGACTGAG ACTTACGAAA CTGTGAATCC 3720  
 CACTGGGAAA AAGACTTTTT GTACATTTGG AAAAGACAAG CGAGAGCACA CTATTTCTAT 3780  
 TGCCAAAGTT AAACCTTATT TAAAAGCCAA ACGTGCCCTG AGCCCTCTCC TCCAAGAGGT 3840  
 CCCCTCAGCA TCAAGCAGCC CAACCAAGGC GTGCATCGAG CCTTGCACTT CAACAAAAGG 3900  
 CTCCCTGAGT GGCTGTGAAG CAACCAAGG AGCCCTGGCT GAAGCAAGCA GTCACTACTT 3960  
 GCGCACTGAC AGTCAATATC TGTACCTAG TAAGCAACCA AGAGACCCCT CTTTATGCG 4020

5  
 10  
 15

```

TTCGATCAG ATGGCAAGGG TCTTTGCAGA TGTGCATTC AGAGCCAGCC GGGATTCCAG 4080
TGAGATGGGT GCTGTTCTTG AGCAGCTTGA CCACCCCAAC AGGGATCTGG GCAGAGAGTC 4140
TGTGGATGCA GAGGAAGTTG TGAGAGAAAT TGATAAGCTT TTGCAAGACT GCCGGGGAAA 4200
CGACCCCTGT GCTGTGAGAA AGTGAAAAAA GAAAAAAAAG AAGGCATTGG CATTTCCTTG 4260
TCTCTTCTGT TGATTTAAAA ATGATCCCTC CTGGTGATAA CCCATTTTAC AGGGATGAAG 4320
AAAGACCAAT GCTGCTTTAA GGCTTTTAGT GAACATCTGA AGTGCCCA CA AGTATGTTCT 4380
TTCCACTGCT GATTTCCTTT TCAGAGATAA CAATGGTTTC GTTTTGACCA AACTTGTATT 4440
AGGACAGAAT TAATGATGCT TAAAGAGAAA AGAAAAAAG AGAGAAGAAA AAGGAGAGAT 4500
GAAAAAGGAG GATGAGGAGA AGAATTACCT TTTGACAATC TGTTAGGAAG GTATGCAGTG 4560
TGAGAACTGA AGTATTTCTG ATCACTCTCA GACTGTCCTC CGTGATTAT GCTGACTTAA 4620
CTGTTTACCT ATAAACCCCA TACAAAGCAG GGTATAATT TGTGATCTGT GGTGGATTTC 4680
TAGCAGTCAT CACAGGCTTC TACTGAAAGT CCGTAAAAGA CCTTGCACTA GTCCAAGCTA 4740
CACCAACAT TAACACATAT TTGTGGTAAA CATTTCCTGA TAAAGTTACC TGACACACAT 4800
ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAACAA AAACAAAAAA AAAACCTTTG 4860
GTCATTTGTA AGACATCTCA TGTATATAA AAGTTAAATG TAAAAAGATA CAGTCCATTT 4920
TGTCTGCAC ACAGTAGAC TAATTCAGT CAAAAAAA AAAAAA 4966
  
```

20

```

Seq ID NO: C67 DNA Sequence
Nucleic Acid Accession #: NM_005601.2
Coding sequence: 101..598
  
```

25  
 30  
 35

```

1 11 21 31 41 51
| | | | |
CCCAGGAGTC TGGGTGCACA GCTCCTTCT CTCTGAGATT CAAGAGTCTG ATCAGCAGCC 60
TCTTCTCTCT CCAGGACCCA GAAGCCCTGA GCTTATCCCC ATGGAGCTCT GCGGTCCTCT 120
GGCCCTGCTG GGGGGCTCCC TGGGCTGAT GTTCTGCCCTG ATTGCTTTGA GCACCGATT 180
CTGGTTTGA GCTGTGGGTC CCACCCACTC AGCTCACTCG GGCTCTGGC CAACAGGGCA 240
TGGGACATC ATATCAGGT ACATCCAGT GACGACAGCC TTCAGCATT TGGCTGTTCT 300
GTGGGCCCTG GTGTCCGTTA GCTTCTGGT CCGTCTCTGC TCCCCCTCAC TGTTCCTCCC 360
AGGCCACGGC CCGCTTGTCT CAACCAACGC AGCCTTGTCT GCAGCCATCT CCATGGTGGT 420
GGCCATGGCG GTGTACACCA GCGAGCGGTG GGACCAAGCT CCACACCCCA AGATCCAGAC 480
CTTCTTCTCC TGGTCTTCT ACCTGGGCTG GGTCTCAGCT ATCCTCTTGC TCTGTACAGG 540
TGCCCTGAGC CTGGGTGCTC ACTGTGGCGG TCCCGTCTCT GGCTATGAAA CCTTGTGAGC 600
AGAAGGCAAG AGCGCAAGA TGAGTTTGA GCGTGTGATT CCAAGGCGCT CATCTGGAGC 660
CTCGGGAAG TCTGTCTCA CATTGCCCCG CCTTCCAGC CCTTCCCCAG CCCTCCTCT 720
TGTTTCTTCA TTCATTCAAC AAAATTGGC TGGAAAAAAA AAAAAAAA AAAAAAAA 783
AAA
  
```

40

```

Seq ID NO: C68 DNA Sequence
Nucleic Acid Accession #: NM_006433.2
Coding sequence: 129..566
  
```

45  
 50  
 55

```

1 11 21 31 41 51
| | | | |
GTATCTGTGG TAAACCCAGT GACACGGGGG AGATGACATA CAAAAAGGGC AGGACCTGAG 60
AAAGATTAA GCTCAGGCTC CCGCCCATTA AAACAGGGTG TGAAAGGCAT CTCAGCGGCT 120
GCCCAACCAT GGTACCTGG GCGCTCCTGC TCCTTGACAG CATGCTCCTG GGCAACCCAG 180
GTCTGTCTCT CTCTGCTCTG AGCCCTGAGT ACTACGACCT GGCAAGAGCC CACCTGGCTG 240
ATGAGAGAAA ATCTGCTCCG TGCTGGGCCC AGGAGGGCCC CCAGGGTGAC CTGTTGACCA 300
AAACACAGCA GCTGGGCGGT GACTACAGGA CCTGTCTGAC GATAGTCCAA AAACCTGAAGA 360
AGATGTGGA TAAGCCCAAC CAGAGAAGTG TTTCCAATGC TGCGACCCCG GTGTGTAGGA 420
CGGGGAGGTC ACGATGGCGC GACGCTGCA GAAATTTTAT GAGGAGGTAT CAGTCTAGAG 480
TTACCAAGCG CCTCTGGGCC GGAGAAACTG CCCAGCAGAT CTGTGAGGAC CTCAGGTTGT 540
GTATACCTCT TACAGTCCC CTCTGAGCCC TCTCACTTGT TCCTGTGGAA GAAGCAGAGG 600
CTCTGTCTCT CAGATCCCGG GAACCTCAGC AACCTCTGCC GGCTCCTGCT TTCCTGATC 660
CAGATCCAC TCTCAGTCT CCCTCCCTG ACTCCTCTG CTGTCTCTCC CTCTCAGAG 720
AATAAAGTGT CAAGCAAG 738
  
```

60

```

Seq ID NO: C69 DNA Sequence
Nucleic Acid Accession #: NM_002985.2
Coding sequence: 69..344
  
```

65  
 70  
 75  
 80

```

1 11 21 31 41 51
| | | | |
GCTGCAGAGG ATTCCTGCAG AGGATCAAGA CAGCAGTGG ACCTGACACA GCTCTCCCA 60
CAGGTACCAT GAAGGTCTCC GCGGCAGCCC TCGCTGCAT CCTATTGCT ACTGCCCTCT 120
GCGCTCCTGC ATCTGCCTCC CCATATTCTT CGGACACCAC ACCCTGCTGC TTTGCTTACA 180
TTGCCCGCCC ACTGCCCGGT GCCCAGATCA AGGAGTATTT CTACACCACT GGCAAGTGCT 240
CCAAACCAAG AGTCTCTTT GTCAACCGAA AGAACCGCCA AGTGTGTGCC AACCCAGAGA 300
AGAAATGGGT TCGGGAGTAC ATCAACTCTT TGGAGATGAG CTAGGATGGA GAGTCTTGA 360
ACCTGAACCT ACACAAATT GCCTGTTTCT GCTTGTCTT GTCTAGCTT GGGAGGCTTC 420
CCCTCACTAT CCTACCCAC CCGCTCCTTG AAGGGCCAG ATTCTACCAC ACAGCAGCAG 480
TTACAAAAAC CTTCGCCAGG CTGACGCTGG TGGCTCAGC CTGTAATCCC AGCATTGTTG 540
GAGGCCAAGT TGGGTGGATC ACTTGAGGTC AGGAGTTTGA GACCAGCCTG GCCAACATGA 600
TGAAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGGTAGC GGGGCGCTGT 660
AGTCCAGCT ACTCGGGAGG CTGAGGCAGG AGAATGGGCT GAACCCGGGA GCGGAGCTTT 720
GCAGTGAGCC GAGATCGCGC CACTGCACCT CAGCCTGGGC GACAGAGCGA GACTCCGTCT 780
CAAAAAAATA AAAAAAATA AAATACAAA AATTAGCCGG GCGTGGTAGC CCACGCTGT 840
AATCCAGCT ACTCGGGAGG CTAAGGCAGG AAAATTGTTT GAACCCAGGA GGTGGAGGCT 900
GCAGTGAGCT GAGATTGTGC CACTTCACCT CAGCCTGGGT GACAAAGTGA GACTCCGTCT 960
CAACACACAC AAAAAAAGC TTCCCAACT AAAGCTAGA AGAGCTCTG AGGCGTGTCT 1020
TTGTCAAAAG GAAGTCTCTA GGTCTGAGC TCTGGCTTTG CCTTGGCTTT GCCAGGGCTC 1080
  
```

TGTGACCAGG AAGGAAGTCA GCATGCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC 1140  
 TTAAGCTTCC GCCGTCTCAA CCCCTCACAG GAGCTTACTG GCAACATGA AAAATCGGCT 1200  
 TACCATTAAA GTTCTCAATG CAACCATAAA AAAAAA 1237

Seq ID NO: C70 DNA Sequence  
 Nucleic Acid Accession #: NM\_022154.2  
 Coding sequence: 1381..1722

10 1 11 21 31 41 51  
 AGTGTGGTTT TAGTTTTTCC TAAGAAGTGG CGTGGTTTGG GGCTTTATAT CCGGGAGGAG 60  
 CATATGTACG CAATCCTGCG GCGCTTTGCA AACCGGATC CGGGCGCTCT GGCCCATGTC 120  
 CCGGCGGGGC GTTTGAGGGC TACTGCCACG CAGCGTTTCT GGAGCCTGCC GGCTGGTGCC 180  
 15 CTGGTGCCCT TTATCTCTGT CCCCTTTGT CCTCTTTATC TCAGGCTCTC CAGGAGGCCG 240  
 GGGGGCCAC TCAGCCTATC GCTCCCTCG GCTACGCTGC CACTCCAATG CCCGCGAGGT 300  
 CGGAGCTGC TGTCTTTG AAGCGCGCG AGAACGAGG GCGTCCCGCG CCACCTCTGA 360  
 CTGGAGCAG CGCCGAGCAC TGACGCTCCC GCCCTTGGGC AAGGACGCCA GTGCGCCCGC 420  
 GCGCGTCCCT CTGCGCGGCA GCCCGTCGCG GGCCCTCAAG GGGAGGCCA GGCCAGGATG 480  
 20 GCCCGGGTGC GCGCGTGGC CGGCTCCTG TTGCTGGCGG CCGCGGCCCT CGGAGGAGTG 540  
 CCGGAGGGGC CAGGCGTAGC CTTGAGCGAG GATGTGCTGA CCGTGTTCGG CGCGAATCTG 600  
 AGCCTGTGCG CGCGCGAGCT CCAGCACTTG CTGGAGCAGA TGGAGCGCGC CTCGCGGTG 660  
 GCGTCCCGG AGCCTGGCCA GCTGCACTTC AACCAGTGT TAAGTGTGA AGAGATCTTT 720  
 25 TCCTTCATG GCTTTTCAA TGCTACCCAA ATAACCACT CCAATTTCTC TGTCTCTGT 780  
 CCAGCAGTCT TACAGCAAT GAACCTTAC CCATGTGAGG ATCGGCCCAA GCACAAACAA 840  
 AGACCAAGTC ATTCAGAAAT TTGGGGATAT GGATTCCTGT CAGTGACGAT TATTAACTG 900  
 GCATCTCTCC TCGGATTGAT TTTGACTCCA CTGATAAGA AATCTTATT CCACAAAGATT 960  
 TTGACCTTTT TTGTTGGGCT GGCTATTGGG ACTCTTTTTT CAAATGCAAT TTTCACCTT 1020  
 30 ATTCAGAGG CATTGGGAT TGATCCCAA GTGACAGTT ATGTTGAGAA GGCAGTTGCT 1080  
 GTGTTGGTG GATTTTACCT ACTTTCTTT TTGAAAGAA TGCTAAAGAT GTTATTAAAG 1140  
 ACATATGGTC AGAATGGTCA TACCCACTTT GGAATGATA ACTTTGGTCC TCAAGAAAAA 1200  
 ACTCATCAAC CTAAGCATT ACCTGCCATC AATGGTGTGA CATGCTATGC AAATCCTGCT 1260  
 GTCACAGAAG CTAATGGACA TATCCATTTT GATAATGTCA GTGTGTATC TCTCAGGAT 1320  
 35 GGAAAAAAG AGCCAAGTTC ATGTACCTGT TTGAAGGGG CCAACTGTGC AGAAATAGGG 1380  
 ACGATTGCCT GGATGATAAC GCTCTGCGAT GCCCTCCACA ATTTTCATGA TGGCCTGGCG 1440  
 ATTGGGGCTT CTGCACTTT GTCTCTCCTT CAGGGACTCA GTACTTCCAT AGCAATCCTA 1500  
 TGTGAGGAGT TTCGCCAGA GTTAGGAGAC TTGTGATCC TACTCAATGC AGGGATGAGC 1560  
 ACTGCAAG CTTGCTATT CAACCTCCTT TCTGCTATGT CCGCTATGT TGGGCTAGCT 1620  
 40 TTTGGCATT TTGTTGGGCA CAATTTGCT CCAATATTA TATTGCACT TGCTGGAGGC 1680  
 ATGTTCTCT ATATTCTCT GGCAGATATG TTTCAGAGA TGAATGATAT GCTGAGAGAA 1740  
 AAGTAAGTC GAAGAAAAAC CGATTTCACC TTCTTCATGA TTCAGAATGC TGGAAATGTA 1800  
 ACTGGATTCA CAGCCATTCT ACTCATTACC TTGTATGAG GAGAAATCGA ATTGGAGTAA 1860  
 TAGAAAAAG AAGATGGTGT TGTAAATAA GGCATTAAAT AGATAAAAA ATCTCCAAAA 1920  
 45 AGGATTTGA AGCTGATCCT ATTTAGTTAA AAGATAAAT TTGCTTCA CTGTAGGTCC 1980  
 AGAAAACTAA TTATTGGCAT CAGTCTGTGA AATAGTCCAT TATTGTGTGT TAAAAATGCT 2040  
 TCAAAAGTCT TTAGTGATG GTCTGAGATG CCTGGTATAT AGGAGCCTTT GGGAAATACT 2100  
 TATTTTTCAG TATTCATGCG ATATTAGATA TCACCATGAA GCAAGAGACA TGCAATCTAT 2160  
 AATCATGTAG ACATCAGAC TCAGGGGAAA ATACAGTTA TATCTGAAA GCCTTTAAAA 2220  
 50 CTCTATGGTA GGATCAAGA TTCAAAATGG TTCCAGAGAG TTTTATTTC ATTAAATTTG 2280  
 TCTAGTGCTT TCAAGAGCAA GTACATCAAA ATGTAGAGG TAAAAATGAT GCAACACTAA 2340  
 TATAAATTAT TCCAAGTCTT TAAGGAGCCA AAGAAAAAAA AGATTCTCA CAGCTTTTGT 2400  
 TTCTGTTTGT TATTTCATT AGGAACTTGC AGTATTATT TGAACCAT TCTAAAAATA 2460  
 TAGSAGTTAG GAAATAATA AAGTTTGTCT AGCCCTGCTA AGTTCAGGCT TAGAGGCTTA 2520  
 55 TCGCTAAGTN TAACTTCAC CAGATTCCAC GAAAAGCTGG ATAGCTTTT TTCTGACTTA 2580  
 TGTGTGGTT GCACCCCTCA CAAATGGCAG AACAGTATGT AAAGCTGGTA ACACCTCGGT 2640  
 TTAGTGAGC CATGTGTTG CTTTGTGAAG GTGAAGAATA TGTGTGTTA GAGAAAGAAA 2700  
 TTGGATGTAA TTTATGCAA TTTACTTTA AAGACAAACA TAACATTTA GCAGAGAATA 2760  
 TTTTATAAAA TGCAAACAA CAGCTGGACT GCTGTACATC AAGGACAGAT TAACTGGAAA 2820  
 60 ACATATGTT CTTATGTGTG ATTGAGAGCC ATTCAGAAAA GACTTCCTTT GTGTTGAGCC 2880  
 TATACTTTT CATATGGTAT ACCTTGAAAA AATTAGCAC ACCATGGTTA TTTTCTTACC 2940  
 TTTTATAAAA GACAGAGCCT GTTACTCAT TTAGAAGATA GAGAAATTTG GTCTAAAAAT 3000  
 GAACATCCTA GATTCACTC CCCAAGTCAC TTAAGGTGAT TTGATGGTGA GGAATATGAT 3060  
 TGACAAAGCC CAACATGAT CTCAGGAATT ACATTTTCCA ACAGACCAA AAATGTTTTC 3120  
 65 ATGTAGCAGC AATGCAGATT TGGTGAATAT TTAATATATA TTTTAGTAGT TATTTCATT 3180  
 TATGACTGAC AATTAAAAA TATTGTTTGG CCAATAGTA AACACCTTT TGAACCATG 3240  
 AAAAAA 3246

Seq ID NO: C71 DNA Sequence  
 Nucleic Acid Accession #: NM\_004184.2  
 Coding sequence: 188..1603

75 1 11 21 31 41 51  
 CGAAAAAAGA GGGGAAGAGT ATTAAGACC ATTTCTGGCT GGGCAGGGCA CTCTCAGCAG 60  
 CTCACCTGCC CAGCGTGACC AGTGGCCACC TCTGCAGTGT CTTCCACAAC CTGGTCTTGA 120  
 CTGCTCTGCT GAACAAATCC TCTGACCTCA GGCCGGCTGT GAACGTAGTT CCTGAGAGAT 180  
 AGCAACATG CCCACAGTG AGCCCGCATC TCTGCTGGAG CTGTTCAACA GCATCGCCAC 240  
 80 ACAAGGGGAG CTCGTAAGGT CCTCAAAGC GGGAAATGCG TCAAGGATG AAATTGATTC 300  
 TGCAGTAAAG ATGTTGGTGT CATTAAAAAT GAGCTACAAA GCTGCCCGG GGGAGGATTA 360  
 CAAGGCTGAC TGTCTCCAG GGAACCCAGC ACCTACCAGT AATCATGGCC CAGATGCCAC 420  
 AGAAGCTGAA GAGGATTTTG TGGACCATG GACAGTACAG ACAAGCAGT CAAAAGGCAT 480  
 AGACTACAGT AAGCTCATTT TCGGTTTGG AAGTAGTAAA ATTGACAAAG AGCTAATAAA 540  
 CCGAATAGAG AGAGCCACCG GCCAAGACC ACACCACTTC CTGCGCAGAG GCATCTCTTT 600

5	CTCACACAGA	GATATGAATC	AGGTTCTTGA	TGCCTATGAA	AATAAGAAGC	CATTTTATCT	660
	GTACACGGC	CGGGGCCCTC	CTTCTGAAGC	AATGCATGTA	GGTCACTCA	TTCATTAT	720
	TTTCAAAAG	TGGCTCCAGG	ATGTATTTAA	CGTGCCCTTG	GTCACTCCAGA	TGACGGATGA	780
	CGAGAAGTAT	CTGTGAAGG	ACCTGACCC	GGACCAGGCC	TATGGCGATG	CTGTGAGAA	840
	TGCCAAGGAC	ATCATGCGCT	GTGGCTTTGA	CATCAACAAG	ACTTTCATAT	TCTCTGACCT	900
10	GGACTACATG	GGGATGAGCT	CAGGTTTCTA	CAAAAATGTG	GTGAAGATTG	AAAAGCATGT	960
	TACCTTCAAC	CAAGTGAAAG	GCATTTTCGG	CTTCACTGAC	AGCGACTGCA	TGGGAAGAT	1020
	CAGTTTCTCT	GCCATCCAGG	CTGCTCCCTC	CTTCAGCAAC	TCATTCCCA	AGATCTTCCG	1080
	AGACAGGACG	GATATCCAGT	GCCTTATCCC	ATGTGCCATT	GACCAGGATC	CTTACTTTAG	1140
	AATGACAAGG	GAGGTGCGCC	CCAGGATCGG	CTATCTTAAA	CCAGCCCTGT	TGCATCCAC	1200
15	CTTCTTCCCA	GGCTTCCAGG	GCGCCAGAC	CAAAATGAGT	GCCAGCGACC	CAAACTCCTC	1260
	CATCTTCTCT	ACCGACACGG	CCAAGCAGAT	CAAAACCAAG	GTCAATAAGC	ATGCGTTTTC	1320
	TGGAGGGAGA	GACACCATCG	AGGAGCACAG	GCAGTTTGGG	GGCAACTGTG	ATGTGGACGT	1380
	GTCTTTTCATG	TACCTGACCT	TCTTCTCGA	GGACGACGAC	AAGCTCGAGC	AGATCAGGAA	1440
	GGATTACACC	AGCGGAGCCA	TGCTCACCGG	TGAGCTCAAG	AAGGCACTCA	TAGAGGTTCT	1500
20	GCAGCCCTTG	ATGCTCAGAG	ACCAGGCCCG	GCGCAAGGAG	GTCAAGGATG	AGATAGTGAA	1560
	AGAGTTTCATG	ACTCCCGGGA	AGCTGTCTCT	CGACTTTTCA	TAGCACTCGT	TTTACATATG	1620
	CTTATAAAG	AAGTATGATG	TCAGTAAATC	ATCAATAATC	CCAGCCCACT	CAAGCAGCG	1680
	CCACCTGTAG	GCTTCTGTCT	CATGGTAATT	ACTGGGCTTG	GCCTCTGTAA	GCCTGTGTAT	1740
	GTATACAATA	CTGTTTCTTC	CTGTGAGTTC	CATTATTTCT	ATCTCTTATG	GGCAAAGCAT	1800
25	TGTGGGTAAT	TGGTGTCTGC	TAACATTGCA	TGGTCGGATA	GAGAAGTCCA	GCTGTGAGTC	1860
	TCTCCCAAAA	GCGACCCCA	AGTGGAGCCT	TGGGCTGGAA	GTCCATGGGC	CACCTCTGTC	1920
	TGTTCATGG	AGGACTTCCG	AGGGTTCCAA	GTATACTCTT	AAGACCCACT	CTGTTTAAAA	1980
	ATATATATT	TATGTATGCG	TATATGGAAT	TGAATGTCA	TTATTGTAA	CTAGAAAGTG	2040
	CTTTGAAATA	TGATGTGGG	GAGGTTTATT	GAGCACAGA	TGATTTTCAG	CCCATGCCCC	2100
30	CTCCAAAAA	GAAATTGATA	AGTAAAGCT	TCGTTATACA	TTTGAATAAG	AAATCACCCA	2160
	GCTTTAAAGC	TGCTTTTAA	AATGAAGATT	GAACAGAGTT	CAGCAATTTT	GATTAAATTA	2220
	AGACTTGGG	GTGAAACTTT	CCAGTTTACT	GAACCTCAGA	CCATGCATGT	AGTCCACTCC	2280
	AGAAATCATG	CTCGCTTCCC	TGGGCACAC	AGTGTCTTCC	TGCCAAATGA	CCCTAGACCC	2340
	TCTGTCTCTG	AGAGTCAGG	TGGCTTTTCC	CCTGACTGTG	TCCGATGCCA	AGGAGTCTCT	2400
35	GCCTCCGCG	ATGCTTCAAT	TGACCCCTTG	GCTGCAGTGG	AAGTCAGCAC	AGAGCAGTGC	2460
	CCTGGCTGTG	TCTTGGACGG	GTGGACTTAG	CTAGGGAGAA	AGTCAGGACA	GCGACCCCTG	2520
	AGGCCCTCAC	AGATGTCTAG	GCAGGCCCTCA	TTTCATCACG	CAGCATGTGC	AGGCCGTGAA	2580
	GAGCAAGGCC	AAATCTCAGG	GAAGTCTCTG	GTGTGATGAT	CTGGGTCTCC	TCTGGAGCAC	2640
	TCTGCCCTCC	TGTCACCCAG	TAGAGTAAAT	AAACTTCCTT	GGCTCCTAAA	AAA	2693

Seq ID NO: C72 DNA Sequence

Nucleic Acid Accession #: NM\_004938.1

Coding sequence: 337..4632

40	1	11	21	31	41	51	
	CGGAGGACAG	CGGAGCCGAG	CCAAAGCCGG	GGACTTTGTT	CCCTCCACGG	AGGGGACTCG	60
	GCAACTCGCA	GCGGCGAGGT	CTGGGGCCGG	CGCTCGGGAG	GGATCTGGCG	CCCCCACTCA	120
45	CTCCCTAGCT	GTGTTCCCGC	CGCGCCCGCG	GCTAGTCTCC	GGCGCTGGCG	CCTATGGTGG	180
	GCCTCCGACA	GCGCTCCGGA	GGGACCGGGG	GAGCTCCAG	GCGCCCGGGA	CTGGAGACTG	240
	ATGCATGAGG	GGCCTACGGA	GGCGCAGGAG	CGGTGGTGAT	GGTCTGGGAA	GCGGAGCTGA	300
	AGTCCCTTGG	CTTTGGTGA	GGCGTGACAG	TTTATCATGA	CGGTGTTCAG	GCAGGAAAC	360
	GTGGATGATT	ACTAGCAGAC	CGGCGAGGAA	CTTGGCAGTG	GACAGTTTGC	GGTTGTGAAG	420
50	AAATGCGGTG	AGAAAAGTAC	CGGCTCCAG	TATGCCGCCA	AATTCATCAA	GAAGAAGGAG	480
	ACTAAGTCCA	GCGGCGGGGG	TGTGAGCCGC	GAGGACATCG	AGCGGGAGGT	CAGCATCCCTG	540
	AAGGAGATCC	AGCAACCCAA	TGTATCACC	CTGCAGAGG	TCTATGAGAA	CAAGACGGAC	600
	GTATCTCATG	TCTTGAAC	CGTTGCAGGT	GCGAGCTGT	TTGACTTCTT	AGCTGAAAAG	660
	GAATCTTTAA	CTGAAGAGGA	AGCAACTGAA	TTTCTCAAC	AAATCTTAA	TGTTGTTTAC	720
55	TACCTGCACT	CCCTTCAAAT	CGCCCACTTT	GATCTTAAAG	CTGAGAACAT	AATGCTTTTG	780
	GATAGAAATG	TCCCAAAAC	TGGATCAAG	ATCAATGACT	TTGGGTGGCG	CCATAAAATT	840
	GACTTTGGAA	ATGAATTTAA	AAACATATTT	GGGACTCCAG	AGTTTGTGCG	TCTTGAGATA	900
	GTCAACTATG	AACTCTTGG	TCTTGAGGCA	GATATGTGGA	GTATCGGGGT	AATAACCTAT	960
60	ATCCTCTTAA	GTGGGGCTCT	CCCATTTCTT	GGAGACACTA	AGCAAGAAAC	GTTAGCAAAT	1020
	GTATCCGCTG	TCAACTACGA	ATTTGAGGAT	GAATACTTCA	GTAAATACCA	TGCCCTAGAC	1080
	AAAGATTTCA	TAAGAAGACT	TCTGGTCRAG	GATCCAAAGA	AGAGAATGAC	AATTCRAGAT	1140
	AGTTTGCAGC	ATCCCTGGAT	CAAGCCATAA	GATACACRAC	AGGCACCTAG	TAGAAAAGCA	1200
	TCAGCAGTAA	ACATGGAGAA	ATTCAAGAAG	TTTGCAGCCC	GGAAAAAATG	GAACCAATCC	1260
65	GTTCGCTTGA	TATCACTGTG	CCAAAGATTA	TCCAGGTCTAT	TCTGTCCAG	AAGTAACATG	1320
	AGTGTGCCA	GAAGCGATGA	TACTCTGGAT	GAGGAAGACT	CCTTTGTGAT	GAAGCCATC	1380
	ATCCATGCCA	TCAACGATGA	CAATGTCCCA	GGCTGCAGC	ACCTTCTGGG	CTCATTATCC	1440
	AACATATGAT	TTAAACCAAC	CAACAAGCAC	GGGACACCTC	CATTACTCAT	TGCTGTGGC	1500
	TGTGGGAATA	TTCAATACT	ACAGTTGCTC	ATTAAAAAG	GCTCGAGAAT	CGATGTCCAG	1560
70	GATAAGGGCG	GGTCCAATGC	CGTCTACTGG	GCTGCTCGCG	ATGGCCACGT	CGATACCTTG	1620
	AAATTTCTCA	GTGAGAACAA	ATGCCCTTTG	GATGTGAAAG	ACAAGTCTGG	AGAGATGGCC	1680
	CTCCAGCTGG	CAGCTCGCTA	TGGCCATGCT	GACGTGGCTC	AAGTTACTTG	TGCAGCTTCG	1740
	GCTCAAAATCC	CAATATCCAG	GACAAAGGAA	GAAGAAACCC	CCCTGCACGT	TGCTGCTTGG	1800
	CACGGCTATT	ACTCTGTGGC	CAAGCCCTTT	TGTGAAGCCG	GCTGTAACTG	GAACATCAAG	1860
75	AACCGAGTAG	GAGAGACGCC	CCTCTTGACA	GCCTCTGCCA	GGGGCTACCA	CGACATCGTG	1920
	GAGTGTCTGG	CCGAACATGG	AGCCGACCTT	AATGCTTGGC	ACAAGGACGG	ACACATTGCC	1980
	CTTCACTGG	CTGTAAGACG	GTGTCAAGTG	GAGGTAATCA	AGACTCTCTT	CAGCCAAGGG	2040
	TGTTTCTGTC	ATTATCAAGA	CAGGCACGGC	AATACTCCCC	TCCATGTGGC	ATGTAAAGAT	2100
	GGCAACATCG	CTAGCTGTGT	GGCCCTCTGT	GAAGCAAACT	GCAATTGGGA	CATCTCCAAC	2160
	AAGTATGGGC	GAAGCCTCT	GCACCTTGCG	GCCAAACAAG	GAATCCTAGA	CGTGGTCCGG	2220
80	TATCTCTGTC	TGATGGGAGC	CAGCCTTGAG	GCGCTGACCA	CGGACGGAAA	GACGGCAGAA	2280
	GATCTTGCTA	GATCGGAACA	GCACGAGCAC	GTAGCAGGTC	TCCTTGCAAG	ACTTCGAAAG	2340
	GATACGACCC	GAGGACTCTT	CATCCAGCAG	CTCCGACCCA	CACAGAACCT	GCAGCCAAAG	2400
	ATTAAGCTCA	AGCTGTTTGG	CCACTCGGGA	TCCGGGAAAA	CCACCTTGTG	AGAATCTCTC	2460
	AAGTGTGGGC	TGCTGAGGAG	CTTTTTCAGA	AGGCGTGGCG	CCAGACTGTC	TTCCACCAAC	2520

5 TCCAGCAGGT TCCACCTTC ACCCCTGGCT TCTAAGCCCA CAGTCTCAGT GAGCATCAAC 2580  
 AACCTGTACC CAGGCTGCGA GAACGTGAGT GTGAGGAGCC GCAGCATGAT GTTCGAGCCG 2640  
 GGCTCTACCA AAGGGATGCT GGAGGTGTTT GTGGCCCCGA CCCACCACCC GCACTGCTCG 2700  
 GCCGATGACC AGTCCACAA GGCATCGAC ATCCAGAACG CTTATTGAA TGGAGTTGGC 2760  
 GATTTGAGG GTGTTGGAGT CTCTGGAAAT CCTGTGTATT TCTGCTGTTA TGACTATTTT 2820  
 GCTGCAATG ATCCACGTC AATCCATGTT GTTGTCTTTA GTCTAGAAGA GCCCTATGAG 2880  
 ATCCAGCTGA ACCCAGTGAT TTTCTGGCTC AGTTTCTGTA AGTCCCTGT CCCAGTTGAA 2940  
 GAACCCATAG CCTTCGGTGG CAAGCTGAAG AACCCACTCC AAGTTGTCTT GGTGGCCACC 3000  
 10 CACGCTGACA TCAATGAATG TCCTCGACCG GCTGGAGGCG AGTTTGGATA TGACAAAGAC 3060  
 ACATCGTTGC TGAAGAGATG TAGGAACAGG TTTGGAAATG ATCTTCACAT TTCAAATAAG 3120  
 CTGTTTGTTC TGGATGCTGG GGCCTTCGGG TCAAAGGACA TGAAGGTACT TCGAAATCAT 3180  
 CTGCAAGAAA TACGAAGCCA GATTGTTTCG GTCTGTCTCT CCATGACTCA CCTGTGTGAG 3240  
 AAAATCATCT CCACGCTGCG TTCTGGAGG AAGCTCAATG GACCCAACCA GCTGATGTGG 3300  
 15 CTGCAGCAGT TTGTGTACGA CGTGCAGGAC CAGCTGAACC CCCTGGCCAG CGAGGAGGAC 3360  
 CTCAGGCGCA TTGCTCAGCA GCTCCACAGC ACAGGCGAGA TCAACATCAT GCAAAGTGAA 3420  
 ACAGTTTCAG ACAGTGTGCT CTGGAACCCC CGCTGGCTCT GCACAAAGT CCTGGGGAAG 3480  
 TTGCTGTCCG TGGAGACCCC ACAGGCGCTG CACCACTACC GGGGCGCGTA CACCGTGGAG 3540  
 GACATCCAGC CCCTGGTGGC CGACAGCGAC GTGGAGGAGC TGTGCAATCT CCTGATGCC 3600  
 20 ATGGACATCT GCGCCCCGGA CCTGAGCAGC GGGACCATGG TGGAGTCCCT AGCCCTGATC 3660  
 AAGACAGACA ACCTGCACCG CTCTGGGCTT GATGAGGAGG ACGAGGTGAT GGTGTATGGT 3720  
 GCGGTGCGGT TCGTGCCCGT GGAAACACCT ACCCCCTTCC CATGTGGCAT CTTTCACAA 3780  
 GTCCAGGTGA ACCTGTGCCG GTGGATCCAC CAGCAAGACA CAGAGGGCGA CGCGGACATC 3840  
 GCGCTGTGGG CCAATGGTGG CAAGCTGGCC AACCGTGGGG CCGAGCTGCT GGTGCTGCTG 3900  
 25 GTCAACACAG GCCAGGCGAT TGAGGTCCAG GTCCGTGGCC TGGAGACGGA GAAGATCAAG 3960  
 TGCTGCTGTC TGCTGGACTC GGTGTGACGC ACCATTGAGA ACGTCATGGC CACCACGCTG 4020  
 CCAGGGCTCC TGACGCTGAA GCATTACCTG AGCCCCAGC AGCTGCGGGA GCACCATGAG 4080  
 CCGGTATGA TCTACAGCC AGGGGACTTC TTCCGGGCAC AGACTCTGAA GGAACCTCA 4140  
 CTGACCAACA CAGTGGGGGG GTACAAGGAA AGCTTCAGCA GCATCATGTG CTTGGGTGTG 4200  
 30 CACGACGTCT ACTCACAGGC CAGCCTCGGC ATGGACATCC ATGCATCAGA CCTGAACCTC 4260  
 CTCACCTGGA GGAACATGAG TCGCCTGCTG GACCCGCGCG ACCCCCTGGG GAAGGACTGG 4320  
 TGCTTCTCG CCATGAACTT AGGCCTCCCT GACCTCGTGG CAAAGTACAA CACCAATAAC 4380  
 GGGGCTCCCA AGGATTTCTT CCCCAGCCCC CTCACGCCCC TGCTGCGGGA ATGGACCAAC 4440  
 TACCCTGAGA GCACAGTGGG CACCCCTCATG TCCAAACTGA GGGAGCTGGG TCGCGGGAT 4500  
 35 GCGGACAGCC TTTTGTGAA GGCATCCTCT GTGTTCAAAA TCAACCTGGA TGGCAATGGC 4560  
 CAGGAGGCCCT ATGCTCTGAG CTGCAACAGC GGCACCTCTT ACAATTCCAT TAGCTCTGTT 4620  
 GTATCCCGGT GAGGCGAGCC TCTGGCTTGG ACAGGGTCTG TTTGGACTGC AGAACCAAGG 4680  
 GGGTGATGTA GCCCATCTCT CCCTTGGAG ATGCTGAGGG TGTTCCTTCC TGCAACCACA 4740  
 40 GCCAGGGGAT CCTCCTCCTT TGACCTGTTT CTCTGCGCTC ACCTCCTTCC 4800  
 CCGTCTCATT CCGTTGTCTG TGGATGCTA TTGCAATTTA AGAGCAGAAC AGATCTTTTA 4860  
 CTTTGGCGGC TTGAAAGCTT AGTGTACCTC CTCTCAGTGT TTTGGACTCC ATCTCTCATC 4920  
 CTCAGTACG CTGCTCTTTA CTGATAATTG TGCTGGAATT CCTAAGTTT CAATGACATT 4980  
 TTTTTTAAT ATCATATTGA TTGTCTTTA AAAAGAAAA GTGCATATT ATCCAAAATG 5040  
 45 TGTATTCTT ATACGCTTTT CTGTGTTATA CCAATTCTCT AGCTTATCTC TTTTATATT 5100  
 GTAGGAGAAA CTCCTCATGA TGAATCCCA CTGTATGATT TATAAACAGA CAATATGTGA 5160  
 GTGCCCTTTG CAGAAGAGGG TGTGTTTGAA ATCATCGAG TCAGCCAGGA GCTGTACCA 5220  
 AGGAAACGCT ACCCTCTGTG CCCTTGTCTG ATGCTGATCA TCGCCAGAGG TGCTTCAACC 5280  
 TGAGTTTGT TTGTATTGTT TTTCTGACAG TTTTCTGTT TTGTTTGGCA AGGAAAGGGG 5340  
 50 AGAAGGGAAT CCTCCTCCAG GGTGATTTTA TGATCAGTGT TGTGCTCTA GGAAGACATT 5400  
 TTTCCGTTTG CTTTGTCTCC AATGTCAATG TGAACGTCCA CATGAAACCT ACACACTGTC 5460  
 ATGCTTCATC ATTCCCTCTC ATCTCAGSTA GAAGGTTGAC ACAGTTGTAG GGTACAGAG 5520  
 ACCATGTATA GAATTACAGAA GACCCCTGAC TCATCATTTG TGGCAGTCCC TTATAATTGG 5580  
 TGATAGCAG ATGGTTTCCA CATTTAGATC CTGTTTTCAT AACTTCCTGT ACTTGAAGTC 5640  
 TAAAAGCAGA AATAAAGGA AGCAAGTTTT CTTCCATGAT TTTAAATTGT GATCGAGTTT 5700  
 55 TAAATTGATA GAGGGGAACA TGTCTTAATT CTTCTGTCTT GAGAAGCATG TAATGTTAAT 5760  
 GTTATATCAT ATGATATAT ATATATGCAC TATGATATA CATATATATT AATACTGGTA 5820  
 TTTTACTTAT ATCTATAAAA TGTCGTTAAA AAGTTGTTT TTTTTCCTT TTTTATAAAA 5880  
 TAACTGTGT CTGTTAAAA AAAAAAAAAA 5910

Seq ID NO: C73 DNA Sequence  
 Nucleic Acid Accession #: NM\_002081.1  
 Coding sequence: 222..1898

65 1 11 21 31 41 51  
 | | | | |  
 GGCTGCCGGA GCGAGCGTTC GGACCTGCA CCCCAGCGGC CCGCGCGCGC CGCCGCGCGC 60  
 GGCTTTTGT GTCTCCGCTT CCTCGGCGCG CGCCGCTCT GGACCGGAG CGCGCGCGC 120  
 CGGAGCTTGG GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCGGCGC AGGATCCGAG 180  
 AGAGGCGCGG GCGGGTGGCC GGGGGCGCGC CGGCGCCGCG CATGGAGCTC CGGGCCGAG 240  
 70 GCTGTGGGCT GCTATGTGCG GCGCGAGCGC TGGTGGCTG CCGCGCGCGG GACCGGCGCA 300  
 GCAAGAGCCG GAGCTGCGGC GAGGTCCGCC AGATCTACGG AGCCAAGGC TTGAGCTTGA 360  
 GCGACGTGCC CAGGCGGAG ATCTCGGGTG AGCACTGGG GATCTGTCCC CAGGGCTACA 420  
 CCTGTGTCAC CAGGAGATG GAGGAGAACC TGGCCAAAC CAGCCATGCC GAGCTGGAGA 480  
 CCGGCTTCGG CAGCAGCAGC CGCTCTGTC AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540  
 75 TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGGG GACGCTGCG GGCACCTTCC 600  
 CCGGCGCCTT CGGAGAGCTG TACAGCAGA ACGCGAGGGC CTTCCGGGAC CTGTACTCAG 660  
 AGCTGCGCCT CATCTACCGG GGTGCCAACC TGCACTTGA GGAGACGCTG GCGGAGTTCT 720  
 GGGCGCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCTGATG 780  
 ACTACCTGGA CTGCTGGGG AAGCAGGCGG AGGCGCTGG GCGCTTGGG GAGGCCCGGA 840  
 80 GAGAGCTGCG CCGCGGCGCC ACCCGTGCTT TCGTGGCTGC TCGCTCCTTT GTGAGGGGCC 900  
 TGGGCGTGGC CAGCGAGCTG GTCCGGAAG TGGCTCAGGT CCCCCTGGGC CGGAGTGCT 960  
 CGAGAGCTGT CATCAAGCTG GTCTACTGTG CTCACGTGCT GGGAGTCCCC GCGCCAGGCT 1020  
 CCGCTGCTGA CTATTGCGGA AATGTGCTCA AGGGCTGCTT TGCCAAACAG GCGACCTGG 1080  
 AGCGCGATG GAGGAACCTC CTGGAATCCA TGGTGTCTAT CACCGACAAG TTTGGGGTA 1140  
 CATCGGTGTG GAGAGGTGTC ATCGGCAGCG TGACACGCTG GCTGCGGAG GCCATCAAG 1200

5  
10  
15  
20  
25  
30  
35  
40

```

CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGGAAACCCCA 1260
AGSTCAACCC CCAGGGCCCT GGGCCTGAGG AGAAGCGGCG CCGGGGCAAG CTGGCCCCGC 1320
GGGAGAGGCC ACCTTCAGGC ACGCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
GGGACGTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC 1440
TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGATGGC CAGAGGCCGG TACCTCCCCG 1500
AGGTCAATGG TGACGGCCTG GCCAACCA TCAACAACCC CGAGGTGGAG GTGGACATCA 1560
CCAAGCCGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCCGC 1620
TGCGCAGGCG CTACAACGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG 1680
GCTCGGGCAG CGGTGATGGC TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA 1740
GCTCCAGCTC CGGACGCCCC TTGACCCATG CCTTCCAGG CCTGTGAGAG CAGGAAGGAC 1800
AGAAGACCTC GGTGAGCAGC TGCCCCCAGC CCCCAGCTT CTCTCTGCCC CTCTCTCTCT 1860
TCCTGGCCCT TACAGTAGCC AGGCCCCGGT GCGGTAACT GCCCCAAGGC CCCAGGGACA 1920
GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGAGC ATATTTAATT CACCTCAGCC 1980
TGGAGAGGCC TGGGGTGGGA CAGGGAGGCG CGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040
GTCCAGCCCC CAGGCTGGC CTGCGCTGCC TTCTGCCTT TTAATTTTGT ATGAGGTCTT 2100
CAGGTCACTC GGTGAGCAGT GTGCCCAAAA GGCATGTATT TCAGGGACCT CAGGGGCACC 2160
TCCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGCAACGCGC CAGAAGCAGC CCTTCGAGGC 2220
CTACAGAGGA GGCTCAAAAG CAACCCGCTG GAGCCACAGC CGAGCCTGTG CCTTCTCTCC 2280
CGCTTCTTCC CACTGGGACT CCCAGCAGAG CCCACAGGCC AGCCCTGGCC CACCCCCCAG 2340
CTCCAGAGA AGCCCGCAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400
TCTGAGATGA TGCATGATGC CTCCCTCA GCGCAGGCTG CAGAGCCCGC CCCCACCTCC 2460
CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGTGACGCGC TGAGACAGCA CCATGCTGA 2520
GGAGTCTGAG GACTGTCTTC CCACAGACCC TGCACTGAGG GGCCTCCAT GCGCAGATGA 2580
GGGGCACTG ACCCACTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCCAG 2640
GGAGGCAGCG TGGGCTCTGC CAATGTGGGC TGCCCCCGC ACACAGGGCT CACAGGGCAG 2700
GCCTTCTGCG GGTCCAGGGC GTTTGAGGGA CCCCAGGGGC TGAGGAGCAG CCAGGACCCG 2760
CCTGTCTCCA TCCTCACCCA GATCAGGAAC CAGGGCTCTC CTGTTCAGG TGACACAGGT 2820
CAGGGCTCAG AGTGACCTTC GGCTGTCAAC TGCTCACAGG GATGCTGGTG GCTGTGAGA 2880
CCCCGCACTG CACACGGGAA TGCTAGGTC CCTTCCGAC CCAGCCAGCT GCACTGCAAG 2940
GCACGGGAGC CTGATAGTT AAGGGCTTT CCAACATGCG ATCCATTAC TGACACTTCC 3000
TGTCCTTGT TGTGAGAGG GTTCTGCTCC TCCAGATGG CTTGAGGGC CCGCAGGGCC 3060
CACCTTGGAC CCTGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120
CTGGAGGGGC CCTCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGTGG 3180
TGTGGTGTG GGAAGGGTTC CTGAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
TCCTGAACCG ACTGACCTG AGGAGGGCGC TTATGTCTGC TTGTCTTTC ATCACCGTCC 3300
CGCACGTGG ACGGAGGTCC CCGGTTGCTG GTCAGTCCC CATGGCTGT TCTCTGGAAC 3360
CTGACITTAG ATGTTTTGGG ATCAGGAGCC CCCACACAG GCAAGTCCAC CCCATAATA 3420
CCTTGCCAGT GCCAGGGTGG GCTGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTCA TGGTCAGGG AGTGCCCAAG CCTGTCTGT 3600
CTTCTCTCA CAAGGTCCCC CCACCGCTCA GTGTACGCG GTGACGTGTG TTCTTTTGG 3660
TCCTTGTATG AATAAAGGC TGAACCTA AA 3692

```

45 Seq ID NO: C74 DNA Sequence  
Nucleic Acid Accession #: BC030205.1  
Coding sequence: 45..878

50  
55  
60  
65  
70  
75

```

1 11 21 31 41 51
| | | | |
GTGAGCAGCC CTAACAGGC TGTTACTTCA CTACAACGTA CGATATGATC ATCTTAATTT 60
ACTTATTCTT CTGCTATGCG GAAGACACTC AAGGATGGGG ATTCAAGGAT GGAATTTTTC 120
ATAACTCCAT ATGGCTTGAA CGAGCAGCCG GTGTGTACCA CAGAGAAGCA CGGTCTGGCA 180
AATACAAGCT CACCTAOCGA GAAGCTAAGG CGGTGTGTGA ATTTGAAGGC GGCCATCTCG 240
CAACTTACAA CGAGCTAGAG GCAGCCAGAA AAATTGGATT TCATGTCTGT GCTGCTGGAT 300
GGATGGCTAA GGGCAGAGTT GGATACCCCA TTGTGAAGCC AGGGCCCAAC TGTGATTG 360
GAAAAACTGG CATTATTGAT TATGGAATCC GTCTCAATAG GAGTGAAGA TGGGATGCTT 420
ATTGTACAA CCCACACGCA AAGGAGTGTG GTGGCGTCTT TACAGATCCA AAGCAAATTT 480
TTAAATCTCC AGGCTTCCCA AATGAGTACG AAGATAACCA AATCTGCTAC TGGCACATTA 540
GACTCAAGTA TGGTCAGCGT AITCACTGTA GTTTTTTGA TTTTGACCTT GAAGATGACC 600
CAGGTTGCTT GGCTGATTAT GTTGAATAT ATGACAGTTA CGATGATGTC CATGGCTTTG 660
TGGGAAGATA CTGTGAGAT GAGCTTCCAG ATGACATCAT CAGTACAGGA AATGTCATGA 720
CCTTGAAGTT TCTAAGTAT GCTTCAGTGA CAGCTGGAGG TTTCCAAATC AAATATGTTG 780
CAATGGATCC TGTATCCAAA TCCAGTCAAG GAAAAAATAC AAGTACTACT TCTACTGGAA 840
ATAAAAACCT TTTAGCTGGA AGATTTAGCC ACTTATAAAA AAAAAAAGG GATGATCAAA 900
ACACACAGTG TTTATGTTGG AATCTTTTGG AACTCCCTTG ATCTCACTGT TATTATTAAC 960
ATTATTTTAT TATTTTCTTA AATGTGAAAG CAATACATAA TTTAGGGAAA ATTGGAAAA 1020
ATAGGAAACT TTAACAGAGA AAATGAARCC TCTCATAATC CCACTGCATA GAAATAACAA 1080
CGGTTAACAT TTTTATATTT TTTTCTTTCA GTCATTTTTT TATTTGTGGT ATATGTATAT 1140
ATGTACCTAT ATGTATTTGC ATTGAAATTT TTGGAATCCT GCTCTATGTA CAGTTTTGTA 1200
TTATATCTTT TAAATCTTGA ACTTTATAAA CAITTTCTGA AATCATTGAT TATTCTACAA 1260
AAACATGATT TTAACAGCT GTAAAATATT CTATGATATG AATGTTTTAT GCATTATTTA 1320
AGCCTGTCTC TATTGTTGGA ATTTGAGTTC ATTTTCATAA ATATTGTTGC AATAAATATC 1380
CTTGAACACA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA 1430

```

80 Seq ID NO: C75 DNA Sequence  
Nucleic Acid Accession #: NM\_001982.1  
Coding sequence: 199..4227

```

1 11 21 31 41 51
| | | | |
CTCTCACACA CACACACCCC TCCCCTGCCA TCCCTCCCCG GACTCCGGCT CCGGCTCCGA 60
TTGCAATTTG CAACCTCCGC TGCCGTGCGC GCAGCAGCCA CCAATTCGCC AGCGGTTTCA 120

```



	GTGGCTCTTG	CCTCGATGTC	CTAGCCTAGG	GGCCCCCGGG	COGGACTTGG	CTGGGCTCCC	180
	TTACCCCTCT	GCGGAGTCAT	GAGGGCGAAC	GACGCTCTGC	AGGTGCTGGG	CTTGCTTTTC	240
	AGCCTGGCCC	GGGGCTCCGA	GGTGGGCAAC	TCTCAGGCAG	TGTGTCTCTG	GACTCTGAAT	300
5	GGCCTGAGTG	TGACCGGCGA	TGCTGAGAAC	CAATACCAGA	CACTGTACAA	GCTCTACGAG	360
	AGGTGTGAGG	TGGTGTATGG	GAACCTTGAG	ATTGTGCTCA	CGGGACACAA	TGCCGACCTC	420
	TCCTTCCCTG	AGTGGATTGG	AGAAGTGACA	GGCTATGTCC	TCGTGGCCAT	GAATGAATTC	480
	TCTACTCTAC	CATTGCCCAA	CCTCCGCGTG	GTGCGAGGGA	CCCAGGTCTA	CGATGGGAAG	540
	TTTGCCATCT	TCGTCATGTT	GAACATAAAC	ACCAACTCCA	GCCACGCTCT	GCGCCAGCTC	600
10	CGCTTGATCT	AGCTCACCGA	GATTCTGTCA	GGGGTGTGTT	ATATTGAGAA	GAACGATAAG	660
	CTTTGTGACA	TGGACACAAT	TGACTGGAGG	GACATCGTGA	GGGACCGAGA	TGCTGAGATA	720
	GTGGTGAAGG	ACATGGGACG	AAGCTGTCCC	CCCTGTCTAT	AGGTTTGCAA	GCGGCGATGC	780
	TGGGGTCTTG	GATCAGAAGA	CTGCCAGACA	TTGACCAAGA	CCATCTGTGC	TCCTCAGTGT	840
	AATGGTCACT	GCTTTGGGGC	CAACCCCAAC	CAGTGCTGCC	ATGATGAGTG	TGCCGGGGGC	900
15	TGCTCAGGCC	CTCAGGACAC	AGACTGCTTT	GCCTGCCGGC	ACTTCAATGA	CAGTGGAGCC	960
	TGTGTACCTC	GCTGTCCACA	GCCTCTTGTG	TACAACAAGC	TAACTTTCCA	GCTGGAACCC	1020
	AATCCCAACA	CCCTGGACCG	GTATGGAGGA	GTTTGTGTAG	CCAGCTGTCC	CCATAACTTT	1080
	GTGGTGGATC	AAACATCCTG	TGTCAGGGCC	TGTCTCTCTG	ACAAGATGGA	AGTAGATAAA	1140
	AATGGGCTCA	AGATGTGTGA	GCCTTGTGGG	GGACTATGTC	CCAAAGCCTG	TGAGGGAACA	1200
20	GGCTCTGGGA	GCGGCTTCCA	GACTGTGGAC	TCGAGCAACA	TTGATGGATT	TGTGAACCTG	1260
	ACCAAGATCC	TGGGCAACCT	GGACTTTCTG	ATCACCGGCC	TCAATGGAGA	CCCTTGGCAC	1320
	AAGATCCCTG	CCCTGGACCC	AGAGAAAGCTC	AATGTCTTCC	GGACAGTACG	GGAGATCACA	1380
	GGTTACCTGA	ACATCCAGTC	CTGGCCGCCC	CACATGCACA	ACTTCAGTGT	TTTTTCCAAT	1440
	TTGACAACCA	TTGGAGGCAG	AAGCCTCTAC	AACCGGGGCT	TCTCATGTTT	GATCATGAAG	1500
25	AACTTGAATG	TCACATCTCT	GCGCTTCCGA	TCCCTGAAGG	AAATTAGTGC	TGGGGGTATC	1560
	TATATAAGTG	CCAATAGGCA	GCTCTGTCTC	CACCACTCTT	TGAATGGAC	CAAGGTGCTT	1620
	CGGGGGCCTA	CGGAGAGGCG	ACTAGACATC	AAGCATAATC	GGCCGCGCAG	AGACTGCGTG	1680
	GCAGAGGGCA	AAGTGTGTGA	CCCACTGTGC	TCTCTGGGGG	GATGCTGGGG	CCCAGGCCCT	1740
	GGTCAGTGCT	TGTCCTGTGC	AAATTATAGC	CGAGGAGGTG	TCTGTGTGAC	CCACTGCAAC	1800
30	TTTCTGAATG	GGGAGCCTCG	AGAATTGGCC	CATGAGGCGG	AATGCTTCTC	CTGCCACCCG	1860
	GAATGCCAAC	CCATGGGGGG	CAGTGCACCA	TGCAATGGCT	CGGGCTCTGA	TACTTGTGCT	1920
	CAATGTGCCC	ATTTTGTAGA	TGGGCCCCAC	TGTGTGAGCA	GCTGCCCCCA	TGGAGTCCCTA	1980
	GGTGCCAAAG	GCCCAATCTA	CAAGTACCCA	GATGTTTACA	ATGAATGTGC	GGCCTGCCAT	2040
	GAGAACTGCA	CCCGGGGGTG	TAAAGGACCA	GAGCTTCAAG	ACTGTTTAGG	ACAAACACTG	2100
35	GTGCTGATCG	GCAAAACCCA	TCTGACAATG	GCTTTGACAG	TGATAGCAGG	ATTGGTAGTG	2160
	ATTTTTCATGA	TGCTGGGCGG	CACCTTTCTC	TACTGGCGTG	GGGCGCGGAT	TCAGAAATAA	2220
	AGGGCTATGA	GGCGATACCT	GGAAACGGGT	GAGAGCATAG	AGCCTCTGGA	CCCCAGTGAG	2280
	AAGGCTAACA	AAGTCTTGGC	CAGAATCTTC	AAAGAGACAG	AGCTAAGGAA	GCTTAAAGTG	2340
	CTTGGCTCGG	GTGTCTTTGG	AACGTGTCAC	AAAGGAGTGT	GGATCCCTGA	GGGTGAATCA	2400
40	ATCAAGATTC	CAGTCTGCAT	TAAAGTCATT	GAGGACAAGA	GTGGACGGCA	GAGTTTTCAA	2460
	GCTGTGACAG	ATCATATGCT	GGCCATTGGC	AGCCTGGACC	ATGCCACCAT	TGTAAAGGCTG	2520
	CTGGGACTAT	GCCCAAGGTC	ATCTCTGCAG	CTTGTCACTC	AATATTGTCC	TCTGGGTCTC	2580
	CTGCTGGATC	ATGTGAGACA	ACACCGGGGG	GCACTGGGGC	CACAGCTGCT	GCTCAACTGG	2640
	GGAGTACAAA	TTGCCAAGGG	AATGTACTAC	CTTGAAGAAC	ATGGTATGGT	GCATAGAAAC	2700
45	CTGGCTGCCC	GAAAGGTGCT	ACTCAAGTCA	CCAGTTCAGG	TTCAAGTGGC	AGATTTTGGT	2760
	GTGGCTGACC	TGCTGCCCTC	TGATGATAAG	CAGTGTCTAT	ACAGTGAGGC	CAAGACTCCA	2820
	ATTAAGTGGG	TGGCCCTTGA	GAGTATCCAC	TTTGGGAAT	ACACACACCA	GATGTAGTGC	2880
	TGGAGCTATG	GTGTGACAGT	TTGGGAGTTG	ATGACCTTCG	GGGCAGAGCC	CTATGCAGGG	2940
	CTACGATTGG	CTGAAGTACC	AGACCTTGCTA	GAGAAGGGGG	AGCGTGTGGC	ACAGCCCCAG	3000
50	ATCTGCACAA	TTGATGTCTA	CATGGTGATG	GTCAAGTGTG	GGATGATTGA	TGAGAACATT	3060
	CGCCCAACCT	TTAAAGAACT	AGCCAATGAG	TTCAACAGGA	TGGCCCGAGA	CCCAACACGG	3120
	TATCTGGTCA	TAAAGAGAGA	GAGTGGGCCT	GGAAATAGCC	CTGGGCCACA	GCCCCATGGT	3180
	CTGACAAACA	AGAAGCTAGA	GGAAGTAGAG	CTGGAGCCAG	AACCTAGACCT	AGACCTAGAC	3240
	TTGGAAGCAG	AGGAGGACAA	CCTGGCAACC	ACCACACTGG	GCTCCGCCCT	CAGCCTACCA	3300
55	GTGGGAACAC	TTAATCGGCC	ACGTGGGAGC	CAGAGCCTTT	TAAGTCCATC	ATCTGGATAC	3360
	ATGCCCATGA	ACCAGGGTAA	TCTTGGGGGG	TCTTGGCCAG	AGTCTGCAGT	TTCTGGGAGC	3420
	AGTGAACCGT	GCCCCCGTCC	AGTCTCTCTA	CACCCAATGC	CAOGGGATG	CCTGGCATCA	3480
	GAGTCATCAG	AGGGGCATGT	AACAGGCTCT	GAGGCTGAGC	TCCAGGAGAA	AGTGTCAATG	3540
	TGTAGAAGCC	GGAGCAGGAG	CCGAGGCCCA	CGGCCACGGG	GAGATAGCGC	CTACCATTCC	3600
60	CAGCGCCACA	GCTGCTGAC	TCTGTATTAC	CCACTCTCCC	CACCCGGGTT	AGAGGAAGAG	3660
	GATGTCAACG	GTTATGTGAT	GCCAGATACA	CACCTCAAGG	GTACTCCCTC	CTCCCGGGAA	3720
	GGCACCCCTT	CTTCAGTGGG	TCTCAGTTCT	GTCCTGGGTA	CTGAAGAAGA	AGATGAAGAT	3780
	GAGGAGTATG	AATACATGAA	CCGAGGAGGA	AGGCACAGTC	CACCTCATCC	CCCTAGGCCA	3840
	AGTTCGCCCT	AGGAGCTGGG	TTATGAGTAC	ATGGATGTGG	GGTCAGACCT	CAGTGCCTCT	3900
65	CTGGGCAGCA	CACAGAGTTG	CCCCTCCAC	CCTGTACCCA	TCATGCCCAC	TGCAGGCACA	3960
	ACTCCAGATG	AAGACTATGA	ATATATGAAT	CGGCAACGAG	ATGGAGGTGG	TCCTGGGGGT	4020
	GATTATGACG	CCATGGGGGC	CTGCCACGCA	TCTGAGCAAG	GATATGAAGA	GATGAGAGCT	4080
	TTTCAGGGGC	CTGGACATCA	GGCCCCCAT	GTCCATTATG	CCCGCCTAAA	AACCTACAGT	4140
	AGCTTAGAGG	CTACAGACTC	TGCCTTTGAT	AACCTGATT	ACTGGCATAG	CAGGCTTTTC	4200
70	CCCAAGGCTA	ATGCCAGAG	AACGTAACCT	CTGCTCCCTG	TGGCACTCAG	GGAGCAITTA	4260
	ATGGCAGCTA	GTGCCCTTAG	AGGGTACCGT	CTTCTCCCTA	TTCCCTCTCT	CTCCAGGCTC	4320
	CCAGGCCCTT	TTCGCCAGTG	CCAGACAATT	CCATTCAATC	TTTGGAGGCT	TTTAAACATT	4380
	TTGACACAAA	ATTCCTATGG	TATGTAGCCA	GCTGTGCACT	TTCTCTCTTT	TCCCAACCCC	4440
	AGGAAAGGTT	TTCCCTATT	TGTGTGCTTT	CCAGTCCCA	TTCTCTCAGT	TCTTCAACAG	4500
75	CACCTCTGGA	GATATGAAGG	ATTACTCTCC	ATATCCCTTC	CTCTCAGGCT	CTTGACTACT	4560
	TGGAACTAGG	CTCTTATGTG	TGCCCTTTGT	TCCCATCAGA	CTGTCAAGAA	GAGGAAAGGG	4620
	AGGAAACCTA	GCAGAGGAAA	GTGTAATTTT	GGTTTATGAC	TCTTAACCCC	CTAGAAAGAC	4680
	AGAAAGCTAA	AATCTGTGAA	GAAGAGGTTT	AGGAGTAGAT	ATTGATTACT	ATCATAATTC	4740
	AGCACTTAAC	TATAGCCAG	GCATCATACT	AACTTCACC	TACATTACT	CACCTAGTTC	4800
80	TTTATCATCC	TTAAACAAT	TCTGTGACAT	ACATATTATC	TCAITTTTACA	CAAAGGGAAG	4860
	TGGGCGATGG	TGGCTCATGC	CTGTAACTCT	AGCACTTTGG	GAGGCTGAGG	CAGAAGGATT	4920
	ACCTGAGGCA	AGGAGTTTGA	GACCACTTGA	GCCAAACATG	TAAAGCCGCC	ATCTC	4975

Nucleic Acid Accession #: NM\_001216.1  
Coding sequence: 43..1422

```
5 1 11 21 31 41 51
| | | | |
GCCCCATACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 60
AGCCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
10 AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC TGGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATACAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
AATAATGCCC ACAGGACAA AGAAGGGGAT GACCAGAGTC ATTGGGCTA TGGAGGCGAC 480
15 CGCCCTGGC CCGCGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC 540
CGCCCCCAGC TCGCCGCTTC CTGCCCAGCC CTGGGCCCCC TGGAACTCCT GGGCTTCCAG 600
CTCCCGCCAG CCGCAGAACT GCGCCTGCGC AACAAATGGCC ACAGTGTGCA ACTGACCCCTG 660
CCTCTGGGCG TAGAGATGGC TCTGGGTCCC GGGCGGAGT ACCGGCTCT GCAGCTGCAT 720
CTGCACTGGG GGGCTGTCAG TCGTCCGCGC TCGGAGCACA CTGTGGAGG CCACGTTTC 780
20 CCTGCGAGA TCCAGTGGT TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCCCTG 840
GGGCGCCCGG GAGGGCTGGC CGTGTGCGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
AGTGCTATAG AGCAATGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
CAGGTCCAGG GACTGGAGAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020
TATGAGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGAC TGTGTTTAA 1080
25 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCTT GTGGGACCT 1140
GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGAGC CTTTGAATGG GCGAGTGATT 1200
GAGGGCTCCT TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATTCTGCTC TGCTGCTGG TGACATCTTA GCCCTGGTTT TTGGCTCCT TTTTGTGCTC 1320
ACCAAGCGCG CGTCTCTGTG GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGTG 1380
30 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GAGGCCGTA ACTGTCTGT CTTGCTCATT 1500
ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT 1552
```

Seq ID NO: C77 DNA Sequence

Nucleic Acid Accession #: NM\_004207.1  
Coding sequence: 63..1460

```
35 1 11 21 31 41 51
| | | | |
GGGAGAGGCG GGGCTGAGGC GGGCCAGCGG CGGCAGGTGA GGGGGAACCA ACCCTCCTGG 60
40 CCATGGGAGG GGCCTGTGTT GACGAGGGCC CCACAGGCGT CAAGGCCCTT GACGGCGGCT 120
GGGGCTGGCG CGTGTCTTTC GGCTGTTTCG TCATCACTGG CTTCTCTAC GCCTTCCCA 180
AGGCGCTCAG TGCTTCTTTC AAGGAGCTCA TACAGGAGTT TGGGATCGGC TACAGCGACA 240
CAGCCTGGAT TCTCTCCATC CTGCTGGCCA TGCTCTACGG GACAGGTCCG CTCTGCAGTG 300
45 TGTGGGTGAA CCGCTTTGGC TGCCGGCCCG TCATGCTTGT GGGGGGTCTC TTTGCGTGGC 360
TGGGCATGTT GGTGTGCTCC TTTTGCAGGA GCATCATCCA GGTCTACCTC ACCACTGGGG 420
TCATCAGCGG GTTGGGTTTG GCACTCAACT TCCAGCCCTC GCTCATCATG CTGAACCGCT 480
ACTTCAGCAA GCGCGCGCCC ATGGCCAAAG GGTGCGCGGC AGCAGGTAGC CCTGTCTTCC 540
TGTGTGCCCT GAGCCGCTG GGGCAGCTGC TGCAGGACCG CTACGGCTGG CGGGCGGCT 600
50 TCTTCATCCT GGGCGGCTG CTGCTCAACT GCTGCGTGTG TGCCGCACTC ATGAGGCCCC 660
TGTGTGTCAC GGCCTAGCGG GGTCTGCGGC CGCCGCGACC CTCCCGCGCG CTGCTAGACC 720
TGAGCGTCTT CCGGGAACGC GGCTTTGTGC TTTACGCCGT GGCCGCTCG GTCATGGTGC 780
TGGGGCTCTT CGTCCGCCC GTGTTCTGTG TGAGCTACGC CAAGGACCTG GGGGTGCCCG 840
ACACCAAGGC CGCCTTCTG CTCACCATCC TGGGCTTCAT TGACATCTTC GCGCGGCGCG 900
55 CCGCGGCTT CGTGGCGGGG CTTGGGAAGG TGCGGCCCTA CTCGTCTAC CTCTTCAGCT 960
TCTCCATGTT CTTCAAGCGC CTGCGGACC TGCGGGGCTC TACGGCGGGC GACTACGGCG 1020
GCCTGTGCTT TCTCTGATC TCTCTACGG CATGTGGGG CATGTGGGG GGCCTGAGT 1080
TCGAGGTGCT CATGGGCATC GTGGGACCCC ACAAGTCTC CAGTGCCATT GGCCTGGTGC 1140
TGCTGATGGA GCGCGTGGC GTGCTCGTGG GGCCTCTTTC GGGAGGCAAA CTCCTGATG 1200
60 CGACCCAGCT CTACATGTAC GTGTTCATCC TGGCGGGGCG CGAGGTGCTC ACCTCCTCCC 1260
TGATTTTGCT GCTGGGCAAC TTCTTCTGCA TTAGGAAGAA GCCCAAAGAG CCACAGCCCTG 1320
AGGTGCGCGC CCGGAGGAG GAGAAGCTCC ACAAGCCTCC TGCACTCTCG GGGGTGGACT 1380
TGCGGAGGCT GGAGCATTTC CTGAAGGCTG AGCCTGAGAA AAGCGGGGAG GTGGTTCACA 1440
CCCGGGAAC AAGTGTCTGA GTGGCTGGGC GGGCGCGGCA GGCACAGGGA GGAGGTACAG 1500
65 AAGCCGCAAA CGCTGTCTAT TTATTTTACA AACTGGAGTG GCTCAGGCAG GGCACGGCT 1560
GGGCTCCAGC TGCCGGCCCA GCGGATCGTC GCCCGATCAG TGTTTTGAGG GGAAGGTGG 1620
CGGGGTGGGA ACCGTGTCTAT TCCAGAGTGG ATCTGCGGTG AAGCCAAGCC GCAAGGTATC 1680
AAGGCATCCT CACCAAGGGC CCGCCTGCT GCTCCAGGT GGCCTGCGCG CACTGCTATG 1740
CTCAAGGACC TGGAAACCCA TGCTTCGAGA CAACGTGACT TTAATGGGAG GGTGGGTGGG 1800
70 CGCAGACAG GCTGGCAGGG CAGGTGCTGC GTGGGCGCT CTCCAGCCCG TCTTACCCCTG 1860
GGCTCACATG GGGCTGTGTC CCAACCTCTT TGAGTGTCTT GGGGACAGCT CTTTCCACCC 1920
CTGGAAGATG GAAATAAAC TCGTGTGGG TGGAGTGTTC TCGTCCGAA TTCAAAAGC 1980
TT 1982
```

Seq ID NO: C78 DNA Sequence

Nucleic Acid Accession #: NM\_000358.1  
Coding sequence: 48..2099

```
80 1 11 21 31 41 51
| | | | |
GCTTGGCCGT CGTCTGCTAG CTGCTCGGT GCGCGTGTGC CGCTCCATG GCGCTCTTGG 60
TGCGGCTGCT GGTCTCTGCC CTGGCTCTGG CCTTGGGCC CGCCGCGACC CTGGCGGGTC 120
CGCCCAAGTC GCGCTACAG CTGGTGTGTC AGCACAGCAG GCTCGGGGCG GCCACGACAG 180
GCCCCAACGT GTGTGCTGTG CAGAAGGTTA TTGGCACTAA TAGGAAGTAC TTCACCACT 240
```

5	GCAAGCAGTG	GTACCAAAGG	AAAACTCTGTG	GCAAAATCAAC	AGTCATCAGC	TACGAGTGCT	300
	GTCCCTGGATA	TGAAAAGGTC	CCTGGGGAGA	AGGGCTGTCC	AGCAGCCCTA	CCACTCTCAA	360
	ACCTTTACGA	GACCCCTGGG	GTCCGTTGGAT	CCACCACCAC	TCAGCTGTAC	ACGGACCGCA	420
	CGGAGAGCT	GAGGCCTGAG	ATGGAGGGGC	CCGGCAGCTT	CACCATCTTC	GCCCCTAGCA	480
	ACGAGGCTG	GGCCTCCTTG	CCAGCTGAAG	TGCTGGACTC	CCTGGTCAGC	AATGTCAACA	540
	TTGAGCTGCT	CAATGCCCTC	CGCTACCATA	TGGTGGGCAG	GCGAGTCTCT	ACTGATGAGC	600
	TGAAAACACGG	CATGACCCCTC	ACCTCTATGT	ACCAGAATTC	CAACATCCAG	ATCCACCACT	660
	ATCCTAATGG	GATTGTAAC	GTGAAGTGTG	CCCGGCTCCT	GAAAAGCCGAC	CACCATGCAA	720
10	CCAAACGGGT	GGTGACCTC	ATCGATAAGG	TCATCTCCAC	CATCACCAAC	AACATCCAGC	780
	AGATCATTTGA	GATCGAGGAC	ACCTTTGAGA	CCCTTCGGGC	TGCTGTGGCT	GCATCAGGGC	840
	TCAACACGAT	GCTTGAAGGT	AACGCCAGT	ACACGCTTTT	GGCCCCGACC	AATGAGGCCT	900
	TCGAGAAGAT	CCCTAGTGTG	ACTTTGAACC	GTATCCTGGG	CGACCCAGAA	GCCCTGAGAG	960
	ACCTGTCTGAA	CAACCAATC	TTGAAGTCAG	CTATGTGTGC	TGAAGCCATC	GTTCGGGGGC	1020
	TGCTGTGAGA	GACCTCTGAG	GGCAGCAGC	TGGAGGTGGG	CTGCAGCGGG	GACATGCTCA	1080
15	CTATCAACCG	GAGCGCGATC	ATCTCCAATA	AAGACATCCT	AGCCACCAAC	GGGGTGATCC	1140
	ACTACATTGA	TGAGCTACTC	ATCCCAAGT	CAGCCAAGAC	ACTATTTGAA	TTGGCTGCAG	1200
	AGTCTGATGT	GTCCACAGCC	ATTGACCTTT	TCAGACAAGC	CGGCCCTCGG	AATCATCTCT	1260
	CTGGAAGTGA	CGGTTTGACC	CTCCTGGCTC	CCCTGAATTC	TGTATTCAAA	GATGGAAACC	1320
	CTCCAATTGA	TGCCCATACA	AGGAATTTGC	TTCCGAAACCA	CATAATTAAA	GACCAGCTGG	1380
20	CCTCTAAGTA	TCTGTACCAT	GGACAGACCC	TGGAACTCT	GGCGGCCAAA	AAACTGAGAG	1440
	TTTTTGTTTA	TGTAATAGC	CTCTGCATTC	AGAACAGCTG	CATCGCGGCC	CACGACAAGA	1500
	GGGGGAGGTA	CGGAGCCCTG	TTCAAGATGG	ACCGGGTGCT	GACCCCCCCA	ATGGGGACTG	1560
	TCATGGAATGT	CCTGAAGGGA	GACAAATCGT	TTAGCATGCT	GGTAGCTGCC	ATCCAGTCTG	1620
25	CAGGACTGAC	GGAGACCCCT	AACCGGGGAG	GAGTCTACAC	AGTCTTTGCT	CCCAACAATG	1680
	AAGCCTTCGG	GAGCCTGCCA	CCAAGAGAAC	GGAGCAGACT	CTTGGGAGAT	GCCAAGGAAC	1740
	TTGCCAACAT	CCTGAAATAC	CACATTGGTG	ATGAAATCCT	GGTTAGCGGA	GGCATCGGGG	1800
	CCCTGGTGGC	GCTAAAGTCT	CTCCAAGGTG	ACAAGCTGGA	AGTCAGCTTG	AAAAACAATG	1860
	TGGTGAGTGT	CAACAAGGAG	CCTGTTGGCG	AGCCTGACAT	CATGGCCACA	AATGGCGTGG	1920
30	TCCATGTCTC	CACCAATGTT	CTGCAGCCTC	CAGCCAAACG	ACCTCAGGAA	AGAGGGGATG	1980
	AACTTGCAGA	TCTGCGCTT	GAGATCTTCA	AACAAGCATC	AGCGTTTTCC	AGGGCTTCCC	2040
	AGAGGTCTGT	GCGACTAGCC	CCTGTCTATC	AAAAGTTATT	AGAGAGGATG	AAGCATTAGC	2100
	TTGAAGCACT	ACAGGAGGAA	TGCACCAACG	CAGCTCTCCG	CCAATTTCTC	TCAGATTTCC	2160
	ACAGAGACTG	TTTGAATGTT	TTCAAAACCA	AGTATCACAC	TTTAATGTAC	ATGGGCCGCA	2220
35	CCATAATGAG	ATGTGAGCCT	TGTGCATGTG	GGGGAGGAGG	GAGAGAGATG	TACTTTTTAA	2280
	ATCATGTTC	CCCTAAACAT	GGCTGTTAAC	CCAATGATG	CAGAACTTG	GATGTCACTG	2340
	CCTGACATTC	ACTTCCAGAG	AGGACCTATC	CCAATGTGG	AATTGACTGC	CTATGCCAAG	2400
	TCCCTGGAAA	AGGAGCTTCA	GTATTGTGGG	GCTCATAAAA	CATGAATCAA	GCAATCCAGC	2460
	CTCATGGGAA	GTCTTGGCAC	AGTTTTTGTA	AAGCCCTTGC	ACAGCTGGAG	AAATGGCATC	2520
40	ATTATAAGCT	ATGAGTTGAA	ATGTTCTGTC	AAATGTGTCT	CACATCTACA	CGTGGCTTGG	2580
	AGGCTTTTAT	GGGGCCCTGT	CCAGGTAGAA	AAGAATGGT	ATGTAGAGCT	TAGATTTCCC	2640
	TATGTGACA	GAGCCATGGT	GTGTTGTGTA	TAATAAAACC	AAAGAAACAT	A	2691

45 Seq ID NO: C79 DNA Sequence  
Nucleic Acid Accession #: NM\_006536.2  
Coding sequence: 109..2940

50	1	11	21	31	41	51	
	ACCTAAAACC	TTGCAAGTTC	AGGAAGAAAC	CATCTGCATC	CATATTGAAA	ACCTGACACA	60
	ATGTATGCAG	CAGGCTCAGT	GTGAGTGAAC	TGGAGGCTTC	TCTACAACAT	GACCCAAGG	120
	AGCATTTGCA	GTCTTATTGG	CAACCTGAAG	TTTGTGACTC	TCCTGGTTGC	CTTAAGTTCA	180
	GAACTCCCAT	TCCTGGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
55	ATTGCAATTA	ATCCTCAGGT	ACCTGAGAAT	CAGAACCTCA	TCTCAACAT	TAAGGAAATG	300
	ATAACTGAAG	CTTCAATTTA	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
	ATAAAGATT	TAATACCTGC	CACATGGAAG	GCTAATAATA	ACAGCAAAAT	AAAAACAAGAA	420
	TCATATGAAA	AGGCAAAATG	CATAGTGACT	GACTGGTATG	GGGCACATGG	AGATGATCCA	480
	TACACCTAC	AATACAGAGG	GTGTGGAAAA	GAGGGAAAAAT	ACATTCATTT	CACACCTAAT	540
60	TTCTTACTGA	ATGATAACTT	AACAGCTGGC	TACGATCAC	GAGGCCGAGT	GTTTGTCCAT	600
	GAATGGGGCC	ACCTCCGTTG	GGGTGTGTTT	GATGAGTATA	ACAATGACAA	ACCTTTCTAC	660
	ATAAATGGGC	AAAATCAAAT	TAAAGTGACA	AGGTGTTTAT	CTGACATCAC	AGGCATTTTT	720
	GTGTGTGAAA	AAGGTCCTTG	CCCCAAGAA	AACGTATTTA	TTAGTAAGCT	TTTTAAGAA	780
	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTTCATGCA	840
	AGTTTATCTT	CTGTGGTTGA	ATTTTGTAA	GCAAGTACCC	ACAACCAAGA	AGCACCAAAAC	900
65	CTACAGAAC	AGATGTGCAG	CCTCAGAAAT	GCATGGGATG	TAATCACAGA	CTCTGCTGAC	960
	TTTACACACA	GCCTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCAC	ATTCTCGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCACAGCA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAACAAGCC	GCAGAAATTT	ATTTGATGCA	GATTGTTGAA	1140
70	ATTATACCT	TGCTGGGCAT	TGCCAGTTTC	GACAGCAAGG	GAGAGATCAG	AGCCAGCTA	1200
	CACCAAAATTA	ACAGCAATGA	TGATCGAAAG	TTGCTGGTTT	CATATCTGCC	CACCACTGTA	1260
	TCAGCTAAAA	CAGACATCAG	CATTGTTTCA	GGGCTTAAGA	AAGGATTGGA	GGTGGTTGAA	1320
	AAACTGAATG	GAAAAGCTTA	TGGCTCTGTG	ATGATATTAG	TGACCACGGG	AGATGATAAG	1380
	CTTCTTGCA	ATTGCTTACC	CACCTGTGCTC	AGCAGTGGTT	CAACAATTCA	CTCCATTGGC	1440
75	CTGGGTTTAT	CTGCAGCCCC	AAATCTGGAG	GAATATACAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTT	CAGATATATC	AAACTCCAAT	AGCATGATGG	ATGCTTTTCA	TAGAAATTTCC	1560
	TCCTGAACTG	GAGACATTTT	CCAGCAACAT	ATTGAGCTTG	AAAGTACAGG	TGAAAATGTC	1620
	AAACCTCAC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CCTCTGAGA	TTATATTATT	TGATCTGTAT	1740
80	GGACGAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTGGGAC	AGCTAGTCTT	1800
	TGGATTTCAG	GAAACGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAAACAA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGGCGCT	CCAATCTCAG	TGTGCCCCCA	1920
	GCCACTGTGG	AAGCCTTTTG	GGAAAGAGAC	AGCCTCCATT	TTCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAAACAGGG	ATTTTATCCC	ATTCCTTAATG	CCACTGTGAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

GTTATAAAAA ATGATGGAAT TTAATCGAGG TATTTTTTCT CTTTGTCTGC AAATGGTAGA 2160
TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCAGC. CCACCTCTATT 2220
CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCTT TGATGTGTTT 2400
CCACCATGCA AAATTATTGA CTTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2460
TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAAATG 2520
AGTAAAAGTC TACAGAATAT CCAAGATGAC TTAAACAATG CTATTTTAGT AAATACATCA 2580
AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCCTACC CCAGATTTCCT 2640
ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTATATGT 2700
GCAATAGCAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCGAGCG 2760
CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTGCCC TTATTATAGT TGTGACACAT 2880
CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
ATAAATATCC AAAGTGTCTT CCTCTTAGA TATAAGACCC ATGSCCTTCG ACTACAAAAA 3000
CATACTAACA AAGTCMAATT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060
ATACAGATAA GATTTTATCA TGGTAGATCA ACAATTCTTT TTGGGGGTAG ATTAGAAAAA 3120
CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAGTAATG GTCTTTAAAG 3180
GCAAGGGGAA GGGTAAAGTC GGACCAAGTG CAAGGAAAGT TTGTTTTATT GAGGTGGAAG 3240
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAAGTGTCTG TGTGAAGCAA 3300
TCATTTAGTT ACCTTGATTA ATTTTCTTTT TCTCCTTATC TGTGCAGTAC AGGTGTGCTG 3360
TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAG CTCTTTACCT 3420
CTGTCTATTG TGTCTATAT ATTTAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
TTTATGACAA AGGTCTATTG AATTATTG TGTGTAAGTT TCTACTCCCA TCAAGCAGC 3600
TTTCTAAGTT TATTGCCTTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660
TACCTAGGAA A
  
```

Seq ID NO: C80 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

1 11 21 31 41 51  
 35  
 40  
 45  
 50  
 55  
 60

```

ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC 60
AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATTT 120
TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAAAATGA AATATAGTGG AAACCTAATG 180
AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240
ACATCTAACC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCGATGT CCATCATTTT 300
AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360
TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAAGC TTTCGAAGTA 420
TGGAGTAATG TTACCCCTTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480
GTGGTTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540
CTAGCCCATG CTTTGGACCT TGGATCTGGC ATTGGAGGGG ATGCACATT CTGATGAGGAC 600
GAATTCCTGA CTACACATTC AGGAGGCACA AACTGTGTTT TCACTGCTGT TCAAGGATTT 660
GGCCATTCTT TAGGTCTTGG CCATCTAGT GATCCAAAGG CGTAAATGTT CCCACCTTAC 720
AAATATGTTG ACATCAACAC ATTTGGCCTC TCTGCTGATG ACATACGTGG CATTCACTCC 780
CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGCAAAATC AGAACCCAGT 840
CTCTGTGACC CCAATTTGAG TTTTGTGCT GTCACTACCG TGGGAAATAA GATCTTTTTT 900
TTCAAAGACA GGTCTCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960
ATTCTCTCCT TATGGCCAAC CTGCGCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTT CTAACCTTGT GAAAAAATTT 1140
GATGCAGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAAACCATAT 1200
TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCTGGTT ATCCCAAACT GATTACCAAG 1260
AACTTCCAAG GAATCGGGCC TAAATTTGAT GCATCTTCTT ACTCTAAAAA CAAATACTAC 1320
TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCACAG TATCACCAAA 1380
ACACTGAAAA GCAATAGCTG GTTGGTTTGT TGA
  
```

Seq ID NO: C81 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

65  
 70  
 75  
 80

```

1 11 21 31 41 51
ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC 60
AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATTT 120
TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAAAATGA AATATAGTGG AAACCTAATG 180
AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240
ACATCTAACC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCGATGT CCATCATTTT 300
AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360
TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAAGC TTTCGAAGTA 420
TGGAGTAATG TTACCCCTTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480
GTGGTTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540
CTAGCCCATG CTTTGGACCT TGGATCTGGC ATTGGAGGGG ATGCACATT CTGATGAGGAC 600
GAATTCCTGA CTACACATTC AGGAGGCACA AACTGTGTTT TCACTGCTGT TCAAGCCATT 660
GGCCATTCTT TAGGTCTTGG CCATCTAGT GATCCAAAGG CGTAAATGTT CCCACCTTAC 720
AAATATGTTG ACATCAACAC ATTTGGCCTC TCTGCTGATG ACATACGTGG CATTCACTCC 780
CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGCAAAATC AGAACCCAGT 840
CTCTGTGACC CCAATTTGAG TTTTGTGCT GTCACTACCG TGGGAAATAA GATCTTTTTT 900
TTCAAAGACA GGTCTCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960
ATTCTCTCCT TATGGCCAAC CTGCGCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTT CTAACCTTGT GAAAAAATTT 1140
  
```

5 GATGACGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCACTAT 1200  
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCCTGGT ATCCCAACT GATTACCAAG 1260  
 AACTTCCAAG GAATCGGGCC TAAAATTGAT GCAGTCTTCT ACTCTAAAAA CAAATACTAC 1320  
 TATTCTTCCC AAGGATCTAA CCAATTGAA TATGACTTCC TACTCCAACG TATCACCAAA 1380  
 ACACGAAAA GCAATAGCTG GTTTGGTTGT TGA 1413

Seq ID NO: C82 DNA Sequence  
 Nucleic Acid Accession #: NM\_006952.1  
 Coding sequence: 11..793

10 1 11 21 31 41 51  
 AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCTGTGC TTCCAGGGCC TGCTGATTTT 60  
 TGGAAATGTG ATTATTGGTT GTTGGCGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120  
 15 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180  
 GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCTCTTTC TGCTGTCTCG TTCTAGGCAT 240  
 TGTAGGCATC ATGAAGTCCA GCAGSAAAAT TCTTCTGGCG TATTTCATTC TGAATTTTAT 300  
 AGTATATGCC TTGTAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360  
 20 ACCCAACCTC TTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAACAA 420  
 TGATGACCAAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480  
 CAATTGCTGT GCGGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540  
 TGAGAAATAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600  
 AGAACCTCTC AACCTGGAGG CTGTAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660  
 25 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTGG CCTGGTTTGG 720  
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780  
 AATTGAATAT TAAGAA 796

Seq ID NO: C83 DNA Sequence  
 Nucleic Acid Accession #: NM\_001793.2  
 Coding sequence: 71..2560

30 1 11 21 31 41 51  
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGCCCGTGGC GGCAGTGTCT TCACCCCTCT 60  
 35 CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGGTCT CTCTCCCTTC TCCAGTTTG 120  
 CTGGCTGCAG TGCGCGCCT COGAGCCGTG COGGCGGTG TTCAGGGAGG CTGAAGTGAC 180  
 CTGGAGGGG GAGAGCGGG AGCAGGAGCC CGGCCAGGG CTGGGGAAAG TATTCTATGG 240  
 CTGCCCTGG GAGAGCCAG CTCGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300  
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360  
 40 ATCCAAACGT ATCTTAGCAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420  
 TGAAAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480  
 AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCC CTGAGGGTGT 540  
 CTTGCTGTA GAGAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGAGGA 600  
 GATTGCCAAG TATGAGCTCT TTGGCCAGC TGTGTGAGG AATGTTGCT CAGTGGAGGA 660  
 45 CCCCATGAAC ATCTCCATCA TGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720  
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780  
 GACAGCCAGG GATGAGGATG ATGCCATCTA CACTACAAAT GGGTGGTGT CTTACTCCAT 840  
 CCATAGCCAA GAACCAAGG ACCCACAGA CCTCATGTTT ACCATTACCC GGAGCAGG 900  
 CACCATCAGC GTCATCTCCA GTGGCTGGA CCGGAAAAA GTCCCTGAGT ACACACTGAC 960  
 50 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCACCAACC ACGGCACTGG CAGTAGTGA 1020  
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTGACCCC CAGAAGTAGG AGGCCATGT 1080  
 GCCTGAGATG GCGATGGGCC ATGAGGTGCA GAGGCTGAGC GTCACTGATC TGGAGCCCC 1140  
 CAACTCACCA AGCTGGCGTG CCACCTACCT TATCATGGGC GGTGACGAG GGGACCATTT 1200  
 TACCATCACC ACCCACTCTG AGAGCAACCA GGCATCCTG ACAACAGGA AGGGTTTGA 1260  
 55 TTTTGAGGCC AAAAACCAGC ACACCTGTA CGTTGAAGTG ACCAAGAGG CCCCTTTTGT 1320  
 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380  
 ACCTGTGTTT GTCCCACTCT CCAAGTCTGT TGAGGTCCAG GAGGCACTCC CACTGGGGA 1440  
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500  
 CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560  
 60 TGTGGGCACC CTGACCGGTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620  
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680  
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCTGAGCCC CGTCAGATCA CCTCTGCAA 1740  
 CCAAGCCCTG GTGCGCCAGG TGCTGAACAT CAAGGACAAG GACCTGTCTC CCCACCTC 1800  
 CCCTTTCCAG GCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860  
 65 GGAAGGTGAC ACAGTGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGAOGT 1920  
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCACTGT 1980  
 GTGCGACTGC CATGGCCATG TOGAAACCTG CCTTGGACCC TGGAAAGGAG GTTTCATCCT 2040  
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGGT 2100  
 70 GAGAAAGAA CCGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGGTGACAA 2160  
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220  
 GTCCACCGA GGTCTGGAGG CCGAGCCCGA GGTGGTCTC CGCAATGAGC TGGCAACCA 2280  
 CATCATCCCG ACACCATGT ACCGTCTCTG GCCAGCCAC CCAGATGAAA TCGGCAACTT 2340  
 TATAATTGAG AACCTGAAG CCGCTAACAC AGACCCCA GCGCCGCTT ACGACACCTT 2400  
 75 CTGTGTGCTG GACTATGAGG GCAGCGGCTC CGACGCGCG TCCCTGAGCT CCCTCACCTC 2460  
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCTTCAA 2520  
 GAAGCTGGCA GACATGTACG GTGGCGGGA GGACGACTAG CGCGCTGCC TGCAGGGCTG 2580  
 GGGACCAAC GTACGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCC TTCAGCTGAG 2640  
 GACTTCGGAG CTGTGACAGA AGTGGCGGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700  
 80 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760  
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGCCCAAGTT TCCAGAAGCC 2820  
 TCTTACCTGC CGTAAATATG TCAACCTGT GTCTGGGCC TGGGCTGCT GTGACTGACC 2880  
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940  
 TTTTATTAAT GCTATCTTCA AAAAGTTAGA GAAAGTCTT CAAAGTGCA GCCCAGAGCT 3000  
 GCTGGGCCCA CTGGCCCTCC TGCAATTTCT GTTTCAGAC CCAATGCTT CCCTTCGGA 3060

TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTATTITTT TATTTTCCCT 3120  
 GTTGCCTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180  
 TAAAGAAACT TTTCCAGAAA AAAA 3205

5 Seq ID NO: C84 DNA Sequence  
 Nucleic Acid Accession #: NM\_005629.1  
 Coding sequence: 639..2546

10 1 11 21 31 41 51  
 | | | | | |  
 TAGTCGGAGC GAGGTGGCGA GTCGCTGAGC CCGCCGCGGC CCCGAGAGCG GCTGCAGCCG 60  
 CCGCCGCGCG GAAGGAGAGG GCGAGGCGCG CCCGAGCGCG CCGCCGCGCG GCCACCGCGG 120  
 CCGCCGCGCAC CACCGCCACC GGAGTCGCGG GCCAGCGCGG CAGCCTCCGC GGGCCCGCGC 180  
 CCGGGCGGGG GCGCGCGGCC ACAGGCCCTT GCTCCGCGCG TCGTTTGAGC ACCCGGGGGG 240  
 15 CCGATGTGCG CCGCGCGCGG TTAGGATGAG TCTCGGGTGG GCGGAGGAGC CGCCGCGAGC 300  
 GCGCCGCGCC CCGCGCGCGG CAGGAGCCTC GGGAGCGCGC GCGCCGCGCG CCGCGCGCGG 360  
 GCGCGCGCCC GAGCGCGCCC GCGCGCGCCC GGGCCCGCGA CACACATGAG ATTCTTCAGG 420  
 CTCACITTC AATGCTTCGT GACTGCTTC TACTGCGCG CCGCGCGCGC CGCACCCCGC 480  
 20 CGTCCGCGCG CCGCCCGGTC CCGCGCGCGC GCGCCCGCGC GCGCCCGCGC GCGCCCGCGC 540  
 CTTCCGCGCG CTCCCGGTTG CCGCGCGGTC CCGCCCGCGC ACCCGCGCGC CCCGTGAGGC 600  
 GCGCGCGCCC CCGCGCGCGC GTGCGCGCGC CCGGGGCCAT GGCGAAGAG AGCGCGGAGA 660  
 ACGGCATCTA TAGCGGTGCC GCGAGCAGAG AGAAGGGGCC CCTCATCGCG CCGCGCGCGC 720  
 CCGGGCGCCG GGGCAAGGGC GAGCGCGCGC TGGGCTGGG GACACCGCGC GCGCGCGCTG 780  
 CCGTGCGCGC GCGCGAGACC TGGACGCGCC AGATGGAATT CATCATGTCG TGCCTGGGCT 840  
 25 TCGCGGTGGG CTTGGGCAAC GTGTGGCGCT TCCCTACCT GTGCTACAAG AACCGCGGAG 900  
 GTGTGTTCTT TATTCTCTAC GTCTGATGCG CCCTGGTTGG AGGAATCCCC ATTTTCTTCT 960  
 TAGAGATCTC GCTGGGCGAG TTCTATGAAG CCGCGAGCAT CAATGTCTGG AACATCTGTC 1020  
 CCCTGTCTCA AGGCTTGGCG TACGCTTCCA TGGTGATCGT CTTCTACTCG AACACCTACT 1080  
 ACATCATGCT GCTGGCTCGG GGCTTCTATT ACCTGGTCAA GTCTTTTACC ACCACGCTGC 1140  
 30 CCTGGGCCAC ATGTGGCCAC ACCTGGAACA CTCCGAGTGG CGTGGAGATC TTCCGCCATG 1200  
 AAGACTGTGC CAATGCCAGC CTGGCCAAAC TCACCTGTGA CCAGCTTGCT GACCGCGCGT 1260  
 CCCTGTCTAT CGAGTCTCGG GAGAACAAAG TCTTGAGGCT GTCTGGGGGA CTGGAGGTGC 1320  
 CAGGGGCCCT CAATCGGGAG GTGACCTTTT GTCTGCTGGC CTGCTGGGTG CTGGTCTACT 1380  
 TCTGTGCTCG GAAGGGGGTC AATCCACCGG GAAAGATCGT GTACTTCACT GCTACATTC 1440  
 35 CCTACGTGCT CCGGTCTGTC CTGCTGGTGC GTGAGTGTCT GCTGCTGGC GCCCTGGATG 1500  
 GCATCATTTA CTATCTCAAG CTTGACTGGT CAAAGCTGGG GTCCCTCAG GTGTGGATAG 1560  
 ATCGGGGAGC CCAGATTTC TTTCTTACG CCATTTGGCT GGGGGCCCTC ACAGCCCTGG 1620  
 GCAGCTACAA CCGCTTCAAC AACAACTGCT ACAAGGACGC CATCATCTG GCTCTCATCA 1680  
 ACAGTGGGAC CAGCTTCTTT GCTGGCTCG TGGTCTTCTC CATCTGGGC TTCTAGGCTG 1740  
 40 CAGAGCAGGG CGTGCAATC TCCAAGTGG CAGAGTCAGG GCCGGGCGTG GCCTTCATCG 1800  
 CCTACCGCGG GCGTGTCAAG CTGATGCCAG TGGGCCACTC CTGGCTGCCC CTGTTCTTCT 1860  
 TCATGCTGTT GCTGCTGGT CTGACAGGCC AGTTTGTAGG TGTGGAGGGC TTCTATCACC 1920  
 GCTCTCTCGA CCTCTCCCG GCTCTCTACT ACTTCCGTTT CCAAGGGGAG ATCTCTGTGG 1980  
 CCCTCTGTGG TGGCCTCTGC TTTGTCTATG ATCTCTCCAT GGTGACTGAT GGGGGGATGT 2040  
 45 ACGTCTTCCA GCTGTTTGAC TACTACTCGG CCAGCGGCAC CACCTGCTC TGGCAGGCCT 2100  
 TTTGGGAGTG CGTGGTGGTG GCTGGGTGTG ACGGAGCTGA CCGCTTCATG GACGACATTG 2160  
 CCTGTATGAT CCGGTACCGA CCTTGGCCCT GGATGAAATG GTGCTGTGTC TTCTTCACCC 2220  
 CGCTGGTCTG CCGCTTCAAC TTCTCTTCA ACGTTGTGTA CTACGAGCGC CTGGTCTACA 2280  
 50 ACAACACCTA CGTGTACCGG TGGTGGGGTG AGGCCATGGG CTGGGCTTTC GCCCTGTCTT 2340  
 CCATGCTGTG CGTGCCGCTG CACCTCTGCG GCTGCTCCT CAGGGCCAGG GGCACCATGG 2400  
 CTGAGCGCTG GCAGCAGCTG ACCCAGCCCA TCTGGGGCCT CCACCACTTG GAGTACCGAG 2460  
 CTCAGGACGC AGATGTGAGG GGCCTGACCA CCCTGACCCC AGTGTCCGAG AGCAGCAAGG 2520  
 TCGTGTGGT GGAGAGTGTG ATGTGACAAC TCAGCTCACA TCACCACTC ACCTCTGTGA 2580  
 55 GCCATAGCAG CCGCTGCTTC AGCCCCACCG CACCCCTCCA GGGGGCTGCG CTTTCCCTGA 2640  
 CACTTTTGGG GTCTGCTGCG GGGAGGAGGG GAGAAAGCAC CATGAGTGT CACTAAAACA 2700  
 ACTTTTTCCT TTTTAAATAA AACGCCAAAA ATATCACAAC CCACCAAAA TAGATGCCCT 2760  
 TCCCTCTCCA GCGCTAGCGG AGCTGTCTCT AGGCCCGGCC TAGTGCCCTA CCCCACCCA 2820  
 CAGTGTGCTA CTCTCTCTCG CCGTCCACCG CCCACCCCTT GCGCACTCT CCAGGCTCTG 2880  
 60 CTCTGACAGA CACCGGTGGG TGACCCCTCA CCCCAGAGC AGCAGTGGCA GCTTGGGAAA 2940  
 TGTGAGGAAG GGAAGGAGGG AGAGACCGGA GGGAGGAGAG AGAGGAGAAG GGAGGCAGGG 3000  
 GAGGGGCGAG AGAACCAAGG CAAATATTTC AGCTGGGCTA TACCCCTCTC CCCATCCCTG 3060  
 TTATAGAAGC TTAGAGAGCC AGCCAGCAAT GGAACCTTCT GGTTCCTGCG CCAATCGCCA 3120  
 CCAGTATCAA TTGTTGAGC TTGGGTGCGA GTGCACGCGT GCGTGAGTAC GGAGAGTATA 3180  
 65 TATAGATCTC TATCTCTTAG CAAAGGTGAA TGCCAGATGT AATGCGGCC TCTGGGCAAA 3240  
 GGAGGCTTGT ATTTTGCACA TTTTATAAAA ACTTGAGAGA ATGAGATTTC TGCTGTGATA 3300  
 TTTCTAAAAA GAGGAAGGAG CCAAAACCAT CCTCTCTTCA CCACTCCCAT CCCTGTGAGC 3360  
 CCTACCTTAC CCCTCTGCCC CTAGCCAAGG AGTGTGAATT TATAGATCTA ACTTTCATAG 3420  
 GCAAAACAAA AGCTTCGAGC TGTGCGTGT GTGAGTCTGT TGTGTGATG TCGTGTGTGT 3480  
 70 GTCCCGAGCC CCGACTGGA TTGGAAGAGT GCATGGTGGG GGCCTCGGGG CTGTCCCCAC 3540  
 GCTGTCCCTT TGCCCAAGT CTGTGGGGCA AGAGGCTGCA ATATTCCGTC CTGGTGTCTT 3600  
 GGGCTGTCTA CCGTGCCTGC TCAGGCTTCC CACCTGTGCG GGGGCACACC CCCAGGAAGG 3660  
 GACCTGTGAG ACGGCTCCCA CGTCCAGGCT TAAGTGTGAT GCACTTCCCG CACCTCCAGT 3720  
 CTTCTGTGTA GCAGCTTTAA CCAAGCTTTC TCTGTCAAGT CCACTCCCGA GAGGCTGAG 3780  
 75 TGACCCCAAG AAGAGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGTGGGTGTA 3840  
 GGGTGGCGGG CCGTGGGGGA CATTCTACTG TGCTAAAAAG CCACTGCAGA CATAGCAATA 3900  
 AAAACATGTC ATTTTCC 3917

80 Seq ID NO: C85 DNA Sequence  
 Nucleic Acid Accession #: NM\_006516.1  
 Coding sequence: 180..1658

1 11 21 31 41 51  
 | | | | | |  
 TAGTCGCGGG TCCCCGAGTG AGCACGCCAG GGAGCAGGAG ACCAAACGAC GGGGGTGGGA 60

5 GTCCAGAGTCG CAGTGGGAGT CCCCGGACCG GAGCACGAGC CTGAGCGGGA GAGCGCCGCT 120  
 CGCACGCCCG TCGCCACCCG CGTACCGGCG GCAGCCAGAG CCACCAGCGC AGCGCTGCCA 180  
 TGGAGCCCGAG CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC 240  
 TTGGCTCCCT GCACTTTGGC TACAACACTG GAGTCATCAA TGCCCCCAG AAGGTGATCG 300  
 AGGAGTTCTA CAACACAGACA TGGGTCCACC GCTATGGGGA GAGCATCCTG CCCACCACGC 360  
 TCACCACGCT CTGGTCCCTC TCAGTGGCCA TCTTTTCTGT TGGGGGCATG ATTGGCTCCT 420  
 TCTCTGTGGG CCTTTTCTGT AACCGCTTTG GCCCGCGGAA TTCAATGCTG ATGATGAACC 480  
 TGCTGGCCTT CGTGTCCGCG GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA 540  
 10 TGCTGATCCT GGGCCGCTTC ATCATCGGTG TGACTCGGG CTGACCACA GCTTCTGTGC 600  
 CCATGTATGT GGGTGAAGTG TCACCCACAG CCTTTCGTGG GCGCTGGGC ACCCTGCACC 660  
 AGCTGGGCAAT CTGCTCGGCG ATCCTCATCG CCCAGGTGTT CGGCTGGAC TCCATCATGG 720  
 GCAACAAGGA CCTGTGCCCC CTGCTGTGTA GCATCATCTT CATCCCGGCC CTGCTGCAAT 780  
 GCATCGTCTT GCCCTTCTGC CCCGAGAGTC CCCGCTTCTT GCTCATCAAC CGCAACGAGG 840  
 15 AGAACCAGGC CAAGAGTGTG CTAAAGAAGC TGCGCGGAC AGCTGACGTG ACCATGACC 900  
 TGCAGGAGAT GAAGGAAGAG AGTCGCGAGA TGATGCGGGA GAAGAAGGTC ACCATCCTGG 960  
 AGCTGTTCCG TTCCCGCGCC TACCGCCAGC CCATCTCAT CTGTGTGGT CTGCAGCTGT 1020  
 CCCAGCAGCT GTCTGGAGCT AACGCTGTCT TCTATTACTC CACGAGCATC TTGAGAAAGG 1080  
 CGGGGTGCA GCGAGCTGTG TATGCCACCA TTGGCTCCGG TATCGTCAAC ACGGCTTCA 1140  
 20 CTGTCTGTGC GCTGTTTGTG GTGAGCGGAG CAGGCGCGCG GACCTGCAC CTATAGGCC 1200  
 TGCTGGCAT GCGGGGTGT GCCATCTCA TGACCATCGC GCTAGCACTG CTGGAGCAGC 1260  
 TACCTGTGAT GTCCCTATCT AGCATCGTGG CCATCTTTGG CTTTGTGGCC TTCTTTGAAG 1320  
 TGGGTCTCG CCCCATCCCA TGGTTCATCG TGGCTGAAT CTTCAGCCAG GGTCCACGTC 1380  
 CAGCTGTGCA GCGCTGTGCA GGCTTCTCCA ACTGGACCTC AAATTTCTAT GTGGGCATGT 1440  
 25 GCTTCCAGTA TGTGGAGCAA CTGTGTGTGC CTAAGTCTT CATCATCTTC ACTGTGCTCC 1500  
 TGGTCTGTGT CTTCATCTTC ACCTACTTCA AAGTTCCTGA GACTAAAGGC CGGACCTTCG 1560  
 ATGAGATCGC TTCCCGCTTC CGGCGGGGG GAGCCAGCCA AAGTGATAAG ACACCCGAGG 1620  
 AGCTGTTCCA TCCCTCGGGG GCTGATTCCT AAGTGTGAGT CGCCCGAGAT CACGAGCCCG 1680  
 GCGTGTCTCC AGCAGCCCTC AGGATCTCTC AGGAGCAGAG GCAGCTGGAT GAGACTTCCA 1740  
 30 AACCTGACAG ATGTGACCGG AGCCGCGCCT GGGCTCTCTT TCTCCAGCCA GCAATGATGT 1800  
 CCAGAAGAAT ATTCAGGACT TAACGGCTCC AGGATTTTAA CAAAAGCAAG ACTGTTGCTC 1860  
 AAATCTATTC AGACAAAGCA CAGGTTTTAT AATTTTTTAA TTACTGATT TGTATTTTTT 1920  
 ATATCAGCCT GAGTCTCTCG TGCCACATC CCAGGCTTCA CCTGTAATGG TTCCATGCCT 1980  
 GAGGTGTGAG AGTGAAGCCT GTGAGACAC TTGCTTCTT CACCCAGCTA ATCTGTAGGG 2040  
 35 CTGGACCTAT GTCTTAAGGA CACATAATC GAACATGAA CTACAAAGCT TCTATCCAG 2100  
 GAGGTGGCTA TGGCCACCGG TTCTGCTGGC CTGGATCTCC CACTCTAGG GGTGAGGCTC 2160  
 CATTAGGATT TGCCCTTCC CATCTCTCC TACCCAAACA CTCAAATTAA TCTTTCTTTA 2220  
 CCTGAGACCA GTTGGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAAAGGCC AGTCTGGGCT 2280  
 GCGGCTTCT AGTCTCTTTT GCACTGAGG CCACATAAT ACCATGAGAA GAGGCTCTGT 2340  
 40 GGGAGCCTGC AAACCTACTG CTCAAGAAGA CATGGAGACT CCTGCCCTGT TGTGTATAGA 2400  
 TGCAAGATAT TTATATATAT TTTTGGTGT CAATATTAAA TACAGACACT AAGTTATAGT 2460  
 ATATCTGAGC AAGCCCACTT GTAAATACAC CACTCACTC CTGTACTTCA CCTAAACAGA 2520  
 TATAAATGGC TGGTTTTAG AAACATGGTT TTGAAATGCT TGTGGATGA GGGTAGGAGG 2580  
 TTTGATGGAG AGTGAGACAG AAGTAAAGTG GGTGCAACC ACTGCAACGG CTTAGACTTC 2640  
 45 GACTCAGGAT CCACTCCCTT ACACGTACCT CTCATCAGT TCCTCTTGT CAAAATCTG 2700  
 TTTGATCCCT GTTACCCAGA GAATATATAC ATTCTTATC TTGACATTCA AGGCATTCT 2760  
 ATCAGATATT TGATAGTTGG TGTTCAAAA AACACTAGTT TTGTGCCAGC CGTGATGCTC 2820  
 AGGCTTGAAG TCGCATTATT TTGAATGTGA AGGGAA 2856

Seq ID NO: C86 DNA Sequence  
 Nucleic Acid Accession #: XM\_035292.2  
 Coding sequence: 53..1576

55 1 11 21 31 41 51  
 | | | | |  
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCGCGGCC GGTGCGCAGA GCATGGCGGG 60  
 TCGGGGCCCG AAGCGGCGCG CGCTAGCGGC GCGCGCGGCC GAGGAGAAGG AAGAGGCGCG 120  
 GGAGAAGATG CTGGCGGCCA AGAGCGCGGA CGGCTCGGCG CCGCGAGCGC AGGGCGAGGG 180  
 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATG TGGGGACCAT 240  
 60 TATCGGCTCG GGCATCTCG TGACGCCAC GGGGCTGCTC AAGGAGGCG GCTCGCGGG 300  
 GCTGGGCTG GTGGTGTGG CCGGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360  
 CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTACA TGCTGGAGGT 420  
 CTACGCTCG CTGCGCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGCGCTTC 480  
 ATCGCAGTAC ATCGTGGGCC TGGTCTTGC CACCTAAGCT CTCGAGCGGC TCTTCCCCAC 540  
 65 CTGCGCGGTG CCCGAGGAG CAGCCAAAGCT CGTGGCCTGC CTCTGCTGTC TGCTGCTCAC 600  
 GGCCTGAAC TGCTACAGCG TGAAGGCCGC CACCGGCTC CAGGATGCTT TTGCGCGGCG 660  
 CAAGCTCCTG GCCCTGGGCC TGATCATCTT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720  
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAATCGGATG TGGGGAACAT 780  
 70 TGTGCTGGCA TTATACAGCG GCCTCTTTC CTATGGAGGA TGAATTAAT TGAATTTCTG 840  
 CACAGAGGAA ATGATCAACC CCTACAGAAA OCTGCGGCTG GCCATCATCA TCTCCCTGCC 900  
 CATGCTGAGC CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACACCC TTGTCAACGA 960  
 GCAGATGCTG TCGTCCGAGG CGTGGCGGT GACTTCGGG AACTATCACC TGGGCTCAT 1020  
 GTCTGAGATC ATCCCGTCT TCGTGGGCTT GTCTGCTTC GGCTCCGTC ATGGGTCTCT 1080  
 GTTCAATATC TCCAGGCTCT TCTTCTGGG GTCCCGGGA GGCACCTGC CCTCATCTCT 1140  
 75 CTCCATGATC CACCAACAG TCCTCACCCC CGTGGCGTCC CTGCTGTTC CTGTGTGAT 1200  
 GACGCTGCTC TACGCTTCT CCAAGGACAT CTCTCTGTC ATCAACTTCT TCAGCTTCTT 1260  
 CAACCTGGCT TCGTGGGCC TGGCCATCAT CGGCATGATC TGGCTGGCC ACAGAAAGCC 1320  
 TGAGCTTGAO CCGCCATCA AGGTGAACCT GGCCTGCTT GTGTCTTCA TCCTGGGCTC 1380  
 CACTTCTCTG TCCGCGTCT CCTTCTGGAA GACACCGTG GAGTGTGGCA TCGGCTTCA 1440  
 80 CATCATCTC AGCGGCTGC CGCTCACTT CTTCGGGCTC TGGTGGAAA ACAAGCCCAA 1500  
 TGGGCTCTCT CAGGCGATCT TCTCCAGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560  
 CCCCAGGAG ACATAGCCAG GAGGCGAGT GGCTGCCGGA GGAGCATGC 1609

Seq ID NO: C87 DNA Sequence  
 Nucleic Acid Accession #: NM\_005268.1

Coding sequence: 168..989

	1	11	21	31	41	51	
5							
	TAAAAAGCAA	AAGAATTGCG	GGCCGGGTGCG	ACACGGGGCTT	CCCCGAAAAC	CTTCCCCGCT	60
	TCTGGATATG	AAATTCAAGC	TGCTTGCTGA	GTCTATTGCG	GGCTGCTGG	GAGCCAGGAG	120
	AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGGGTGG	GTCCACCATG	AATGGAGTA	180
	TCITTTGAGG	ACTCCTGAGT	GGGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
10	TGTCCTGGT	CTTCATCTTC	CGCGTGCTGG	TGTACTGGT	GACGGCCGAG	CGTGTGTGGA	300
	GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTGCCAGGCC	CGGCTGCTCC	AACGTCTGCT	360
	TTGATGAGTT	CTTCCTCTGT	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGGTGA	420
	CATGCCCTCT	ACTGCTCGTG	GTGATGCAGC	TGGCCTACCG	GGAGGTTTCA	GAGAAGAGGC	480
	ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTTACCT	GAACCCCGGC	AAGAAGGGG	540
15	GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT	600
	TTCTCTATGT	GTTCACACTA	TTCTACCCCA	AATATATCCT	CCCTCTGTGT	GTCAAGTGCC	660
	ACGCAATCC	ATGCCCCAAT	ATAGTGGACT	GCTTCATCTC	CAAGCCCTCA	GAGAAGAAC	720
	TTTTCAACCT	CTTCATGGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
	TCATCTACCT	GGTGAGCAAG	AGATGCCACG	AGTGCCTGGC	AGCAAGGAAA	GCTCAAGCCA	840
20	TGTGCACAGG	TCATCACCCC	CACGGTACCA	CCTCTTCTCT	CAAAACAAGAC	GACCTCCTTT	900
	CGGGTGACCT	CATCTTTCTG	GGCTCAGACA	GTCTCTCTCC	TCTCTTACCA	GACCGCCCCC	960
	GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGGTCTG	GCAGGTTGGG	1020
	CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGG	GGAGCTAAGC	1080
	CATGAGGTAG	GGCAGGCCAA	GAGAGAGGAT	TCAGAGCTCT	TGGGAGCCAG	TTCTAGTCC	1140
25	TCAACTCCAG	CCACCTGCCC	CAGCTCGACG	GCACTGGGCC	AGTCCCCCT	CTGCTCTGCA	1200
	GCTCGGTTTC	CTTTTCTAGA	ATGGAATAG	TGAGGGCCAA	TGC		1243

Seq ID NO: C88 DNA Sequence  
Nucleic Acid Accession #: NM\_005130  
Coding sequence: 98..802

30	1	11	21	31	41	51	
	CTCTACCTGA	CACAGCTGCA	GCCTGCAATT	CACTCCCACT	GCCTGGGATT	GCACTGGATC	60
35	CGTGTGCTCA	GAACAAGGTG	AACGCCACGC	TGCAGCCATG	AAGATCTGTA	GCCTCACCTT	120
	GCCTCTCTTC	CTCTACTCTG	CTGCTCAGGT	GCTCCTGGTG	GAGGGGAAAA	AAAAAGTGAA	180
	GAATGGACTT	CACAGCAAAG	TGGTCTCAGA	ACAAAAGGAC	ACTCTGGGCA	ACACCCAGAT	240
	TAAGCAGAAA	AGCAGGCCCG	GGAAACAAAG	CAAGTTTGTC	ACCAAAGACC	AAGCCAAGCT	300
	CAGATGGGCT	GCTACTGAGC	AGGAGGAGGG	CATCTCTCTC	AAGGTTGAGT	GCACTCAATT	360
40	GGACCATGAA	TTTTCTGTGT	TCTTTGCTGG	CAATCCAACC	TCATGCCTAA	AGCTCAAGGA	420
	TGAGAGAGTC	TATTGGAAAC	AAGTTGCCCC	GAATCTGCGC	TCACAGAAAG	ACATCTGTAG	480
	ATATTCCAAG	ACAGCTGTGA	AAACCAAGAT	GTGCAGAAAG	GATTCTCCAG	AATCCAGTCT	540
	TAAGCTAGTC	AGCTCCACTC	TATTGGGAAA	CACAAAGCCC	AGGAAGGAGA	AAACAGAGAT	600
	GTCCCCCAGG	GAGCACAATCA	AGGGCAAAGA	GACCAACCCC	TCTAGCCTAG	CAGTGACCCA	660
45	GACCATGGCC	ACCAAAGCTC	CCGAGTGTGT	GGAGGACCCA	GATATGGCAA	ACCAGAGGAA	720
	GACTGCCCTG	GAGTTCGTGT	GAGAGACTTG	GAGCTCTCTC	TGCACATTCT	TCCTCAGCAT	780
	AGTGCAGGAC	ACGTCTGTGT	AATGAGGTCA	AAAGAGAAAG	GTTTCTTTTA	AGAGATGTCA	840
	TGTGTAAGTT	CCCTCTGTAT	ACTTTAAAGC	TCTCTACAGT	CCCCCAAAAA	TATGAACCTT	900
	TGTGCTTAGT	GCTAGTCAAG	AAATATTTAA	ACAAGTTTGT	TATTTTGTGT	TTTTGTGTTT	960
50	TGGAATTTGC	CTTATTTTTC	TTGATGCGA	TGTTCAAGAG	CTGTTTCTGT	CAGCATGTAT	1020
	TTCCATGGCC	CACACAGCTA	TGTGTTTGAG	CAGCGAAGAG	TCCTTGAGCT	GAATGAGCCA	1080
	GAGTGATAAT	TTCAAGTCAA	CGAACCTTCT	GCTGAATTAA	TGGTAATAAA	ACTCTGGGTG	1140
	TTTTTCAAAA	AAAAAATAAA	AAA				1163

Seq ID NO: C89 DNA Sequence  
Nucleic Acid Accession #: BC022542  
Coding sequence: 274..927

55	1	11	21	31	41	51	
60	ACTTGGTCCC	AGCCGATAAA	TCTGGGGCAG	CGCGCGGTAG	GAGCTGCGGG	CGGCCAGGCC	60
	CCCTCCCTGG	TCCGCACCTG	GCCCCGCGCG	CCCTCTCGGG	GGGTCCGGCT	TCCGGCGTCC	120
	TGGCGGGCTG	GGTGGCGGGG	GTTGCGGGCG	CGGCTGGGCT	GCTCTCGGG	GCGGGGAGGG	180
	GGCTCAGCGT	CGGGCCCGCC	ACGGCCTTCA	CCGCGCGCGG	CTCTGACGCC	GGCATAAGGG	240
65	CCATGTGTTT	TGAAATTATT	TTGAGGCAAG	AAGTTTGTAA	AGATGGTTTC	CACAGAGACC	300
	TTTTAATCAA	AGTGAAGTTT	GGGGAAAGCA	TTGAGGACTT	GCACACGTGC	CGTCTCTTAA	360
	TTAAACAGGA	CATTCTTGCA	GGACTTTATG	TGGATCCGTA	TGAGTTGGCT	TCATTACGAG	420
	AGAGAAACAT	AACAGAGGCA	GTGATGGTTT	CAGAAAAATT	TGATATAGAG	GCCCCTAAGT	480
	ATTTGTCCAA	GAGTCTGAAA	GTTCTCATTT	ATGCCAGACG	AGATTACAGT	TGCATTGACT	540
70	GTTTTCAGCG	CTTTTTCGCT	GTGCACTGCC	GCTATCATCG	GCGCACAGT	GAAGATGGAG	600
	AAGCCTCGAT	TGTGGTCAAT	AACCCAGATT	TGTTGATGTT	TTGTGACCAA	GAGTTCGCGA	660
	TTTTGAAATG	CTGGGCTCAC	TCAGAAAGTG	CAGCCCCCTG	TGCTTTGGAT	AATGAGGATA	720
	TATGCCAATG	GAACAAGATG	AAGTATAAAT	CAGTATATAA	GAATGTGATT	CTACAAGTTC	780
	CAGTGGGACT	GACTGTACAT	ACCTCTCTAG	TATGTTCTGT	GACTCTGCTC	ATTACAATCC	840
75	TGTGCTCTAC	ATTGATCCTT	GTAGCAGTTT	TCAATATGCG	CCATTTTCCC	CTATAAGTTT	900
	TATGTAGTTA	AATGCTTCTT	AGAAACCTAA	ATAAGATCTA	TTAATTTCTG	ACGAGAGGTG	960
	TTCTCTAGTA	ATTAAATTACT	TTTATCTTTT	GTCTTCATTT	GTGGCCAAAA	TTATGTTTAC	1020
	TAGAGGAAAT	TTGGGATCAT	TCTCAGCTAA	TTCCAAAATG	TAGTGTCTTA	TTGCATGGAT	1080
	CCTTGGTAAT	CCTCAAGCAT	CAGATGCCAT	AAGGGGAAAC	TTAATTTCTG	TAAATTAATG	1140
80	TTTATTTTGT	GAGAAAGTAC	TTTATCTTCA	TTTGGGAGTAG	AAAAATTATT	TCITTTATGTA	1200
	GTAGAGACAA	ATTATTTCTA	TTTTGCAAGT	ACTTTCAATT	TAAGCTACAA	ATTGAGAAAA	1260
	CGGTTATATA	TAAGAAATAA	ATAGGCCAGG	CACAGTGGCT	CACACCTGTA	ATCCAGCAC	1320
	TTTGGGAGGC	CGAGGTGGGC	GGATCACCAG	AGGTCAAGAG	TTTGAGACCA	GCTTGGTGAA	1380
	ACCCGTCTCT	TACTAAAAAT	ACAAAAGTTA	GCTGGGGCTG	GTGGTGGGCA	TCTGTAGTCC	1440
	CAGCTAATTG	GAAGGGTGAG	CGCGGAGGAT	CGCTTGAACC	TGGGAGGCGG	AGGTTCCAGA	1500



5 GAGCCAAAGT CGCACCAGT CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA 1560  
 GGAAAAACAA AAAAGAAGAA TAAATAAAT TGGATGAAAA TCATGTTTAT TTAATAGTA 1620  
 ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCATGA AAATCATTAA AGTAGGACAG 1680  
 CTAAGAAAT AATATTAAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCTCTA 1740  
 ACGCACTCCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGSCAA 1800  
 GGACTTGTATG AAACCTGAGTA CTAAGATTG GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860  
 TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAA AAAA 1906

10 Seq ID NO: C90 DNA Sequence  
 Nucleic Acid Accession #: NM\_004994  
 Coding sequence: 20..2143

15 1 11 21 31 41 51  
 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTG GTCTCTGGTG TCTCTGGTGT 60  
 GGGCTGCTGC TTGTCTGCC CCAGACAGCG CCAGTCCACC CTGTGTCTCT TCCCTGGAGA 120  
 CCTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180  
 CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCTGTGCG TGTCTCTTCT 240  
 CCAGAAGCAA CTGTCTCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300  
 GCGAACCCCA CGGTGCGGGG TCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT 360  
 CAAGTGGCAC CACCAACAACA TCACCTATTG GATCCAAAC TACTCGGAAG ACTTGCCGCG 420  
 GGGCGTGATT GACGACGCTC TTGCCCGGCG CTTCGCACTG TGGAGCGCGG TGAACGCGCT 480  
 CACCTTCACT CGCGTGTACA GCGGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540  
 GCAAGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGSCACACG CCTTTCCTCC 600  
 TGGCCCGCGG ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCTTGGGCAA 660  
 GGGCGTGTGT GTTCCAACTC GGTTTGGAAA CGCAGATGGC GGGCGCTGCC ACTTCCCTTT 720  
 CATCTTCGAG GGGCGCTCCT ACTCTGCTCG CACCACGACG GGTGCTCCCG ACGGCTTGCC 780  
 CTGTGTGAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGGGA 840  
 GAGACTCTAC ACCCGGGACG GCAATGTGTA TGGGAAACCC TGCCAGTTTC CATTATCTT 900  
 CCAAGGCCAA TCCTACTCCG CCTGCACACG GGACGGTGGC TCGACGGGCT ACCGCTGGTG 960  
 CGCCACCAAC GCCAATACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCGAGCTGA 1020  
 CTGACGGGTG ATGGGGGGCA ACTCGGGGGG GGAGCTGTGC GTCTTCCCTT CACTTTCCT 1080  
 GGGTAAGGAG TACTCGACCT GTACCAGCGA GGGCGCGGGA GATGGGCGCC TCTGGTGGCG 1140  
 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200  
 TTTGTCTCTC GTGGCGGCGC ATGAGTTCGG CCACGGGCTG GGCTTAGATC ATTCTCAGT 1260  
 GCGGAGGGCG CTCATGTACC CTATGTACCG CTCTACTGAG GGGCCCCCTT TGCATAAGGA 1320  
 CGACGTGAAT GGCATCGCGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC 1380  
 AACCAACACG AACCAGCAGC CCAAGGCTCC CCGACGGTTC TGCCCCACCG GACCCCCAC 1440  
 TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500  
 AGGTCCCCCC ACTGCTGGCC CTCTACGGC CACTACTGTG CCTTGTAGTC CGGTGGACGA 1560  
 TGCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAAACGAG TGTATTGT 1620  
 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCGGGCGCG AGGGCCCCCT 1680  
 CCTTATCGGC GACAAGTGGC CGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740  
 GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC 1800  
 GGTGCTGGGC CGAGGGGCTC TGGACAAGCT GGGCCTGGGA GCGGAGTGG CCCAGGTGAC 1860  
 GGGGGCGCTC CGAGTGGGCA GGGGGAAGAT GCTGCTGTTT AGCGGGCGCG GCTCTGGAG 1920  
 GTTCCGAGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGATGTT 1980  
 CCGGGGGTGC CTTTGGACA CGCAAGAGCT CTTCCAGTAC CGAGAGAAAG CCTATTCTGT 2040  
 CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGAGTGGAG TTGAACCAAG TGGACCAAGT 2100  
 GGGCTACGTG ACCTATGACA TCCTGCAGTG CCTGAGGAC TAGGCTCTCC GTCTTCTCTT 2160  
 CGAGTGGCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCGGGATA 2220  
 CAACTGTGTA TTCTGTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGC CCCTCTCTTC 2280  
 TCACCTTTGT TTTTGTGG AGTGTCTTA ATAACTTGG ATTCTCTAAC CTTT 2334

55 Seq ID NO: C91 Sequence  
 Nucleic Acid Accession #: NM\_000213  
 Coding sequence: 188..5656

60 1 11 21 31 41 51  
 GCGCTGCCG CCTGTCCCC ACCCCCCAAC CCCCCGCGCC CGCCCTGGGA CAGTCCCTGC 60  
 TGCCCGCGCG GCTGCAGCCC CATCTCCTAG CGGCAGCCCA GCGCGGAGG GAGCGAGTCC 120  
 GCGCCGAGGT AGGTCCAGGA CGGGCGCACA GCAGCAGCCG AGGCTGGCCG GGAGAGGGAG 180  
 GAAGAGGATG GCAGGGCCAC GCCCAGCCCT ATGGGCCAGG CTGCTCTGG CAGCCTTGAT 240  
 65 CAGCGTCAGC CTCTCTGGGA CCTTGGCAAA CCGCTGCAAG AAGGCCCCAG TGAAGAGCTG 300  
 CACGGAGTGT GTCCGTGTGG ATAAGGACTG CGCCTACTGC ACAGACGAGA TGTTCAGGGA 360  
 CCGGCGCTGC AACACCCAGG CGGAGCTGCT GCGCGCGGGC TGCCAGCGGG AGAGCATCGT 420  
 GGTCTAGGAG AGCAGCTTCC AAATCACAGA GGAGACCCAG ATTGACACCA CCCTGCGGCG 480  
 CAGCCAGATG TCCCCCAAG GCCTGCGGGT CCGTCTGCGG CCGGTGAGG AGCGGCATTT 540  
 70 TGAGCTGGAG GTGTTTGAGC CACTGGAGAG CCCCCTGGAC CTGTACTTCC TCATGGACTT 600  
 CTCCAACTCC ATGTCCGATG ATCTGGACAA CCTCAAGAAG ATGGGGCAGA ACCTGGCTCG 660  
 GGTCTTGAGC CAGCTCACCA GCGACTACAC TATTGGATTT GGCAAGTTTG TGGACAAGT 720  
 CAGCGTCCCG CAGACGGACA TGAGGCTCTG GAAGCTGAAG GAGCCTTGGC CCAACAGTGA 780  
 CCCCCCTTTC TCCTTCAAGA ACCTCATCAG CTTGACAGAA GATGTGGATG AGTTCGGGAA 840  
 75 TAAACTGCAG GGAGAGCGGA TCTCAGGCAA CTTGAGTGT CTTGAGGCG GCTTCGATGC 900  
 CATCTGCGAG ACAGCTGTGT GCACGAGGGA CATTGGCTGG CCGCCGGACA GCACCCACT 960  
 GCTGGTCTTC TCCACGAGT CAGCCTTCCA CTATGAGGCT GATGGCGCCA AGTGCTGGC 1020  
 TGGCATCATG AGCGCAACG ATGAACGGTG CCACTGGGAC ACCACGGGCA CCTACACCCA 1080  
 GTACAGGACA CAGGACTACC GGTGCGTGGC CACCTGGGTG CGCCTGCTCG CCAAGCACAA 1140  
 80 CATCATCCCC ATCTTTGCTG TCACCAACTA CTCCTATAGC TACTACGAGA AGCTTCACAC 1200  
 CTATTTCCCT GTCTCTCAC TGGGGGTGCT GCAGGAGGAC TCGTCCAACA TGTGGAGCT 1260  
 GCTGGAGGAG GCCTTCAATC GGATCCGCTC CAACCTGGAC ATCCGGGGCC TAGACAGCCC 1320  
 CGAGGCGCTT CGGACAGAGG TCACCTCCAA GATGTTCCAG AAGACGAGGA CTGGGTCTCT 1380  
 TCACATCCGG CGGGGGGAAG TGGGTATATA CCAGGTGCAG CTGCGGGGCC TTGAGCACGT 1440

	GGATGGGACG	CACGTGTGCC	AGCTGCCGGA	GGACCAGAAG	GGCAACATCC	ATCTGAAACC	1500
	TTCTTTCTCC	GACGGCTCTCA	AGATGGAGCG	GGGCATCATC	TGTGATGTGT	GCACCTGCGA	1560
	GCTGCAAAAA	GAGGTGCGGT	CAGCTCGCTG	CAGCTTCAAC	GGAGACTTCG	TGTGCGGACA	1620
5	GTGTGTGTGC	AGCGAGGGCT	GGAGTGGCCA	GACCTGCAAC	TGCTCCACCG	GCTCTCTGAG	1680
	TGACATTTCAG	CCCTGCTCTG	GGGAGGGGCA	GGACAAGCCG	TGCTCCGGCC	GTGGGGAGTG	1740
	CCAGTGGGGG	CAGTGTGTGT	GCTACGGGCA	AGGCCGCTAC	GAGGGTCAGT	TCTGCGAGTA	1800
	TGACAACTTC	CAGTGTCCCC	GCACTTCCGG	GTTCTGTGTC	AATGACCGAG	GACGCTGCTC	1860
	CATGGGCCAG	TGTGTGTGTG	AGCCTGGTTG	GACAGGCCCA	AGCTGTGACT	GTCCCCCTAG	1920
10	CAATGCCACC	TGCATCGACA	GCAATGGGGG	CACTGTGAAT	GGACGTGGCC	ACTGTGAGTG	1980
	TGGCGCTGTC	CAGTGCACAC	AGCAGTCTGT	CTACACGGAC	ACCATCTGCG	AGATCAACTA	2040
	CTCGGCGATC	CACCCGGGCT	TCTGCGAGGA	CCTACGCTCC	TGCGTGCAGT	ACCAGGCGTG	2100
	GGGACCGGCG	GAGAAAGAGG	GGCGCACGTG	TGAGGAATGC	AACCTCAAGG	TCAAGATGGT	2160
	GGACGAGCTT	AAGAGAGCCG	AGGAGGTGGT	GGTGCGCTGC	TCCTTCCGGG	ACGAGGATGA	2220
15	CGACTGCACC	TACAGCTACA	CCATGGAAGG	TGACCGCGCC	CCTGGGCCCA	ACAGCACTGT	2280
	CCTGGTGCAC	AAGAAGAAGG	ACTGCCCTCC	GGGCTCCTTC	TGGTGGCTCA	TCCCCCTGCT	2340
	CCTCTCTGTC	CTCGCGCTCC	TGGCCCTGCT	ACTGCTGCTA	TGCTGGAAGT	ACTGTGCTTG	2400
	CTGCAAGGCC	TGCTTGGCAC	TTCTCCCGTG	CTGCAACCGA	GGTCACATGG	TGGGCTTTAA	2460
	GGAAAGACTT	CATCATCTGC	GGGAGAACCCT	GATGGCTCTC	GACCACTTGG	ACACGCCCAT	2520
20	GCTGCGCAGC	GGGAACCTCA	AGGGCCGTGA	CGTGGTCCGC	TGGAAGGTCA	CCAACAACAT	2580
	CGAGCGGGCT	GGCTTTGGCA	CTCATGCCGC	CAGCATCAAC	CCCACAGAGC	TGGTGGCCCTA	2640
	CGGGCTGTCT	TTGCGGCTGG	CCCGCCTTTG	CACCGAGAAC	CTGCTGAAGC	CTGACACTCG	2700
	GGAGTGGGCC	CAGCTGCGCC	AGGAGGTGGA	GGAGAACCCT	AACGAGGTCT	ACAGGCAGAT	2760
	CTCGGTGTTA	CACAAGCTCC	AGCAGACCAA	GTTCCGGCAG	CAGCCCAATG	CCGCGAAAAA	2820
25	GCAAGACCAC	ACCATTGTGG	ACACAGTGCT	GATGGCGCCC	CGTCCGGCCA	AGCCGGCCCT	2880
	GCTGAAGCTT	ACAGAGAAGC	AGGTGGAACA	GAGGGCTTTC	CACGACCTCA	AGGTGGCCCC	2940
	CGGCTACTAC	ACCTCACTG	CAGACCAGGA	CGCCCGGGGC	ATGCTGGAGT	TCCAGGAGGG	3000
	CGTGGAGCTG	GTGGAGCTAC	GGGTGCCCTC	CTTTATCCGG	CCTGAGGATG	ACGACGAGAA	3060
	CGAGCTGTCT	GTGGAGGCCA	TGCACTGTCC	CGCAGGCAC	GCCACCTCG	GCCGCGCCCT	3120
30	GGTAAACATC	ACCATCATCA	AGGAGCAAGC	CAGAGACGTG	GTGTCTTTTG	AGCAGCCTGA	3180
	GTCTCTGCTC	AGCCGCGGGG	ACCAGGTGGC	CCGCATCCCT	GTCTCTCGGC	GTGTCTCTGA	3240
	CGCGCGGAAG	TCCAGAGTCT	CCTACCGCAC	ACAGGATGGC	ACCGCGCAGG	GCAACCGGGA	3300
	CTACATCCCC	GTGGAGGGTG	AGCTGCTGTT	CCAGCCTGGG	GAGGCCCTGA	AAGAGCTGCA	3360
	GGTGAAGCTC	CTGGAGCTGC	AAGAAGTTGA	CTCCCTCCTG	CGGGGCGGCC	AGGTCCGCGG	3420
35	TTTCCACGTC	CAGCTCAGCA	ACCCTAAGTT	TGGGGCCAC	CTGGGCCAGC	CCCACTCCAC	3480
	CACCATCATC	ATCAGGAGCC	CAGATGAACT	GGACCGGAGC	TTCACGAGTC	AGATGTTGTC	3540
	ATCACAGCCA	CCCGCTCAGC	CGGACCTGGG	CGCCCGCAG	AACCCCAATG	CTAAGGCCCG	3600
	TGGGTCCAGG	AAGATCCATT	TCAACTGGCT	GCCCCCTCTC	GGCAAGCCAA	TGGGGTACAG	3660
	GGTAAAGCTC	TGATTCAGG	CGGACTCCGA	ATCCGAAGCC	CACCTGCTCG	ACAGCAAGGT	3720
40	GCCCTCAGTG	GAGCTCACCA	ACCTGTACCC	GTATTGCGAC	TATGAGATGA	AGGTGTGGGC	3780
	CTACGCGGCT	CAGGGCGAGG	GACCTACAG	CTCCCTGGTG	TCCTGCGGCA	CCCACCAAGG	3840
	AGTGGCCAGC	GAGCCAGGGC	GTCTGGCCTT	CAATGTGCTC	TCCTCCACGG	TGACCCAGCT	3900
	GAGCTGGGCT	GAGCCGGCTG	AGACCAACGG	TGAGATCACA	GCCTACGAGG	TCTGCTATGG	3960
	CCTGTGCAAC	GTGCAACAAC	AGCCTATTGG	GCCCATGAAG	AAAGTGTCTG	TTGCAACCC	4020
45	TAAGAACCAG	ATGCTGCTTA	TTGAGAACCT	TCGGGAGTCC	CAGCCCTACC	GCTACACGGT	4080
	GAAGGCGGCG	AAGCGGGGCG	GCTGGGGGCC	TGAGCGGGAG	GCCATCATCA	ACCTGGCCAC	4140
	CCAGCCCAAG	AGGCCCATGT	CCATCCCAT	CATCCCTGAC	ATCCCTATCG	TGGACGCCCA	4200
	GAGCGGGGAG	GACTACGACA	GCTTCCCTAT	GTACAGCGAT	GACGTTCTAC	GCTCTCCATC	4260
	GGGCGAGCAG	AGGCCAGCG	TCTCCGATGA	CAGTGGCTGC	GGCTGGAAGT	TGAGCCCTCT	4320
50	GCTGGGGGAG	GAGCTGGACC	TGCGGCGGCT	CACTGGCGGG	CTGCCCGCGG	AGCTCATCCC	4380
	GCGCCTGTCT	GCCAGCAGCG	GGCGCTCTC	CGACGCGGAG	GCCCCCAGCG	CCCCCGGAC	4440
	GACGCGCGCG	CGGGCGGGAA	GGGCGGCAGC	CGTGGCGGCG	AGTGGGACAC	CGGGGCCCTC	4500
	CGGAGAGCAC	CTGGTGAATG	GCCGGATGGA	CTTGGCTTTC	CGGGGAGACA	CCAACCTCCT	4560
	GCAAGAGTAT	ACCACGACCA	GTGCTGCTGC	CTATGGCACC	CACCTGAGCC	CACAGCTGCC	4620
55	CCACCGCGTG	CTAAGCAAT	CCTCCACCT	CACAGGGAC	TACAACTCAC	TGACCGGCTC	4680
	AGAACACTCA	CAGTCCAGCA	CAGTCCCGAG	GGACTACTCC	ACCTTCACTC	CGTCTCTCTC	4740
	CCAGCACTCT	CGCTGACTCT	CTGGTGTGCC	CGACACGCCC	ACCGGCTTGG	TGTTCTCTGC	4800
	CCTGGGGCCC	ACATCTCTCA	GAGTGAAGTG	GCAGAGAGCG	CGGTGCGAGC	GGCGGCTGCA	4860
	GGGCTACAGT	GTGGAGTACC	AGCTGCTGAA	CGGCGGTGAG	CTGCATCGGC	TCAACATCCC	4920
60	CAACCTGCCC	CAGACCTCGG	TGGTGGTGGG	AGACCTCTCT	CCCAACCACT	CCTACGTGTT	4980
	CCGCGTGGCG	GCCAGAGGCC	AGGAAGGCTG	GGGCGGAGAG	CGTGGGGGTC	TCATCAACAT	5040
	TGAATCCAG	GTGCAACCCG	AGAGCCCACT	GTGTCCCTTG	CCAGGCTCCG	CCTTCACTTT	5100
	GAGCACTCCC	AGTGCCCGAG	GCCCGCTGGT	GTCTACTGCC	CTGAGCCCGG	ACTGCTGCA	5160
	GCTGAGCTGG	GAGCGGCCAC	GGAGGCCCAA	TGGGGATATC	GTGCGCTACC	TGGTGAACCTG	5220
65	TGAGATGGCC	CAGGAGGAG	GGCCAGCCAC	CGCATTCGCG	GTGGATGGAG	ACAGCCCGGA	5280
	GAGCGGCTG	ACCGTGGCGG	GCCTCAGCGA	GAACGTGCCC	TACAGTTTCA	AGGTGCAGGC	5340
	CAGGACCACT	GAGGGCTTTC	GGCCAGAGCG	CGAGGGCATC	ATCACCATAG	AGTCCAGGGA	5400
	TGAGGAGCCC	TTCCCGCAGC	TGGGCGAGCG	TGCGGGGCTC	TTCCAGCACC	CGCTGCAAGG	5460
	CGAGTACAGC	AGCATCACCA	CCACCCACAC	CAGCGCCACC	GAGCCCTTCC	TAGTGGATGG	5520
70	GCTGACCTCT	GGGGCCGAGC	ACCTGGAGGC	AGGCGGCTCC	CTCACCGGCG	ATGTGACCCA	5580
	GGAGTTTGTG	AGCCGGAGAC	TGACCCAGAG	CGGAACCTTT	AGCACCCACA	TGACCCAAACA	5640
	GTCTTTCCAA	ACTTGACCGC	ACCTGCGCCC	ACCCCGGCCA	TGTCCCACTA	GGGTCTCTCC	5700
	CGACTCTCTT	CCCGGAGCCT	CCTCAGCTAC	TCCATCCTTG	CACCCCTGGG	GGCCAGCCGC	5760
	ACCGCATGTC	ACAGAGCAGG	GGCTAGGTGT	CTCCTGGGAG	GCAATGAAGG	GGCAAGGTC	5820
75	GTCTCTGTGT	GGCCCAAAAC	TATTGTAAAC	CAAGAGCTGT	GGAGCAGCAC	AAGGACCCAG	5880
	CTTTTGTCTT	GCACCTTAATA	AATGGTTTTG	CTACTGCTAA	AAAAAAAAAA	AAAAAAAAAA	5940
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAA	5994

Seq ID NO: C92 DNA Sequence  
 Nucleic Acid Accession #: NM\_023915  
 Coding sequence: 250..1326

1 11 21 31 41 51  
 | | | | |  
 GGCAGAGGG TTTCGTTTTG ATGCTTTACC AGAAAAATCCA CTTCCTGCGC GACCTTAGTT 60

TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120  
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAA CAGGAATAAC CTATGCTGAA 180  
 CCCACGGCTC AATCGTCCCC AAGTGTTCCT TGACACGCAT CTTTGCTTAC AGTGCAATCAG 240  
 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300  
 CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCCTTCAC 360  
 AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTTGT GGCAAGCATC 420  
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480  
 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCTATTGGA 540  
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600  
 TCAGTTTGTG TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660  
 GATCGCTATC TGAAGTGGT CAAGCCATT GGGGACTCTC GGATGTACAG CATAACCTTC 720  
 ACGAAGGTTT TATCTGTTTG TGTGTTGGTG ATCATGGGCT TTTGTCTTT GCCAACATC 780  
 ATCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840  
 CCTTTGGGGG TCAATATGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTGTGGCC 900  
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960  
 AGGCAATTCA TGAAGTCAGT AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020  
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATCC TTTTACTTTT 1080  
 AGTCACTTAG ACAGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA TCGAAAGAA 1140  
 ATTACACTTT TCTGTCTGCT GTGTAAATGT TGCCTGGATC CAATAATTIA CTTTTCATG 1200  
 TGTAGGTCAT TTTCAAGAA GCTGTTCAA AATCAAAATA TCAGAACAG GAGTGAAGC 1260  
 ATCAGATCAC TCGAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320  
 GTGTAGGCCT TTTATTGTTT GTTGGAAATG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380  
 TTCATTATCC TTAATAAAAA AA 1402

25 Seq ID NO: C93 DNA Sequence  
 Nucleic Acid Accession #: NM\_020789.1  
 Coding sequence: 208..3699

30 1 11 21 31 41 51  
 GGCACGAGGG TGGAGCCGAG CGGTGCGGAG CAGATCTGGT GGTCTCCGG AGAGCAGCTT 60  
 CCTTGGGTGT TACATGAGCC AAGCCCTCAC TGTACAGAAG AGTGAGAGCT GAAACCTGTT 120  
 CCTCGAGCTG ATCAGAAGGA CATCCCTTGG CCCCTCCATC TGGGCTCCTG TGGATAGGAG 180  
 GGGCTGGGTG AGCAGGCCAG CTGGGCTATG GTGTGGTGCC TCGGCTCGGC CGTCTCAGC 240  
 35 TGTTGTCATCA GCCAGGGGGC TGACGGTCTGA GGAAGCCCTG AGGTGGTATC GGTGGTGGGC 300  
 CGGGCTGAGG AGAGTGTGGT GCTGGGCTGT GACCTGCTGC CCCCGGCCGG CGGGCCCCC 360  
 CTGATGTCA TCGAGTGGCT CGGCTTTGGA TTCTGCTTC CCATCTTCAT CCAGTTCGGC 420  
 CTCTACTCTC CCCGAATTGA CCTGATTAC GTGGGAGGAG TCGGCTGCA GAAGGGGGCC 480  
 40 TCCTCCAGA TTGAGGTCT CCGGGTGGAA GACCAGGCT GGTACGAGTG CCGGTGTTT 540  
 TTCTGGACC AGCAGATCCC TGAAGAGCAT TTTGCTAACG GCTCCTGGT GCATCTGACA 600  
 GTCAATTAC CCCTCAATT CCAGGAGACA CCTCTGCTG TGTGGGAAGT GCAGGAAGT 660  
 GAGCCTGTGA CCCTGCGTTG TGTGGCCGCT GGCAGCCCC TGCCTCATGT GACGTGAAG 720  
 CTCGAGGAA AGACCTTGG CAGGGCCAG GGCAGGTGC AAGTCAGAA CGGACGCTG 780  
 45 CGGATCGCC GGTAGAGCG AGGCAGCTCT GGGTCTACA CCTGCCAAGC CTCAGCACT 840  
 GAGGGCAGCG CCACCCAGCG CACCAGCTG CTAGTGTAG GACCCCACT CATGTGGT 900  
 CCCCCAAGA ACAGCAAGT CAATGCTCC CAGGATGTTT CATGGGCTG CCATGCTGAG 960  
 GCATACCTG CTAACTCTAC CTACAGCTGG TTCCAGGACA ACATCAATGT CTTCCACATT 1020  
 AGCGGCTGC AGCGCGGGT GCAGATCTCT GTGACGGGA GCCTGCGCT GCTGGCCACC 1080  
 50 CAGCCTGATG ATGCCGGCTG CTACACCTGT GTGCCAGCA ATGGCCTCCT GCATCCACCC 1140  
 TCAGCCTCTG CCTACTCTAC TGTGCTCTGC ATGCCGGGG TGTCCGCTG CCGGTTCGT 1200  
 GCCAACCCCC CACTGCTCTT TGTCACTGG ACCAAGGATG GAAAGGCCCT GCAGCTGGAC 1260  
 AAGTTCCTG GCTGTGCCA GGGCAGAGAA GGCTCACTGA TCATCGCCCT GGGGAACGAG 1320  
 GATCGCAATG CTGTGCTGCT CTGCACCCC TACAACAGTC TTGTTACCGC CGGGCCCTCT 1380  
 55 CCTGTGACCC GCGTCTGCT CAAGGCTCCC CCAGCTTTA TAGAGCGGCC CAAGGAAGAA 1440  
 TATTTCCAG AAGTAGGGCG GGAGCTGCT ATCCCTGCT CGGCCCAAGG GACCCCTCCT 1500  
 CCTGTGTCT CTTGGACCAA GGTGGGCCGG GGGCTGCAAG GCCAGGCCA GGTGGACAGC 1560  
 AACAGCAGCC TCATCTCTCG ACCATTGACC AAGGAGGCC ACGGGCACTG GGAATGCAGT 1620  
 GCCAGCAATG CTGTGGCCCG AGTGGCCACC TCCAGAACG TCTAGTCTG GGGCACTAGC 1680  
 60 CCTCATGTTG TCACCAATGT GTCCGTGGTG GCTTGGCCA AGGTGGCAA TGTCTCTGG 1740  
 GAGCCTGGCT TTGATGGTGG TTATCTGCAG AGATTCAAGT TCTGTATAC CCCACTGGCC 1800  
 AAGCGTCTTG ACCGAATGCA CCATGACTGG GTGTCTTGG CAGTGCCTGT GGGGGCTGCT 1860  
 CACCTCTTAG TGCCAGGGCT GCAGCCCCAC ACCAGTACC AGTTCAGCT GCTAGCTCAG 1920  
 AACAGCTGG GGAGTGGTCC CTTAGCGAA ATCGTCTGT CTGCTCGGA AGGGCTTCTT 1980  
 65 ACCACGCCAG CTGACCCCG GCTTCCCCA ACAGAGATAC OGCTCCCTCT GTCCCTCCG 2040  
 CGGGGTCTGG TGGCAGTGAG GACACCCCG GGGTACTCC TGCAATTGGA TCCCCAGAG 2100  
 CTGCTCCCTA AGAGACTGGA TGGCTACGTC TTGGAAGGCC GGCAAGGCTC CCAGGGCTGG 2160  
 GAGGTGCTG ACCCGGCTGT GGCAGGCACA GAAACAGAGC TGCTGGTGCC AGGCCCTATC 2220  
 AAGGATGTT TCTACAGATT CCGCTCTGTG GCCTTCGCGG GCAGCTTGT CAGCGACCCC 2280  
 70 AGCAACCGG CCAAGCTCT CACTTCCGGT CTGGAGGTCT ACCTTTCGG CAGCAGCTG 2340  
 CGGGCCCTCC TGCCTCAGCC CGTGTGSGCC GCGTGTGGG GCGAGTCTG CTTTCTGGA 2400  
 GTGGCCCTCC TTGTGAGCAT CTTGGCCGCG TGCTCTCTGA ACCGGCGCAG GGCTGCCGCG 2460  
 CGCGCGCGCA AGCGCCTCCG CCAAGATCCA CCTCTTATCT TCTCTCCGAG CGGGAAGTCA 2520  
 GCTGCACCTT CTGCTCTGGG CTCAGGCACT CCGGCAAGCT TGGCAAGCT GAACTCTCAG 2580  
 75 GGATCCCGAG TCCCAGCCT GCGCCAGAG CTGCTCTGG GGGATCCTGC CGGAACCTCC 2640  
 AGCCCCCACC CGGATCTCTC ATCTAGCCGG GACCCCTTAC CTCTGAGGCC CATTGCGCG 2700  
 GGCCCAAGAG GCGCTTGTG GATGGGGGCC ACTGTGGCGG CCCCCAGGA AAGGTGAGC 2760  
 CGGGAGCAGG CAGAACCTCG GACTCCAGCC CAGCGTCTGG CCGGTCTCTT TGAAGTATAG 2820  
 AGCAGCAGC CCAGTGGGGC ACCCCAGCCC CTCTGCAITG AAGACATCAG CCTGTGGCA 2880  
 80 CCCCCTCCAG CAGCCCCACC CAGTCCCTTG CCAGGTCTG GACCCCTGCT CCACTACCTG 2940  
 AGCCTGCCCT TCTTCCGAGA GATGAATGTG GATGGGACT GGGCCCCGCT TGAAGAGCCC 3000  
 AGCCTGCTG CACCCCCAGA TTACATGGAT ACCCGGCGCT GTCCCACTTC ATCTTCTCTT 3060  
 CGTCTCCAG AAAACCCCTC TGTATCCCC AGGGAATCAC TTCTGGGGC TGTGTAGAGG 3120  
 GCTGGGGCCA CTGCAGAGCC CCCTTACACA GCCTGGCTG ACTGACACT GAGGAGCGG 3180  
 CTGCTGCCAG GCTTCTCTCC TGCTGCCCTC GAGGGCAGCC TCACCAAGCA GAGCAGCGG 3240

CGAGGCAGCG CTCTGTTCTC GCGGCCCCCC TCCACAGCCC CCTCTGCAGG AGGCAGCTAC 3300  
 CTCAGCCCTG CTCCAGGAGA CACCAGCAGC TGGGCCAGTG GCCCTGAGAG ATGGCCCCGA 3360  
 AGGGAGCATG TGGTGACAGT CAGCAAGAGG AGGAACACAT CTGTGGACGA GAACTATGAG 3420  
 TGGGACTCAG AATTCCTTGG GGACATGGAA TTGCTGGAGA CTITGCACCT GGGCTTGGCC 3480  
 5 AGCTCCCGGC TCAGACCTGA AGCTGAGACA GAGCTAGGTG TGAAGACTCC AGAGGAGGGC 3540  
 TGCCTCTCTG ACACTGCCCC TGTACTGGC CCTGAGGCCG GCTGTGCTGC CCTTCGGGAG 3600  
 GAATTCCTGG CCTTCGCGCG CCGCCGAGAT GCTACTAGGG CTGCGCTACC AGCCTATCGA 3660  
 CAGCCAGTCC CCCACCCCGA ACAGGCCACT CTGCTGTGAA CATCCCTAAT GTGAGGCTGT 3720  
 10 GAAAAGGCAT ATGGACCTGC AAAGGAGGCC CCCAACCAGA CAGACCTAGT TTCAAACGAG 3780  
 GGCACCTGCC CTGCTGCCCC CTTTGGTGCC CAGGCACAGA CCTGATAGT GGGTTTGGGT 3840  
 CACCTTGGTA TGGAAATGAT GTGCTGACCC CTTAGGTGAG TCTGGGGATT GGAACAGGGA 3900  
 TCTTAGGTCT GCCTCTCTCT CTCTCTCTCT CTCTCTCTCT GTGTGTGTGT 3960  
 GTGTGTGAAG TTTTTCACAG GTGAATAAAC AAAGTTTGAA AGAAAAAATA AAAAAAATAA 4020  
 15 AAAA 4024

Seq ID NO: C94 DNA Sequence  
 Nucleic Acid Accession #: NM\_006875  
 Coding sequence: 186..1190

20 1 11 21 31 41 51  
 GAATTCGGCA CGAGCGCGCG GCGAATCTCA ACGCTGCGCC GTCTGGGGGC GCTTCGGGGC 60  
 CACCACTTTC TCTGCTTTCC ACCCTGGGCG CCCCAGGCC TGGCTCCCA GCTGCGCTGC 120  
 25 CCGCGGGTTC CAGCCCTGCG GGGCTTAGCG GGTTCAGTGG GCTCAATCTG CCGAGCGCCA 180  
 CCTCCATGTT GACCAAGCCT CTACAGGGGC CTCCCGCGCC CCGCGGGACC CCCACGCGCG 240  
 CGCCAGGAGG CAAGGATCGG GAAGCGTTTC AGGCCGAGTA TCGACTCGGC CCCCTCTCGG 300  
 GTAAGGGGGG CTTTGGCACC GTCTTCGAG GACACCGCCT CACAGATCGA CTCAGGTGG 360  
 CATCAAAATG AATCCCGCGG AATCGTGTGC TGGGCTGGTC CCCCTGTGCA GACTCAGTCA 420  
 CATGCCCACT CGAAGTCGCA CTGCTATGGA AAGTGGGTGC AGGTGGTGGG CACCTGGCG 480  
 30 TGATCGCCTT GCTTGACTGG TTTGAGACAC AGGAAGGCTT CATGCTGGTC CTCGAGCGGC 540  
 CTTTGCCCGC CAGGATCTC TTTGACTATA TCACAGAGAA GGGCCCACTG GGTGAAGGCC 600  
 CAAGCCGCTG CTTCCTTGGC CAAGTAGTGG CAGCCATCCA GCACTGCCAT TCCCGTGGAG 660  
 TTGTCCATCG TGACATCAAG GATGAGAACA TCCTGATAGA CCTACGCCGT GGCTGTGCCA 720  
 AACTCATGTA TTTTGGTTCT GGTGCCCTGC TTCATGATGA ACCCTACACT GACTTTGATG 780  
 35 GGACAAGGAT GTACAGCCCC CCAGAGTGGG TCTCTCGACA CCACTACCAT GCACTCCCGG 840  
 CCACTGTCTG GTCACTGGGC ATCTCTCTCT ATGACATGGT GTGTGGGGAC ATTCCTTTTG 900  
 AGAGGGACCA GGAGATCTTG GAAGCTGAGC TCCACTTCCC AGCCCATGTC TCCCAGACT 960  
 CGTGTGCCCT AATCGCGCGG TGCTGGCCCC CCAAACTTTC TTCCGACCC TCACTGGAAG 1020  
 AGATCTCTGT GGACCCCTGG ATGCAACAC CAGCCGAGGA TGTTACCCCT CAACCCCTCC 1080  
 40 AAAGGAGGCC CTGCCCCCTT GGCTGGTCC TTGCTACCCT AAGCCTGGCC TGGCCTGGCC 1140  
 TGGCCCCCAA TGGTCAGAA AGCCATCCCA TGGCCATGTC ACAGGGATAG ATGGACATTT 1200  
 GTTGACTTGG TTTTACAGGT CATTACCACT CATTAAAGTC CAGTATTACT AAGGTAAGGG 1260  
 ATTGAGGTAG AGGGGTAGA AGACATAAAC CAAGTTTGCC CAGTTCCCTT CCAATCTCTA 1320  
 CAAGAGAGCC TTCCTCCAG AACCTGTGGT CCCTGATTTT GGAGGGGAA CTTCTTGCTT 1380  
 45 CTCATTTTGC TAAGGAAGTT TATTTTGGTG AAGTTGTTC CATTTTGAGC CCGGGGACTC 1440  
 TTATTTTGTG ATAGTGTAC CCACATTTGG CACCTCTCTAC TACCACACA CAACCTTAGT 1500  
 TCATATGCTT TTACTTGGGC AAGGGTGCCT TCCTTCCAAT ACCCCAGTAG CTTTATTTT 1560  
 AGTAAGGCTG AACTTTCCCG TAGCCTAGGG TCCCATATG GGTCAAGCTG CTTACCTGCC 1620  
 50 TCAGCCACGG ATTTTATTAT TTGGGGGAGG TAATGCCCTG TTGTACCCCG AAGCCTTCTT 1680  
 TTTTTTTTTT TTTTTTTTTG GGTGAGGGGA CCCTACTTTG TTATCCCAAG TGCTCTTATT 1740  
 CTGTGAGAGA GAACCTTAAT TCCATAATT TGGGAAGGAAT GGAAGATGGA CACCACCGGA 1800  
 CACCACACGA CAATAGGATG GATGGATGG TTTTGTGGG GATGGGCTAG GGGAAATAAG 1860  
 GCTTGTCTGT TGTTTTCTCG GGGCGCTCCC TCCAATTTG CAGATTTTGT CAACCTCCTC 1920  
 55 CTGAGCCGGG ATGTGCAAT TACTAAATG TAAATAATCA CGTATTGTGG GGAGGGGAGT 1980  
 TCCAAGTGTG CCTTCCTTTT TTTTCTGCCC TGGATTATTT AAAAAAGCCAT GTGTGGAAC 2040  
 CCACATTTTA ATAAAGTAA TAGAATCAGA AAAAAAATAA AAAAAAATAA 2088

Seq ID NO: C95 DNA Sequence  
 Nucleic Acid Accession #: NM\_002510.1  
 Coding sequence: 92..1774

60 1 11 21 31 41 51  
 CAGATGCCAG AAGAACTCTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60  
 65 CCTTGAGTGC CTGCGTCCGT GAGAATTCAG CATGGAATGT CTCTACTATT TCCTGGGATT 120  
 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGGCGCCAAA CGATTTCATG ATGTGCTGGG 180  
 CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAATAGGCT GGTCTTCTGA 240  
 TGAATAATGAC TGAATGAAA AACTCTACCC AGTGTGGAAG CGGGAGACA TGAGGTGGAA 300  
 70 AAATCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTGACC AGTGACTCAC CAGCCCTCGT 360  
 GGGCTCAAAAT ATAACATTG CGGTGAACCT GATATTCCTT AGATGCCAAA AGGAAGATGC 420  
 CAATGGCAAC ATAGTCTATG AGAAGAACTG CAGAAATGAG GCTGGTTTAT CTGCTGATCC 480  
 ATATGTTTAC AACTGGACAG CATGGTCAGA GGACAGTGAC GGGGAAATG GCACCGGCCA 540  
 AAGCCATCAT AACGTCTTCC CTGATGGGAA ACCTTTTCTT CACCAACCCG GATGGAGAAG 600  
 75 ATGGAATTTT ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT TGGGACGATG 660  
 TTCAGTGAGA GTTCTCTGTA ACACAGCCAA TGTGACACTT GGGCTCTCAAC TCATGGAAGT 720  
 GACTGTCTAC AGAAGACATG GACGGGCATA TGTTCCTATC GCACAAAGTA AAGATGTGTA 780  
 CGTGGTAACA GATCAGATTC CTGTGTTTGT GACTATGTTT CAGAAGAACG ATCGAAATTC 840  
 ATCCGACGAA ACCTTCTCTA AAGATCTCCC CATTATGTTT GATGTCCTGA TTCATGATCC 900  
 80 TAGCCACTTC CTCATTTATT CTACCAITAA CTACAAGTGG AGCTTCGGGG ATAATACTGG 960  
 CCTGTTTGTG TCCACCAATC ATACTGTGAA TCACACGTAT GTGCTCAATG GAACCTTCAG 1020  
 CCTTAACCTC ACTGTGAAAG CTGCAGCACC AGGACCTTGT CCGCCACCGC CACCACCCAC 1080  
 CAGACCTTCA AAACCCACCC CTTCTTTAGG ACCTGCTGGT GACAACCCCC TGGAGCTGAG 1140  
 TAGGATTCCT GATGAAAAT GCCAGATTAA CAGATATGGC CACTTTCAGG CCACCATCAC 1200  
 AATTGTAGAG GGAATCTTAG AGGTAAACAT CATCCAGATG ACAGACGTCC TGATGCCGGT 1260

5	GCCATGGCCT	GAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
	GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGAGATC	ACCCAGAACA	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCCCT	1500
	GATTTCTGTT	CTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAACA	GTGCCCTGAT	1560
	CTCCGTTGGC	TGCTTGGCCA	TATTTGTAC	TGTGATCTCC	CTCTGGTGT	ACAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAATAGTCC	TGGGAATGTG	GTGAGAAGCA	AAGGCTCGAG	1680
	TGTCTTTCTC	AACCGTGCAA	AAGCGGTGT	CTTCCGGGA	AACCAGGAAA	AGGATCCGCT	1740
10	ACTCAAAAC	CAAGAATTTA	AAGGAGTTTC	TAAATTTTCG	ACCTTGTTC	TGAAGCTCAC	1800
	TTTTCACTGC	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTT	TTCTAAAGA	1860
	TTATTGTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGT	TAAATGTCAAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTATGT	TTCATTATA	AAGTCTTAGG	2040
15	TAAGTAGTAG	GATAGAAACA	CTGTGTCCTG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
	AGCCTAACCC	AGGTTAACTG	CAAGAAGAGG	CGGGATACCT	TCAGCTTTCC	ATGTAAGTGT	2160
	ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCCAC	2220
	TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTGACTTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
20	TGACAACCTA	CTTGTCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCAT	2400
	GGACATTTAG	TTAGTGCTTT	TTATATACCA	GGCATGATCG	TGAGTGACAC	TCCTGTGAT	2460
	ATTTCCAAAT	TTTTGTATAG	TGCTGACACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGTGC	CCTGTTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTCCAC	TCCTTTGTA	2580
	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTTCTTT	TCTCTCTTC	CTGAAAAATA	2640
25	AAGTGTGGGA	AGAGACAAAA	AAAAAAA				2669

Seq ID NO: C96 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1-4247

30	1	11	21	31	41	51	
	ATGCGAATCC	TAAAGCGTTT	CCTCGCTTGC	ATTCAGCTCC	TCTGTGTTTG	COGCTGAGAT	60
	TGGGCTAATG	GATACTACAG	ACAACAGAGA	AAACTTGTG	AAGAGATTGG	CTGTCTCTAT	120
35	ACAGGAGCAC	TGAATCAAAA	AAATTGGGGA	AAGAAATATC	CAACATGTAA	TAGCCCAAAA	180
	CAATCTCCTA	TCAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
	AAATTTCAAG	GTTGGGATAA	AACATCATTG	GAAAAACAT	TCATTCTATA	CAGTGGGAAA	300
	ACAGTGGAAA	TTAATCTCAC	TAATGACTAC	CGTGTGAGCG	GAGGAGTTTC	AGAAATGGTG	360
	TTTAAAGCAA	GCAAGATAAC	TTTTCACTGG	GGAAAATGCA	ATATGTCTATC	TGATGGATCA	420
40	GAGCATAGTT	TAGAAGGACA	AAAATTTCCA	CTTGAGATGC	AAATCTACTG	CTTTGATGCA	480
	GACCGATTTT	CAAGTTTTGA	GGAAGCAGTC	AAAGGAAAAG	GGAAGTTAAG	AGCTTTATCC	540
	ATTTTGTGTT	AGGTTGGGAC	AGAAGAAAAT	TTGGATTCCA	AAGCGATTAT	TGATGGAGTC	600
	GAAAGTGTTA	GTGTTTTTGG	GAAAGCAGCT	GCTTTAGATC	CATTCTACT	GTGAAACCTT	660
	CTGCCAAACT	CACTGACAAA	GTATTACATT	TACAATGGCT	CATTGACATC	TCCTCCCTGC	720
45	ACAGACACAG	TTGACTGGAT	TGTTTTTAAA	GATACAGTTA	GCATCTCTGA	AAGCCAGTTG	780
	GCTGTTTTTT	GTGAAGTTCT	TACAATGCAA	CAATCTGGTT	ATGTCATGCT	GATGGACTAC	840
	TTACAAAACA	ATTTTCGAGA	GCAACAGTAC	AAGTTCTCTA	GACAGGTGTT	TTCTCTATAC	900
	ACTGGAAGAG	AAGAGATTCA	TGAAGCAGTT	TGTAGTTTCA	AACAGAGAAA	TGTTTCAAGCT	960
	GACCCAGACA	ATATACCCAG	CCTTCTTGT	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
50	ACCATGATTG	AGAAGTTTGC	AGTTTGTATC	CAGCAGTTGG	ATGAGAGGGA	CCAAACCAAG	1080
	CATGAATTTT	TGACAGATGG	CTATCAAGAC	TTGGGTGCTA	TTCTCAATAA	TTTGCTACCC	1140
	AATATGAGTT	ATGTTCTTCA	GATAGTAGCC	ATATGCACTA	ATGGCTTATA	TGGAATAATC	1200
	AGGCAACCA	TGATTTGCGA	CATGCCCTACT	GATAATCCTG	AACCTGATCT	TTTCCCTGAA	1260
	TTAATTGAAA	CTGAAGAAAT	AATCAAGGAG	GAGGAAGAGG	GAAAGACAT	TGAAGAAGGC	1320
55	GCTATTGTGA	ATCCTGGTAG	AGACAGTGCT	ACAAACCAAA	TCAGGAAAAA	GGAACCCAG	1380
	ATTTCTACCA	CAACACACTA	CAATCGCATA	GGGACGAAAT	ACAATGAAGC	CAAGACTAAC	1440
	CGATGCCCAA	CAGAGAGAA	TGAATTTCT	GGAAAGGGTG	ATGTTCCCAA	TACATCTTTA	1500
	AAATCCACTT	CCCAACCACT	CACTAAATTA	GCCACAGAAA	AAGATATTTC	CTTGACTTCT	1560
	CAGACTGTGA	CTGAATCTGC	ACCTCACACT	GTGGAAGGTA	CTTCAGCCTC	TTTAAATGAT	1620
60	GGCTCTAAAA	CTGTTCTTAG	ATCTCCACAT	ATGAACCTGT	CGGGGACTGC	AGAATCCTTA	1680
	AATACAGTTT	CTATAACAGA	ATATGAGGAG	GAGAGTTTAT	TGACCAAGTTT	CAAGCTTGAT	1740
	ACTGGAGCTG	AAGATTCTTC	AGGCTCCAGT	CCCGCAACTT	CTGCTATCCC	ATTCATCTCT	1800
	GAGAACATAT	CCCAAGGGTA	TATATTTTCC	TCCGAAAAAC	CAGAGACAAT	AACATATGAT	1860
	GTCTTATACA	CAGAACTCTG	TAGAAATGCT	TCCGAAAGAT	CAACTTCTATC	AGGTTTCAGAA	1920
65	GAATCACTAA	AGGATCTCTC	TATGGAGGGA	AATGTGTGGT	TTCTTAGCTC	TACAGACATA	1980
	ACAGCACAGC	CCGATGTTGG	ATCAGGCAGA	GAGAGCTTTC	TCCAGACTAA	TTACACTGAG	2040
	ATACGTTGTT	ATGAATCTGA	GAAGACAACC	AAGTCTTTT	CTGCAGGCCC	AGTGATGTCA	2100
	CAGGGTCCCT	CAGTTACAGA	TCGTGAAATG	CCACATTATT	CTACCTTTGC	CTACTTCCCA	2160
	ACTGAGGTAA	CACCTCATGC	TTTTACCCCA	TCCTCCAGAC	AACAGGATTT	GGTCTCCACG	2220
70	GTCAACGTGG	TATACTGCGA	GACAACCCAA	CCGTATACAA	ATGAGGCCAG	TAATAGTAGC	2280
	CATGAGTCTC	GTATTGTTCT	AGCTGAGGGG	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	2340
	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	TGCTAGTGG	TTCTTGTGGG	TATTCTCATC	2400
	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	TTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	2460
	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	CCAATTTTCA	ATGATGTGGG	AGCAATTTCA	2520
75	ATAAAGCACT	TTCCAAGACA	TGTTGCAGAT	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	2580
	TTTGAGGAAG	TGCAGAGCTG	TACTGTTGAC	TTAGGTATTA	CAGCAGACAG	CTCCAACCCAC	2640
	CCAGACACAA	AGCACAAGAA	TGATACATA	AATATCGTTG	CCTATGATCA	TAGCAGGGTT	2700
	AAGCTAGCAC	AGCTTGTCTG	AAAGGATGGC	AAACTGACTG	ATTATATCAA	TGCCAATTAT	2760
	GTTGATGGCT	ACAACAGACC	AAAAGCTTAT	ATTGCTGCCC	AAGGCCCACT	GAAATCCACA	2820
80	GCTGAAGATT	TCTGAGAAAT	GATATGGGAA	CATAATGTGG	AAGTTATTGT	CATGATAACA	2880
	AACCTGTGTT	AGAAAGGAAG	GAGAAAATGT	GATCAGTACT	GGCCTGCCGA	TGGAGTGGAG	2940
	GAGTAACGGG	ACTTTCTGTT	CACCTCAGAA	AGTGTGCAAG	TGCTTGCTTA	TTTACTGTG	3000
	AGGAATTTTA	CTCTAAGAAA	CACAAAATAA	AAAAAGGGCT	CCCGAAGAGG	AAGACCCAGT	3060
	GGACGTGTGG	TCACACAGTA	TCATACACG	CAGTGGCCTG	ACATGGGAGT	ACCAGAGTAC	3120
	TCCTGCGCAG	TGCTGACCTT	TGTGAGAAAG	GCAGCCTATG	CCAAGCGCCA	TGCAGTGGGG	3180

5	CCTGTTGTCG	TCCACTGCAG	TGCTGGAGTT	GGAAGAACAG	GCACATATAT	TGTGCTAGAC	3240
	AGTATGTTGC	AGCAGATTCA	ACACGAAGGA	ACTGTCAACA	TATTTGGCTT	CTTAAACAC	3300
	ATCCGTTTAC	AAAGAAATTA	TTTGGTACAA	ACTGAGGAGC	AATATGCTTT	CATTATGAT	3360
	ACACTGGTTG	AGGCCATACT	TAGTAAAGAA	ACTGAGGTGC	TGGACAGTCA	TATTATGCC	3420
	TATGTTAATG	CACTCTCAT	TCTTGGACCA	GCAGGCAAAA	CAAAGCTAGA	GAAACAATTC	3480
	CAGCTCTGTA	GCCAGTCAAA	TATACAGCAG	AGTGACTATT	CTGCAGCCCT	AAAGCAATGC	3540
	AACAGGGAAA	AGAATCGAAC	TTCTTCTATC	ATCCCTGTGG	AAAGATCAAG	GGTTGGCATT	3600
	TCATCCCTGA	GTGGAGAAGG	CACAGACTAC	ATCAATGCCT	CCTATATCAT	GGGCTATTAC	3660
10	CAGAGCAATG	AATTATCAT	TACCCAGCAC	CCTCTCCTTC	ATACCATCAA	GGATTTCGG	3720
	AGGATGATAT	GGGACCATAA	TGCCCACTG	GTGGTTATGA	TTCTGATGG	CCAAAACATG	3780
	GCAGAAGATG	AATTGTTTAA	CTGGCCAAAT	AAAGATGAGC	CTATAAATTG	TGAGAGCTTT	3840
	AAGGTCACTC	TTATGGCTGA	AGAACACAAA	TGCTATCTA	ATGAGGAAAA	ACTTATAATT	3900
	CAGGACTTTA	TCTTAGAAGC	TACACAGGAT	GATTATGTAC	TTGAAGTGAG	GCACITTCAG	3960
15	TGTCCTAAAT	GGCCAAATCC	AGATAGCCCC	ATTAGTAAAA	CTTTTGAAGT	TATAAGTGTT	4020
	ATAAAGAAG	AAGCTGCCAA	TAGGGATGGG	CCTATGATTG	TTCATGATGA	GCATGGAGGA	4080
	GTGACGGCAG	GAACITTCCTG	TGCTCTGACA	ACCCTTATGC	ACCAACTAGA	AAAAGAAAAAT	4140
	TCCGTGGATG	TTTACACAGT	AGCCAAGATG	ATCAATCTGA	TGAGGGCAGG	AGTCTTTGCT	4200
	GACATTGAGC	AGTATCAGTT	TCTCTACAAA	GTGATCCTCA	GCCTTGTGAG	CACAAGGCAG	4260
20	GAAGAGAATC	CATCCACCTC	TCTGGACAGT	AATGGTGCAG	CATTGCCTGA	TGGAATATA	4320
	GCTGAGAGCT	TAGAGTCTTT	AGTTTAA				4347

Seq ID NO: C97 DNA Sequence  
Nucleic Acid Accession #: XM\_031379  
Coding sequence: 148..7095

25	1	11	21	31	41	51	
	CACACATACG	CACGACAGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
30	CAAAAAAAAC	ATTTCCCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGACAGCCG	TCTGGAAATG	CGAATCTCTA	AGCGTTTCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGAAG	AGATTGGCTG	GTCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
35	AACACATTCA	TTCTAAACAC	TGGGAAACAA	GTGGAATTA	ATCTCACTAA	TGACTACCGT	480
	CTCAGCGGAG	GAGTTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
40	GGAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTATAGT	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACCTGT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTATC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTCTTAC	AATGCAACAA	960
45	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCTATG	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACAGCCCT	TCTTGTATCA	1140
	TGGGAAGAGC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
50	GGTGCTATTG	TCAATAATTT	GCTACCCAA	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
	GAGAGGAGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGTTAGAGA	CAGTGCTACA	1500
	AACCAAAATG	GGAAAGGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACCAA	GAGGAAGTGA	ATTCCTGAGA	1620
55	AAGGGTGATG	TCCCAATAT	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCCT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCTCTTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGACGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGATAA	TGAGGAGGAG	1860
	AGTTTATGTA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCCTCAGG	CTCCAGTCCC	1920
60	GCAACTTCTG	CAATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTCTCTCC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAGGATTCAA	CTTCATCAGG	TTCAAGAGAA	TCATAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
65	TGCTTTCTG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCAACCCG	2400
	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCTTACAGTA	GTGAAGTCTT	TCTCTAGTTC	2460
	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
70	TGCGCTTTCG	ATGCTAGGCC	TGTAATTCCT	AGTGTGATG	TGTCATTGTA	ATCCATCCTG	2580
	TCTTCTTATG	ATGGTGACCC	TTTGCTTCCA	TTTTCTCTG	CTTCTCTCAG	TAGTGAATTG	2640
	TTTCGCTATC	TGCATACAGT	TTCTCAAATC	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
	GATAAGTGCG	GTGTAACTTA	TTCTCTGCCA	GTGGCTGGGG	GTGATTGCTT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
75	TTTGTGATGG	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTCTT	TCAGGGCCTG	AACCTTCTTA	TGCCITGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTCCTTACA	GTTCGCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACTTA	TCAGGGTTC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCAATTAATG	AGCCTACTCA	TGCCCTCTCT	3120
80	GGTATGTTGG	TAAGTGTCTG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACTT	GTTCCTGTAG	CTGAATTTAC	ATATACAAAC	3240
	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATAGAG	3300
	ACTGAACCTG	AAATTCCTCT	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420

	ATTCTAGCA	CCAAGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCAG	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	CTGGTGACAC	TTGGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
5	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TTAAAACGTG	TCCTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAAAC	3780
	CCCAAGTTG	ATAAAATTAG	TTCTCAATAG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAACA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
10	ATGCACCTCG	CTTCACCTCA	AGGTTTGACC	ATTTCTCTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTTGTTAA	AAAGTGAAAG	TTCCCAACCA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAA	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AAATGATGAA	CCATTAAATA	CACTAATAAA	TAAGCTTATA	4140
	CATTGATG	AAATTTTAA	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
15	ATTTCAACAG	TGCTTCTGTA	TACATTGTA	TCTACTGATC	ATTCGTGTC	TATAGGAAAT	4260
	GGGCATGTT	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCGTGTA	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGGAAG	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTCTAAG	TGTATGTCAT	GCTCATCCTA	TAGAGAAATCA	4500
20	CAGGAAAAGG	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAAATAAT	4560
	CCAATCTCAT	ACTCAGTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
	TCAGACAGTC	AACTCTGTTAT	GGACAGAAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
25	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTTGCA	4860
	GACACTAATG	AAAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCAC	AGTCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAAT	GTTCACGTT	4980
	TCAGAGGAGC	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTG	5040
	GAATCCGAGA	GAAGGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
30	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAAGT	ATGTCGGAGC	AATTCCAATA	AAGCACTTTC	CRAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	5400
35	CACAAGAAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	5580
	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTATTGTGTA	TGATAACAAA	CCTCGTGGAG	5640
40	AAAGGAAGGA	GAATATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCTTATT	ATACTGTGAG	GAATTTTACT	5760
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTC	5940
	CAGTGCAGTG	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCGA	6000
45	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTTCAAA	6060
	AGAAATTATT	TGGTACAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	6120
	GCCATACTTA	TGAAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTTATGCCTA	TGTTAATGCA	6180
	CTCCTCATTG	CTGGACCAAG	AGGCCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
	CAGTCAAAAT	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAGAG	6300
50	AATCGAATCT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TGGCATTTC	ATCCCTGAGT	6360
	GGAGAAGGCA	CAGACTACAT	CAATGCCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTTCATCATT	CCCAGCACCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
	GACCATATAT	CCCACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
55	ATGGCTGAAG	AACACAAATG	TCTATCTAAT	GAGGAAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
	CCAAATCCAG	ATAGCCCCAT	TAGTAAAACT	TTTGAACCTA	TAAGTGTATT	AAAAGAAGAA	6780
	CGTCCCAATC	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
	ACTTCTCTGT	CTCTGACCA	CCTTATGCAC	CAACTAGAAA	AAGAAAATTC	CGTGGATGTT	6900
60	TACCGAGTAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCTTGTCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAAATCCA	7020
	TCCACCTCTC	TGGACAGTAA	TGGTGACGCA	TTGCCTGATG	GAATATATAG	TGAGAGCTTA	7080
	GAGTCTTTAG	TTTAACACAG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTCTCTC	7140
	TTCTAAAAAT	TAGGCAGGAA	AATCAGTCTA	GTCTCTGTTT	CTGTGTGATT	CCCATCACCT	7200
65	GACAGTAAAT	TTTCATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTTA	CAATGTGTGC	7260
	CATTTTGCAA	GACTGTGTAAT	TTACTTATTA	TGTTTGAAGT	AAAATGATTG	AATTTTACAG	7320
	TATTTCTAAG	AATGGAATTG	TGGTATTTTT	TCTGTATTG	ATTTTAAACAG	AAAATTTCAA	7380
	TTTATAGAGG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAAATTTTA	7440
	GCTGTATTTG	TAGCAATTAT	CAGGTTTGCT	AGAAATATAA	CTTTTAATAC	AGTAGCCTGT	7500
70	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAATACT	GCCCTAGTGT	CTCCATGGAC	CAAAATTTATA	7620
	TTTATAATTG	TAGATTTTTA	TATTTTACTA	CTGAGTCAAG	TTTTCTAGTT	CTGTGTAAAT	7680
	GTTTAGTTTA	ATGACGTAGT	TCATTAGCTG	GTCTTACTCT	ACCAGTTTTT	TGACATTGTA	7740
	TTGTGTTACC	TAGTCAATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAAAATA	7800
75	GAATACCTT	CAITTTGAAA	GAAGTTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTTCA	7860
	AATGGTTTTT	ATCCAAAGAA	TTGCAAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAAAATA	7920
	AAAAAAAATA	AAAAAAAATA	AAAA				7944

Seq ID NO: C98 DNA Sequence  
Nucleic Acid Accession #: NM\_002851  
Coding sequence: 77..4518

1	11	21	31	41	51	
CACACRATAG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60



	CAAAAAAATC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCGCA	120
	CGGCGAGGGG	CGCGAGACCG	TCTGGAAATG	CGAATCTTAA	AGCGTTTCC	CGCTTGCAAT	180
	CAGCTCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAA	240
5	CTTGTGAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCCAAAACA	TCTCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAC	ATCATTGGAA	420
	AACACATTCA	TTCAATACAC	TGGGAAAACA	GTGGAATTA	ATCTCACTAA	TGACTACCGT	480
	GTACGCGGAG	GAGTTTCAGA	AATGGTGT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
10	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	TGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTTAC	840
15	AATGGCTCAT	TGACATCTCC	TCCTTGACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAG	CCAGTTGGCT	GTTTTGTG	AAGTCTTAC	AATGCAACAA	960
	CTGCTTATG	TGATCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCAATG	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCT	TCTGTGTACA	1140
20	TGGGAAAGAC	CTGAGTGTG	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCA	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGTATTC	TCAATAATT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACATATG	GCCTATATGG	AAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCTG	AAGAAATAAT	CAAGGAGGAG	1440
25	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCAACA	CACACTACAA	TCCGATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAG	ATATTCTCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACT	TCACTCTGTG	1740
30	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCATATATG	1800
	AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAAAGAAATA	TGAGGAGGAG	1860
	AGTTTATGAC	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAARACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
35	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTCC	AGCAATAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTCTG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CTTTGCTCTA	CTTCCCACT	GAGGTAACAC	CTCATGCTTT	TACCCATCC	2340
40	TCCAGACAAC	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCACCCG	2400
	GTATACAAAT	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGCAAGAGCG	AGTTATACCC	CTTGATGCTG	TGTCAGCCCT	GACTTTTATC	2520
	TGCTAGTGG	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
	TTTTACTTAG	AGGACAGTAC	ATCCCTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
45	CCAATTTTCA	ATGATGTCGG	AGCAATTCCA	ATAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTATGCGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACCTGTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
50	TACACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCTGT	3060
	GAGAAAGGAA	GGAGAAATGT	TGATCAGTAC	TGGCCTGCGG	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTCTGCG	TCACCTAGAA	GAGTGTGCAA	GTGCTTGCTT	ATTATACTGT	GAGGAATTTT	3180
	ACTCTAAGAA	ACACAATAAT	AAAAAGGGC	TCCCAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
55	GTACACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACA	GGCACAATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATT	AACACGAAGG	AACGTGCAAC	ATATTGCGCT	TCTTAAACAA	CATCCGTTCA	3480
	CAAAAGAAAT	ATTGTTGATA	AACGTAGGAG	CAATATGTCT	TCATTCAATG	TACACTGGTT	3540
60	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGTC	ATATTCAATG	CTATGTTAAT	3600
	GCACTCTCTA	TTCTGGGACC	AGCAGGCAAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCTCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AGAATTCGAA	CTTCTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTGGGCAT	TTCACTCCCTG	3780
	AGTGGAGAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
65	GAATTCATCA	TTACCCAGCA	CCCTCTCTCT	CATACCATCA	AGGATTCTG	GAGGATGATA	3900
	TGGGACCATTA	ATGCCCACT	GGTGGTTATG	ATTCTGATG	GCCAAACAT	GGCAGAAGAT	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGTCTATCT	AATGAGGAAA	AACTTATAAT	TCAGGACTTT	4080
70	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGCTCTAAA	4140
	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAAGAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTCATGATG	AGCATGGAGG	AGTGAACGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAA	TTCCGTGGAT	4320
	GTTTACCCAG	TAGCCAAAGT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTGA	GCACAAGGCA	GGAAAGAAAT	4440
75	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTGCTG	ATGGAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAACA	CAGAAAGGGG	TGGGGGAGCT	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCTTAA	AATTAGGACG	GAAATCAGT	CTAGTTCTGT	TATCTGTGTA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTTATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
80	TGCTTTTGG	CACAGACTGT	AATTTACTTA	TTATGTTTGA	ACTAAAATGA	TTGAATTTTA	4740
	CAGTATTTCT	AAGAAATGAA	TTTGTGTTAT	TTTTCTGTGA	TTGATTTTAA	CAGAAAATTT	4800
	CAATTTATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAAATGT	TTGTTTATAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAATATAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCACT	ATTCACCTAA	4980
	AGTAGAATA	ATCTGTTACT	TATTGTAAAT	ACTGCCCTAG	TGCTTCCATG	GACCAATTTT	5040
	ATATTTATAA	TTGTAGATTT	TTATATTTTA	CTACTGAGTC	AAGTTTCTTA	GTCTGTGTGA	5100



5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

ATTGTTTAGT TTAATGACGT AGTTCATTAG CTGGTCTTAC TCTACCAGTT TTCTGACATT 5160  
 GTATTGTGTT ACCTAAGTCA TTAACCTTGT TTCAGCATGT AATTTTAACT TTGTGGGAAA 5220  
 ATAGAAATAC CTTCAATTTG AAAGAAGTTT TTATGAGAAT AACACCTTAC CAAACATTGT 5280  
 TCAATGGTT TTTATCCAAAG GAATTGCCAA AATAAATATA AATATTGCCA TTAACAAAAA 5340  
 AAAAAA AAAA AAAA AAAA AAAA 5367

Seq ID NO: C99 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 501..4514

1 11 21 31 41 51  
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAARAC ATTTCTCTCG CTCCCTCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CGCGAGACCG TCTGGAAATG CGAATCTTAA AGCGTTTCTT CGCTTGCAAT 180  
 CAGCTCCTCT GTGTTTGGCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTGTGTGAAG AGATTGGCTG GTCTATACA GGAGCACTGA ATCAAAAAAT TGGGGAAGA 300  
 AATATCCAAAC ATGTAATAGC CCAAAACAA CTCTATCAA TATTGATGAA GATCTTACAC 360  
 AAGTAAATGT GAATCTTAAG AAATCTAAAT TTCAGGGTTG GGATAAAACA TCATTGGAAA 420  
 ACACATTCAT TCATAACACT GGGAAAAACAG TGGAAATTA TCTCACTAAT GACTACCGTG 480  
 TCAGCGGAGG AGTTTCAGAA ATGGTGTTTA AAGCAAGCAA GATAACTTTT CACTGGGAAA 540  
 AATGCAATAT GTCATCTGAT GGATCAGAGC ATAGTTTGA AGGACAAAAA TTTCACCTTG 600  
 AGATGCCAAT CTACTGCTTT GATGCGGACC GATTTTCAAG TTTTGAGGAA GCAGTCAAG 660  
 GAAAAGGGAA GTTAAGAGCT TTATCCATT TGTGTGAGT TGGGACAGAA GAAAATTTGG 720  
 ATTTCAAAGC GATTATTGAT GGAGTCGAAA GTGTTAGTGG TTTTGGGAAG CAGGCTGCTT 780  
 TAGATCCATT GTATCTGTTG AACCTTCTGC CAAACTCAAC TGACAAGTAT TACATTTACA 840  
 ATGGCTCATT GACATCTCCT CCTGACAGAG ACACAGTTGA CTGGATTGTT TTTAAAGATA 900  
 CAGTGAATCAG CTCTGAAGAG CAGTTGGCTG TTTTGTGTA AGTTCCTTACA ATGCAACAAT 960  
 CTGTTATGT CATGCTGATG GACTACTTAC AAAACAATT TCGAGAGCAA CAGTACAAGT 1020  
 TCTCTAGACA AGTGTTTTCC TCATACACTG GAAAGGAAGA GATTATGAA GCAGTTTGT 1080  
 GTTCAGAAC AGAAAATGTT CAGGCTGACC CAGAGAATTA TACCAGCCTT CTGTTTACAT 1140  
 GGGAAAGACC TCAGAGTCGT TATGATACCA TGATTGAGAA GTTTGCAGTT TTGTACCAGC 1200  
 AGTTGGTAGG AGAGGACCAA ACCAAGCATG AATTTTGTAC AGATGGCTAT CAAGACTTGG 1260  
 GTGCTATTCT CAATAATTG CTACCAATA TGAGTTATGT TCTTCAGATA GTAGCCATAT 1320  
 GCACTAATGG CTATATAGGA AAATACAGCG ACCAATGAT TGTGACATG CCTACTGATA 1380  
 ATCCTGAATC TGATCTTTT CCTGAATTAA TTGGAACCTG AGAAATAATC AAGGAGGAGG 1440  
 AGAGGGGAAA AGACATTGAA GAAGGCGCTA TTGTGAATCC TGTGAGAGAC AGTGCTACAA 1500  
 ACCAATCAG GAAGAAGGAA CCCCAGATT CTACCAACAC ACCTACAAT CGCATAGGGA 1560  
 CGAAATACAA TGAAGCCAG ACTAACCGAT CCCCAACAG AGGAAGTGAA TTCTCTGGAA 1620  
 AGGGTGATGT TCCCAATACA TCTTTAAAT CCACCTOCCA ACCAGTCACT AAATTAGCCA 1680  
 CAGAAAAAGA TATTCTCTG ACTTCTCAGA CTGTGACTGA ACTGCCACT CACACTGTGG 1740  
 AAGGTACTTC AGCCTCTTTA AATGATGGCT CTAACACTGT TCTTAGATCT CCACATATGA 1800  
 ACTTGTGGG GAGGTCAGAA TCCTTAAATA CAGTTTCTAT AACAGAAAT GAGGAGGAGA 1860  
 GTTTATTGAC CAGTTTCAAG CTTGATCTG GAGCTGAAGA TTCTTCAGGC TCCAGTCCCG 1920  
 CAACCTCTGC TATCCCATTC ATCTCTGAGA ACATATCCCA AGGGTATATA TTTCTCTCG 1980  
 AAAACCCAGA GACAATAACA TATGATGTCC TTATACCAGA ATCTGTAGA AATGCTTCCG 2040  
 AAGATTCAAC TTATCAGGT TCAGAAGAA CACTAAAGGA TCCTTCTATG GAGGGAATG 2100  
 TGTGTTTAC TGGCTCTACA GACATAACAG CACAGCCCGA TGTGAGTCA GGCAGAGAGA 2160  
 GCTTCTCCA GACTAATTAC ACTGAGATAC GTGTTGATGA ATCTGAGAAG ACAACCAAGT 2220  
 CCTTTCTGC AGGCCAGTG ATGTCACAGG GTCCCTCAGT TACAGATCTG GAAATGCCAC 2280  
 ATTAATCTAC CTTTGGCTAC TTCCCACTG AGGTAAACACC TCATGCTTTT ACCCCATCCT 2340  
 CCAGACAACA GGATTGGTC TCACCGTCA AOGTGGTATA CTCGAGACA ACCCAACCGG 2400  
 TATACAAATG GCGCAGTAAT AGTAGCCATG AGTCTGTAT TGGTCTAGT GAGGGGTTGG 2460  
 AATCGAGAA GAAAGCGATT ATACCCCTTG TGATGTGTG AGCCCTGACT TTTATCTGTC 2520  
 TAGTGGTTCT TGTGGGTATT CTACTACTT GGAGGAATG CTTCCAGACT GCACACTTTT 2580  
 ACTTAGAGGA CAGTACATCC CCTAGAGTTA TATCCACACC TCCAACACT ATCTTCCAA 2640  
 TTTGAGTGA TGTGGAGCA ATTCCAATA AGCACTTTC AAAGCATGTT GCAGATTTAC 2700  
 ATGCAAGTAG TGGGTTTACT GAAGAATTG AGACACTGAA AGAGTTTAC CAGGAAGTGC 2760  
 AGAGCTGTAC TGTGACTTA GGTATTACAG CAGACAGCTC CAACCAACCA GACAACAGC 2820  
 ACAAGAATCG ATACATAAAT ATCGTTGCT ATGATCATAG CAGGGTTAAG CTAGCACAGC 2880  
 TTGCTGAAAA GATGCGCAAA CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA 2940  
 ACAGACCAAA AGCTTATATT GCTGCCAAG GCCACTGAA ATCCACAGCT GAAGATTTCT 3000  
 GGAGAATGAT TGGGAACAT AATGTGGAAG TTATTGTAT GATAACAAAC CTCGTGGAGA 3060  
 AAGGAAGGAG AAAATGTGAT CAGTACTGGC CTGCCGATGG GAGTGAGGAG TACGGGAAGT 3120  
 TTCTGGTCAC TCAGAAGAGT GTGCAAGTGC TTGCCATTAT TACTGTGAGG AATTTTACTC 3180  
 TAAGAAACAC AAAAAATAAA AAGGGCTCCC AGAAAGGAAG ACCCAGTGA CGTGTGGTCA 3240  
 CACAGTATCA CTACACGAG TGGCCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC 3300  
 TGACCTTTGT GAGAAAGGCA GCCTATGCCA AGGCCATGC AGTGGGGCCT GTTGTGCTCC 3360  
 ACTGCAGTGC TGGAGTTGGA AGAACAGGCA CATATATTGT GCTAGACAGT ATGTTGCAGC 3420  
 AGATTCAACA CGAAGGAAGT GTCAACATAT TTGCTTCTT AAAACACATC CGTTCACAAA 3480  
 GAAATTTATT GGTACAAACT GAGGAGCAAT ATGTCTTCT TCATGATACA CTGGTTGAGG 3540  
 CCATACTTAG TAAAGAACT GAGGTGCTGG ACAGTCTAT TCATGCTTAT GTTAATGCAC 3600  
 TCCTCAATCC TGGACAGCA GGCAAAACAA AGCTAGAGAA ACAATTCAG CTCTGAGCC 3660  
 AGTCAAAAT ACAGCAGAGT GACTATTCTG CAGCCCTAAA GCAATGCAAC AGGGAAAAGA 3720  
 ATCGAACTTC TTCTATCATC CCGTGGGAAA GATCAAGGGT TGGCATTTC TCCCTGAGTG 3780  
 GAGAAGGCAC AGACTACATC AATGCTCCT ATATCATGGG CTATTACAG AGCAATGAAT 3840  
 TCATCATTAC CCAGCACCTC CTCTCTATA CCATCAAGGA TTTCTGAGG ATGATATGGG 3900  
 ACCATAATGC CCAACTGGTG GTTATGATTC CTGATGGCCA AAACATGGCA GAAGATGAAT 3960  
 TTGTTTACTG GCCAAATAAA GATGAGCCTA TAAATTGTGA GAGCTTTAAG GTCACCTTA 4020  
 TGGCTGAAGA ACACAAATGT CTATCTAATG AGGAAAAACT TATAATTTCAG GACTTTATCT 4080  
 TAGAAGCTAC ACAGGATGAT TATGTACTTG AAGTGAGGCA CTTTCACTGT CCTAAATGGC 4140  
 CAAATCCAGA TAGCCCACTT AGTAAACTT TTGAACCTAT AAGTGTATA AAGAGAAG 4200  
 CTGCCAATAG GATGGGCTT ATGATTGTTC ATGATGAGCA TGGAGGAGTG ACGGAGGAA 4260  
 CTTTCTGTGC TCTGACACC CTTATGCCAC AACTAGAAAA AGAAATTTCC GTGGATGTTT 4320

	ACCAGGTAGC	CAAGATGATC	AATCTGATGA	GGCCAGGAGT	CTTTGCTGAC	ATTGAGCAGT	4380
	ATCAGTTTCT	CTACAAAGTG	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	4440
	CCACCTCTCT	GGACAGTAAT	GGTGCAGCAT	TGCCTGATGG	AAATATAGCT	GAGAGCTTAG	4500
5	AGTCTTTAGT	TTAACACAGA	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTITTCCTCT	4560
	TCCTAAAAAT	AGGCAGGAAA	ATCAGTCTAG	TTCTGTTATC	TGTTGATTTC	CCATCACCTG	4620
	ACAGTAACCT	TCATTGACATA	GGATTCTGCC	GCCAAATTTA	TATCAITTAAC	AATGTGTGCC	4680
	TTTTTGCAAG	ACTTGTAATT	TACTTATTAT	GTITGAACTA	AAATGATTGA	ATTTTACAGT	4740
	ATTTCTAAGA	ATGGAATTGT	GGTATTTTTT	TCTGTATTGA	TTTTAACAGA	AAATTTCAAT	4800
10	TTATAGAGGT	TAGGAATTCC	AAACTACAGA	AAATGTTTGT	TTTTAGTGTC	AAATTTTAG	4860
	CTGTATTGTG	AGCAATTATC	AGGTTTGCTA	GAATATAAC	TTTTAATACA	GTAGCCTGTA	4920
	AATAAAACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
	GAATAATCT	GTACTTATT	GTAATACTG	CCCTAGTGTC	TCCATGGACC	AAATTTATAT	5040
	TTATAATTGT	AGATTTTAT	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATTG	5100
15	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTCTT	GACATTGTAT	5160
	TGTGTACTCT	AAGTCATTAA	CTTTGTTTCA	GCATGTAATT	TTAACTTTTG	TGGAAAAATG	5220
	AAATACCTTC	ATTTTGAAGG	AAGTTTTTAT	GAGAATAACA	CCTTACCATA	CATTGTTCAA	5280
	ATGGTTTTTA	TCCAAGGAAT	TGCAAAAATA	AATATAAATA	TTGCCATTAA	AAAAAAAAAA	5340
	AAAAAAAAAA	AAAAAAAAAA	AAA				5363
20	Seq ID NO: C100 DNA Sequence						
	Nucleic Acid Accession #: Eos sequence						
	Coding sequence: 148..4362						
25	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAAA	ATTTCCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGCGGAGGGG	CGCGAGACCG	TCTGGAAATG	CGAATCCTAA	AACGTTTCCT	CGCTTGCAAT	180
30	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCTATATCA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCCAAACAA	TCTCTATCA	ATATTGATGA	AGATCTTACA	360
	CAGTAATAAT	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TCTATAACAC	TGGGAAAACA	GTGGAATTTA	ATCTCACTAA	TGACTACCGT	480
35	GTCAAGCGAG	GAGTTTCAGA	AATGTTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GGATGTCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTGGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTTC	GTTTGGGAAA	GCAGGCTGCT	780
40	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGT	GAAGTTCTTA	CAATGCAACA	960
	ATCTGGTTAT	GTCACTGCTGA	TGGACTACTT	ACAAAACAA	TTTCGAGAGC	AACAGTACAA	1020
	GTCTCTTACA	CAGGTGTTTT	CCTCATACAC	TGGAAAGGAA	GAGATTCAATG	AAGCAGTTTG	1080
45	TAGTTTCAGAA	CCAGAAAAATG	TTCAAGCTGA	CCCAGAGAA	TATACAGACC	TTCTTGTTAC	1140
	ATGGGAAAGA	CCTCGAGTCG	TTTATGATAC	CATGATTGAG	AAGTTTGCAG	TTTTGTACCA	1200
	GCAGTTGCAA	TCTCTGAAAG	AAACCAAGCA	TGAATTTTGG	ACAGATGGCT	ATCAAGACTT	1260
	GGGTGCTATT	CTCAATTAAT	TGCTACCCAA	TATGAGTTAT	GTTCCTTCAG	TAGTAGCCAT	1320
	ATGCACTAAT	GGCTTATATG	GAATAATACAG	CGACCAACTG	ATTGTGAGCA	TGCTCACTGA	1380
50	TAATCCTGAA	CTTGATCTTT	TCCCTGAATT	AATGGAATCT	GAAGAAATAA	TCAAGGAGGA	1440
	GGAAAGAGGA	AAGACATTGG	AAGAAGGCGC	TATGTGAAT	CCTGGTAGAG	ACAGTGCTAC	1500
	AAACCAATCT	AGGAAAGAGG	AAACCCAGAT	TTCTACCAACA	ACACACTACA	ATCGCATAGG	1560
	GAAGAAATAC	AATGAAGCCA	AGACTAACCG	ATCCCCAACA	AGAGGAAGTG	AAITCTCTGG	1620
	AAAGGGTGAT	GTTCCTCAATA	CATCTTTAAA	TTCCACTTCC	CAACCACTCA	CTAAATTAGC	1680
55	CACAGAAAAA	GATATTTTCT	TGACTTCTCA	GACTGTGACT	GAATCTGCCAC	CTCACACTGT	1740
	GGAAAGTACT	TCAGCTCTTT	TAAATGATGG	CTCTAAACTT	GTTCCTTAGAT	CTCCACATAT	1800
	GAATCTTTCG	GGGAGTGCAG	AATCCTTAAA	TACAGTTTCT	ATAACAGAT	ATGAGGAGGA	1860
	GAGTTTATGT	ACCAGTTTCA	AGCTTGATAC	TGGAGCTGAA	GATTCCTTCAG	GCTCCAGTCC	1920
	CGCAACTTCT	GCTATCCCAT	TCACTCTGTA	GAACATATCC	CAAGGGTATA	TATTTTCCTC	1980
60	CGAAAACCCA	GAGACAATAA	CATATGATGT	CCTTATACCA	GAATCTGCTA	GAAATGCTTC	2040
	CGAAGATTCA	ACTTCATCAG	GTTCAGAAGA	ATCACTAAAG	GATCCTTCTA	TGAGGGGAAA	2100
	TGTGTGGTTT	CCTAGCTCTA	CAGACATAAC	AGCACAGCCC	GATGTTGGAT	CAGGCAGAGA	2160
	GAGCTTTCTC	CAGACTAATT	ACACTGAGAT	ACGTTTGTAT	GAATCTGAGA	AGACAAACAA	2220
	GTCTTTTCT	GCAGGCCCCG	TGATGTCACA	GGGTCCCTCA	GTTACAGATC	TGGAATGGCC	2280
65	ACATTATTCT	ACCTTTGCCCT	ACTTCCCAAC	TGAGGTAACA	CCTCATGCTT	TTACCCCATC	2340
	CTCCAGACAA	CAGGATTGGG	TCTCCACGGT	CAACGTGGTA	TACTGCGAGA	CAACCCAAAC	2400
	GGTATACAAT	GAGGCCAGTA	ATAGTAGCCA	TGAGTCTCGT	ATTGGTCTAG	CTGAGGGGTT	2460
	GGAAATCCAG	AAGAAGGCAG	TTATACCCCT	TGTGATCGTG	TCAGCCCTGA	CTTTTATCTG	2520
	TCTAGTGGIT	CTTGTTGGGT	TTCTCATCTA	CTGGAGGAAA	TGCTTCCAGA	CTGCACACTT	2580
70	TTACTTAGAG	GACAGTACAT	CCCTTAGAGT	TATATCCACA	CCTCCAAAC	CTATCTTTCC	2640
	AAATTCAGAT	GATGTGCGAG	CAATTCCAAT	AAAGCACTTT	CCAAAGCATG	TTGCAGATTT	2700
	ACATGCAAGT	AGTGGGTTTA	CTGAAGAATT	TGAGACACTG	AAAGAGTTTT	ACCAGGAAGT	2760
	GCAGAGCTGT	ACTGTTGACT	TAGGTATTAC	AGCAGACAGC	TCCAACCAAC	CAGACAACAA	2820
	GCACAAGAA	CGATACATAA	ATATCGTTGC	CTATGATCAT	AGCAGGGTTA	AGCTAGCACA	2880
75	GCTTGCTGAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTT	3000
	TGGAGAAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	GAAATATGTA	TCAGTACTGG	CCTGCGGATG	GGAGTGAGGA	GTACGGGAAC	3120
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCTTATT	ATACTGTGAG	GAATTTTACT	3180
80	CTAAGAAACA	CAAAATATAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	AGSTGTGGTC	3240
	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGC	3360
	CACTGCAAGT	CTGAGATTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	3420
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGCTTCT	TAAACACAT	CCGTTCAACA	3480
	AGAAATTATT	TGTTACAAAC	TGAGGAGCAA	TATGCTTCTA	TTCATGATAC	ACTGGTTGAG	3540

5	GCCATACTTA	GTAAGAAGAAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCTA	TGTTAATGCA	3600
	CTCCTCATTC	CTGGACCAGC	AGGCCAAACA	AAGCTAGAGA	AACAAATCCA	GGGTCTCACT	3660
	CTGTACACCA	GGCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCCTCCCT	3720
	GGCTTAACATG	ATCCTCTAC	CTCAGCCTCC	CGAGTGGCTG	GGACTATACT	CCTGAGCCAG	3780
	TCRAATATAC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAAGAAT	3840
	CGAACTTCTT	CTATCATCCC	TGTGGAAGAG	TCAAGGGTTG	GCAATTCATC	CCTGAGTGGG	3900
	GAAGGCACAG	ACTACATCAA	TGCCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	3960
	ATCATTACCC	AGCACCCCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
10	CATAATGCC	AACTGGTGGT	TATGATTCTT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAAAATAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTTTATG	4140
	GCTGAAGAAG	ACAAATGTCT	ATCTAATGAG	GAAAACTTA	TAATTACAGG	CTTTATCTTA	4200
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAGTGTCC	TAAATGGCCA	4260
	AATCCAGATA	GCCCCATTAG	TAAAACCTTT	GAACCTATAA	GTGTTATAAA	AGAAGAAGCT	4320
15	GCCAAATAGG	ATGGCCCTAT	GATTGTTTCT	GATGAGCATG	GAGGAGTGAC	GGCAGGAAC	4380
	TTCTGTGCTC	TGACAAACCTT	TATGCACCAA	CTAGAAAAAG	AAAATTCCTG	GGATGTTTAC	4440
	CAGGTAGCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	4500
	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	GTGGGCACAA	GGCAGGAAGA	GAATCCATCC	4560
	ACCTCTCTGG	CAGATTAATG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
20	TCTTTAGTTT	AACACAGAAA	GGGTGGGGGG	GACTCACATC	TGAGCATTGT	TTCTCTCTTC	4680
	CTAAAATTAG	GCAGAAAAAT	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCC	ATCACCTGAC	4740
	AGTAACTTTC	ATGACATAGG	ATTCTGCGCG	CAAAATTATA	TCATTAACAA	TGTGTGCTTC	4800
	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	4860
	TTCTAAGTAG	GGAATTTGGG	TATTTTCTTC	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	4920
25	ATAGAGGTTA	GGAATTCCAA	ACTACAGAAA	ATGTTTGTTT	TTAGTGTCAA	ATTTTGTAGCT	4980
	GTATTTGTAG	CAATTATCAG	GTTTGCTAGA	AAATAAAGTT	TTAATACAGT	AGCCTGTAAA	5040
	TAAAACACTC	TTCCATATGA	TATTCACATG	TTTCAACCTG	CAGTATTCAC	CTAAAGTAGA	5100
	AATAATCTGT	TACTTATTTG	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	5160
	ATAATTGTAG	ATTTTATATG	TTTACTACTG	AGTCAAGTTT	TCTAGTTCTG	TGTAATTTGT	5220
30	TAGTTTAATG	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTCTG	CATTGTATTG	5280
	TGTTACCTAA	GTCAATTAAT	TTGTTTCAGC	ATGTAATTTT	AACTTTTGTG	GAAAATAGAA	5340
	ATACCTTCAT	TTTGAAGAAA	GTTTTTATGA	GAATAACACC	TTACCAACAA	TTGTTCAAAAT	5400
	GGTTTTATATC	CAAGGAATTG	CAAAAATAAA	TATAAATATT	GCCATTAAAA	AAAAAATAAA	5460
	AAAAAATAAA	AAAAAATAAA	A				5481
35	Seq ID NO: C101 DNA Sequence						
	Nucleic Acid Accession #: Eos sequence						
	Coding sequence: 1..3340						
40	1	11	21	31	41	51	
	ATGCGAATCC	TAAAGCGTTT	CCTCGCTTGC	ATTCAGCTCC	TCTGTGTTTG	CCGCTGGAT	60
	TGGGCTAATG	GATACTACAG	ACAACAGAGA	AACTTGTGTG	AAGAGATTGG	CTGGCTCTAT	120
	ACAGGAGCAC	TGAATCAAAA	AAATTGGGGA	AAGAAATATC	CAACATGTAA	TAGCCCAAAA	180
45	CAATCTCCTA	TCAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
	AAATTTCAAG	GTGGGATAA	AACATCATTC	GAAAACACAT	TCATTCATAA	CACCTGGGAA	300
	ACAGTGGAAA	TTAATCTCAC	TAATGACTAC	CGTGTGAGCG	GAGGAGTTTC	AGAAATGGTG	360
	TTTAAAGCAA	GCAAGATAAC	TTTTCACTGG	GGAAAAATGA	ATATGTCTATC	TGATGGATCA	420
	GAGCATAGTT	TGAGAGGACA	AAAATTTCCT	CTTGAGATGC	AAATCTACTG	CTTTGATGCG	480
50	GACCGATTTT	CAAGTTTGA	GGAAGCAGTC	AAAGGAAAAG	GGAAGTTAAG	AGCTTTATCC	540
	ATTTTGTGTT	AGGTTGGGAG	AGAAGAAAAT	TTGGAATTTCA	AAGCGATTAT	TGATGGAGTC	600
	GAAAGTGTTA	GTGCTTTTGG	GAAGCAGGCT	GCTTTAGATC	CATTCACTAT	GTTGAACCTT	660
	CTGCCAAACT	CAACTGACAA	GTATTACATT	TACAATGGCT	CATTGACATC	TCTCCCTGTC	720
	ACAGACACAG	TGAGCTGGAT	TGTTTTTAAA	GATACAGTTA	GCATCTCTGA	AAGCCAGTTG	780
55	GCTGTTTTTT	GTGAAGTTCT	TACAATGCAA	CAATCTGGTT	ATGTCATGCT	GATGGACTAC	840
	TTACAAAACA	ATTTTCGAGA	GCAACAGTAC	AAGTTCTCTA	GACAGGTGTT	TTCCTCATAC	900
	ACTGGAAAGG	AGAGATTCCA	TGAAGCAGTT	TGTAGTTTCA	AACCAAGAAA	TGTTCAAGCT	960
	GACCCAGAGA	ATTATACCA	CCTTCTTGT	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
	ACCATGATTG	AGAAGTTTGC	AGTTTTGTAC	CAGCAGTTGG	ATGGAGAGGA	CCAAACCAAG	1080
60	CATGAATTTT	TGACAGATGG	CTATCAAGAC	TTGGGTGCTA	TTCTCAATAA	TTTGCTACCC	1140
	AATATGAGTT	ATGTTCTTCA	GATAGTAGCC	ATATGCACTA	ATGGCTTATA	TGGAATAATAC	1200
	AGCGACCAAC	TGATTGTGGA	CATGCCCTACT	GATAATCCTG	AGGCCAGTAA	TAGTAGCCAT	1260
	GAGTCTCGTA	TTGTTCTAGC	TGAGGGGTTG	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	1320
	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	1380
65	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	1440
	ATATCCACAC	CTCCACACCC	TATCTTTCCA	ATTTCAAGAT	ATGTCGGAGC	AATTCCAATA	1500
	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	1560
	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	1620
	GCAGACAGCT	CCAACACCCC	AGACAACAAG	CACAAGAATC	GATACATAAA	TATCGTTGCC	1680
70	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	1740
	TATATCAATG	CCAATTATGT	TGATGGCTAC	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	1800
	GGCCCATCTGA	AATCCACAGC	TGAAGATTTT	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	1860
	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	AAAGGAAGGA	GAAATGTGTA	TCAGTACTGG	1920
	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	1980
75	CTTGCTTATT	ATACGTGGAG	GAATTTTACT	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	2040
	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	2100
	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	2160
	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTC	CACCTGAGTG	CTGGAGTTGG	AAGAACAGGC	2220
	ACATATATTG	TGCTAGACAG	TATGTTGCGA	CAGATTCAAC	ACGAAGGAAC	TGTCACACTA	2280
80	TTTGCTTCTT	TAAAACATAT	CCGTTCCAAA	AGAAATTTAT	TGGTACAAAC	TGAGGAGCAA	2340
	TATGTTCTCT	TTCATGATAC	ACTGGTTGAG	GCCATACITTA	GTAAGAAGAC	TGAGGTGCTG	2400
	GACAGTCATA	TTCATGCCTA	TGTTAATGCA	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	2460
	AAGCTAGAGA	ACAATTTCCA	GCTCCTGAGC	CAGTCAAAAT	TACAGCAGAG	TGACTATTCT	2520
	GCAGCGCTAA	AGCAATGCAA	CAGGGAAAAG	AATCGAACTT	CTTCTATCAT	CCCTGTGGAA	2580
	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	GGAGAAGGCA	CAGACTACAT	CAATGCCTCC	2640

	TATATCATGG	GCTATTACCA	GAGCAATGAA	TTCATCATT	CTCAGCACCC	TCTCCTTCAT	2700
	ACCATCAAGG	ATTTCCTGGAG	GATGATATGG	GACCATAATG	CCCAACTGGT	GGTTATGATT	2760
	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	2820
	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	ATGGCTGAAG	AACACAAATG	TCTATCTAAT	2880
5	GAGGAAAAC	TTATAATTCA	GGACTTTATC	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	2940
	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	CCAAATCCAG	ATAGCCCAT	TAGTAAACT	3000
	TTTGAACTTA	TAAGTGTTAT	AAAAGAAGAA	GCTGCCAATA	GGGTGGGCC	TATGATTGTT	3060
	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	ACTTTCGTGT	CTCTGACAAC	CCTTATGCAC	3120
	CAACTAGAAA	AAGAAATTC	CGTGGATGTT	TACCAAGTAG	CCAAGATGAT	CAATCTGATG	3180
10	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	3240
	CTTGTAGCA	CAAGGCAGGA	AGAGAATCCA	TCTACCTCTC	TGGACAGTAA	TGGTGACGA	3300
	TTGCTGATG	GAAATATAGC	TGAGAGCTTA	GAGTCTTAG			3340
	Seq ID NO: C102 DNA Sequence						
15	Nucleic Acid Accession #: Eos sequence						
	Coding sequence: 1..4480						
	1	11	21	31	41	51	
20	ATGCGAATCC	TAAAGCGTTT	CCTCGCTTGC	ATTGAGCTCC	TCTGTGTTTG	CGGCCTGGAT	60
	TGGGCTAATG	GATACCTACAG	ACAACAGAGA	AAACTTGTG	AAGAGATTGG	CTGGTCTCTAT	120
	ACAGGAGCAC	TGAATCAAAA	AAATTGGGGA	AAGAAATATC	CAACATGTAA	TAGCCCAAAA	180
	CAATCTCCTA	TCAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
	AAATTTGAGG	GTGGGATGAA	AACATCACTG	GAAACACAT	TCATTCTATA	CACCTGGGAAA	300
25	ACAGTGGAAA	TTAATCTCAC	TAATGACTAC	CGTGTACGCG	GAGGAGTTTC	AGAAATGGTG	360
	TTTAAAGCAA	GCAAGATAAC	TTTTCACTGG	GGAAATGCA	ATATGTCATC	TGATGGATCA	420
	GAGCATAGTT	TAGAAGGACA	AAAATTTCCA	CTTGAGATGC	AAATCTACTG	CTTTGATGCA	480
	GACCGATTTC	GTGAAGTTTG	GGAAGCAGTC	AAAGGAAAG	GGAAGTTAAG	AGCTTTATCC	540
	ATTTGTTTGG	AGGTTGGGAC	AGAAGAAAT	TTGGATTCTA	AAGCGATTAT	TGATGGAGTC	600
30	GAAAGTGTTA	GTCTTTTGG	GAAGCAGGCT	GCTTAGATC	CATTCTACT	GTTGAACCTT	660
	CTGCCAAACT	CAACTGACAA	GTATTACATT	TACAATGGTT	CATTGACATC	TCCTCCCTGC	720
	ACAGACACAG	TTGACTGGAT	TGTTTTTAAA	GATACAGTTA	GCATCTCTGA	AAGCCAGTGG	780
	GCTGTTTTTT	GTGAAGTTCT	TACAATGCAA	CAATCTGGTT	ATGTCATGCT	GATGGACTAC	840
	TTACAAACAA	ATTTTCGAGA	GCAACAGTAC	AAGTCTCTTA	GACAGGTGTT	TTCTCTATAC	900
35	ACTGGAAAGG	AAGAGATTCA	TGAAGCAGTT	TGTAGTTTCA	AACCAAGAAA	TGTTGAGGCT	960
	GACCCAGAGA	ATTATACCAG	CCTTCTGTG	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
	ACCATGATTG	AGAAGTTTGC	AGTTTGTGAC	CAGCAGTTGG	ATGGAGAGGA	CCAAACCAAG	1080
	CATGAATTTT	TGACAGATGG	CTATCAAGAC	TTGGGTGCTA	TTCTCAATAA	TTTGCTATCC	1140
	AATATGAGTT	ATGTTCTTCA	GATAGTAGCC	ATATGCACTA	ATGGCTTATA	TGGAATAATAC	1200
40	AGGACCAAC	TGATTGTGCA	CATGCCCTACT	GATAATCCTG	AACCTGATCT	TTTCCCTGAA	1260
	TTAATTGGAA	CTGAAGAAAT	AATCAAGGAG	GAGGAAGAGG	GAAAGACAT	TGAAGAAGGC	1320
	GCTATTGTGA	ATCTCGGTAG	AGACAGTGCT	ACAAACCAAA	TCAGGAAAAA	GGAACCCAG	1380
	ATTTCTACCA	CTAACAACCTA	CAATCGCATA	GGGACGAAAT	ACAATGAAGC	CAAGACTAAC	1440
	CGATCCCCAA	CAAGAGGAAG	TGAATCTCT	GGAAAGGGTG	ATGTTCCCAA	TACATCTTTA	1500
45	AATTCACCTT	CCCAACCACT	CACTAAATTA	GCCACAGAAA	AAGATATTTT	CTTGACTTCT	1560
	CAGACTGTGA	CTGAACCTGC	ACCTCACACT	GTGGAAGGTA	CTTCAGCCTC	TTTAAATGAT	1620
	GGCTCTAAAA	CTGTTCTTAG	ATCTCCACAT	ATGAACCTGT	CGGGGACTGC	AGAATCCTTA	1680
	AATACAGTTT	CTATAACAGA	ATATGAGGAG	GAGAGTTTAT	TGACCACTTT	CAAGCTTGAT	1740
	ACTGGAGCTG	AAGATTCTTC	AGGCTCCAGT	CCCGCAACTT	CTGCTATCCC	ATTCTATCTT	1800
50	GAGAACATAT	CCCAAGGGTA	TATATTTTCC	TCGAAAAACC	CAGAGACAAT	AACATATGAT	1860
	GTCTTATATC	GCAAAATCTG	TAGAAATGCT	TCGAAAGATT	CAACTTCATC	AGGTTTCAGAA	1920
	GAATCACTAA	AGGATCTCTC	TATGAGGGGA	AATGTGTGGT	TTCTAGCTC	TACAGACATA	1980
	ACAGCACAGC	CCGATGTGTT	ATCAGGCAGA	GAGAGCTTTC	TCCAGACTAA	TTACTGTAG	2040
	ATACGTGTTG	ATGAATCTGA	GAAGACAACC	AAGTCTTTT	CTGCAAGCCC	AGTGTATGCA	2100
55	TACTGGAGGA	AATGCTTCCA	TCTGGAAATG	CCACATTATT	CTACCTTTGC	CTACTTCCCA	2160
	ACTGAGGTAA	CACCTCATGC	TTTTATCCCA	TCCTCCAGAC	AACAGGATTT	GGTCTCCACG	2220
	GTCAACGTGG	TATACTGCGA	GACAAACCAA	CCGGTATACA	ATGAGGCCAG	TAATAGTAGC	2280
	CATGAGTCTC	GTATTGTTCT	AGCTGAGGGG	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	2340
	CTTGTGATOG	TGTCAGCCCT	GACTTTTATC	TGCTAGTGG	TTCTTGTGGG	TATTCTCATC	2400
60	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	TTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	2460
	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	CCAATTTTCA	ATGATGTGGG	AGCAATTCCA	2520
	ATAAAGCACT	TTCCAAGACA	TGTTGAGAT	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	2580
	TTTGAGACAT	GTAAGAGATT	TTACCAGGAA	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	2640
65	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	AAGCACAAGA	ATCGATACAT	AAATATCGTT	2700
	GCCCATGATC	ATAGCAGGGT	TAAGCTAGCA	CAGCTTGCTG	AAAAGGATGG	CRAACTGACT	2760
	GATTATATCA	ATGCCAATTA	TGTTGATGGC	TACAACAGAC	CAAAGCTTTA	TATTGTCTGC	2820
	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	2880
	GAAAGTTATT	TCATGATAAC	AAACCTCGTG	GAGAAAGGAA	GGAGAAATG	TGATCAGTAC	2940
70	TGGCTGCGG	ATGGGAGTGA	GGAGTACGGG	AACTTCTGCT	TCACTCAGAA	GAGTGTGCAA	3000
	GTGCTTGCTT	ATTATACTGT	GAGGAATTTT	ACTCTAAGAA	ACAAAAAAT	AAAAAAGGGC	3060
	TCCCAGAAAG	GAAGACCCAG	TGGACCTGTG	GTCAACAGAT	ATCACTACAC	GCAGTGGCCT	3120
	GACATGGGAG	TACCAAGATA	CTCCCTGCCA	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	3180
	GCCAAAGCCC	ATGCACTGGG	GCTGTGTTGC	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACAA	3240
	GGCACAATATA	TTGTGCTAGA	CAGTATGTG	CAGCAGATTC	AACACGAAGG	AACTGTCAAC	3300
75	ATATTGGCT	TCTTAAACAA	CATCCGTTCA	CAAGAAATTT	ATTTGGTACA	AACTGAGGAG	3360
	CAATATGCT	TCATTCATGA	TACACTGGTT	GAGGCCATAC	TTAGTAAAGA	AACTGAGGTG	3420
	CTGGACAGTC	ATATTCTATG	CTATGTTAAT	GCACTCCTCA	TTCTGGACC	AGCAGGCCAA	3480
	ACAAAGCTAG	AGAAACAATT	CCAGGCTCTC	ACTCTGTAC	CCAGGCTGGA	GTGCAGAGGC	3540
	ACAACTCGG	CTCACTGCAA	CCTTCTCTC	CCTGGCTTAA	CTGATCCTCC	TACCTCAGCC	3600
80	TCCGAGTGG	TAGGACTAT	ACTCTGAGC	CAGTCAAATA	TACAGCAGAG	TGACTATTCT	3660
	GCAGCCCTAA	AGCAATGCAA	CAGGAAAGAG	AATCGAACTT	CTTCTATCAT	CCCTGTGGAA	3720
	AGATCAAGGG	TTGGCATTTT	ATCCCTGAGT	GGAGAAGGCA	CAGACTACAT	CAATGCCTCC	3780
	TATATCATGG	GCTATTACCA	GAGCAATGAA	TTCACTATTA	CCAGCACACC	TCTCCTTCAT	3840
	ACCATCAAGG	ATTTCCTGGAG	GATGATATGG	GACCATAATG	CCCAACTGGT	GGTTATGATT	3900

5	CCTGATGGCC AAAACATGGC AGAAGATGAA TTTGTTTACT GGCCAAATAA AGATGAGCCT 3960
	ATAAATTGTG AGAGCTTTAA GGTCACTCTT ATGGCTGAAG AACACAAATG TCTATCTAAT 4020
	GAGGAAAAAC TTATAATTCA GGACTTTATC TTAGAAGCTA CACAGGATGA TTATGTACTT 4080
	GAAGTGAGGC ACTTTCAGTG TCCTAAATGG CCAATCCAG ATAGCCCAT TAGTAAACT 4140
	TTTGAACCTA TAAGTGTAT AAAAGAAGAA GCTGCCAATA GGGATGGGCC TATGATTGTT 4200
	CATGATGAGC ATGGAGGAGT GACGGCAGGA ACTTCTGTG CTCTGACAAC CCTTATGCAC 4260
	CAACTAGAAA AAGAAATTC CGTGGATGTT TACCAGGTAG CCAAGATGAT CAATCTGATG 4320
	AGGCCAGGAG TCTTTGCTGA CATTGAGCAG TATCAGTTTC TCTACAAAGT GATCCTCAGC 4380
10	CTTGTGAGCA CAAGGCAGGA AGAGAATCCA TCCACCTCTC TGGACAGTAA TGGTGCAGCA 4440
	TTGCCTGATG GAAATATAGC TGAGAGCTTA GAGTCTTTAG 4480
	Seq ID NO: C103 DNA Sequence
	Nucleic Acid Accession #: Eos sequence
	Coding sequence: 1..4220
15	1 11 21 31 41 51
	ATGCGAATCC TAAAGCGITT CCTCGCTTGC ATTCACTGCC TCTGTGTTTG CCGCCTGGAT 60
	TGGGCTAATG GATACTACAG ACAACAGAGA AAACCTGTGG AAGAGATGGG CTGGTCTTAT 120
20	ACAGGAGCAC TGAATCAAAA AAATGGGGGA AAGAAATATC CAACATGTAA TAGCCCAAAA 180
	CAATCTCTTA TCAATATTGA TGAAGATCTT ACACAAGTAA ATGTGAATCT TAAGAAACTT 240
	AAATTTGAGG GTTGGGATAA AACATCATGG GAAAAACAT TCATTCTATA CACTGGGAAA 300
	ACAGTGGAAA TTAATCTCAC TAATGACTAC CGTGTACGCG GAGGAGTTTC AGAAATGGTG 360
25	TTTAAAGCAA CCAAGATAAC TTTCACTGG GGAATATGCA ATATGTATC TGATGGATCA 420
	GAGCATAGTT TAGAAGGACA AAAATTTCCA CTGAGATGCG AAATCTACTG CTTTGTATCG 480
	GACCGATTTT CAAGTTTGA GGAAGCAGTC AAAGGAAAGG GGAAGTTAAG AGCTTTATCC 540
	ATTTTGTGTT AGTTTGGGAC AGAAGAAAAA TTGGATTCCA AAGCGATTAT TGATGGAGTC 600
	GAAAGTGTGA TCGTTTGGG GAAGCAGGCT GCTTTAGATC CATTCTACT GTTGAACCTT 660
30	CTGCCAACT CAACTGACAA GTATTACATT TACAATGGCT CATTGACATC TCCTCCCTGC 720
	ACAGACACAG TTGACTGGAT TGTTTTAA GATACAGTTA GCATCTCTGA AAGCCAGTTG 780
	GCTGTTTTTT GTGAAGTTCT TACAATGCAA CAATCTGGTT ATGTCTATGCT GATGGACTAC 840
	TTACAAACAA ATTTTCGAGA GCAACAGTAC AAGTTCTCTA GACAGGTGTT TTCTCATAC 900
	ACTGGAAGG AAGAGATTCA TGAAGCAGTT TGTAGTTTCA AACACAGAAA TGTTCAGGCT 960
35	GACCCAGAGA ATTATACCA CTTCTTGTG ACATGGGAAA GACCTCGAGT CGTTTATGAT 1020
	ACCATGATTG AGAAGTTTGC AGTTTGTGAC CAGCAGTTGG ATGGAGAGGA CCAACCAAG 1080
	CATGAATTTT TGACAGATGG CTATCAAGAC TTGGGTGCTA TTCTCAATAA TTTGCTACCC 1140
	AATATGAGTT ATGTTCTTCA GATAGTAGCC ATATGCACTA ATGGCTTATA TGGAAAAATC 1200
	AGGACCAATC TGATTGTGCA CATGCCCTACT GATAATCTG AACTTGATCT TTCCCTGAA 1260
40	TTAATTGSA CTAAGAAAT AATCAAGGAG GAGGAAGAGG GAAAGACAT TGAAGAAGGC 1320
	GCTATTGTGA ATCTCGGTAG AGACAGTGCT ACAACCCAA TCAGGAAAAA GGAACCCAG 1380
	ATTTCTACCA CAACACACTA CAATCGCATA GGGACGAAAT ACAATGAAGC CAAGACTAAC 1440
	CGATCCCCAA CAAGAGGAGG TGAATTTCTT GGAAGGGGTG ATGTTCCCAA TACATCTTTA 1500
	AAITGCACTT CCAACCAAGT CACTAAATTA GCCACAGAAA AAGATATTTC CTTGACTTCT 1560
45	CAGACTGTGA CTGAACGTCC ACCTCACACT GTGGAAGGTA CTTGAGCCTC TTTAAATGAT 1620
	GGCTCTAAAA CTGTTCTTAG ATCTCCACAT ATGAACCTGT CGGGGACTGC AGAATCTTGA 1680
	AATACAGTTT CTATAACAGA ATATGAGGAG GAGAGTTTAT TGACCAGTTT CAAGCTTGAT 1740
	ACTGGAGCTG AAGATTCTCT AGGCTCCAGT CCGCAACTT CTGCTATCCC ATTCATCTCT 1800
	GAGAACATAT CCAAGGGTGA TATATTTTCC TCCGAAAAAC CAGAGACAAAT AACATATGAT 1860
50	GTCCTTATAC CAGAAATGCT TAGAAATGCT TCCGAAGATT CAATTCATC AGGTTTCAAG 1920
	GAATCACTAA AGGATCTTTC TATGGAGGGA AATGTGTGGT TTCCTAGCTC TACAGACATA 1980
	ACAGCACAGC CCGATGTTGG ATCAGGCAGA GAGAGCTTTC TCCAGACTAA TTACACTGAG 2040
	ATACGTGTTG ATGAATCTGA GAAGACAACC AAGTCTCTTT CTGCAAGGCC AGTGATGTCA 2100
	CAGGGTCCCT CAGTTTACAGA TCTGGAATG CCACTATTAT CTACCTTTGC CTACTTCCA 2160
55	ACTGAGGTAA CACCTCATGC TTTTACCCCA TCCTCCAGAC AACAGGATTT GGTCTCCAG 2220
	GTCAACGTGG TATACTCGCA GACAACCCNA CCGTATACA ATGAGGCCAG TAATAGTAGC 2280
	CATGAGTCTC GTATTGGTCT AGCTGAGGGG TTGGAATCCG AGAAGAAGGC AGTTATACCC 2340
	CTTGTGATCG TGTGAGCCT GACTTTTATC TGTCTAGTGG TTCTTGTGGG TATTCTCATC 2400
	TACTGGAGGA AATGCTTCCA GACTGCACAC TTTTACTTAG AGGACAGTAC ATCCCTAGA 2460
60	GTTATATCCA CACCTCCAAC ACCTATCTTT CCAATTTAG ATGATGTGCG AGCAATTCCA 2520
	ATAAAGCACT TTCCAAGCA TGTTCAGAT TTACATGCAA GTAGTGGGTT TACTGAAGAA 2580
	TTTGAGACAC TGAAGAGATT TTACCAGGAA GTGCAGAGCT GTACTGTGA CTTAGGTATT 2640
	ACAGCAGACA GCTCCAACCA CCGACAGAAC AAGCACAAGA ATCGATACAT AAATATCGTT 2700
	GCCTATGATC ATAGCAGGGT TAAGCTAGCA CAGCTTGCTG AAAAGGATGG CAAACTGACT 2760
65	GATTATATCA ATGCCAATTA TGTGTATGGC TACAACAGAC CAAAGCTTGA TATTGCTGCC 2820
	CAAGGCCAC TGAATTCAC AGCTGAAGAT TTCTGGAGAA TGATATGGGA ACATAATGTG 2880
	GAAATTTATT TCAATGATAA AAACCTCGTG GAGAAAGGAA GGAGAAATG TGATCAGTAC 2940
	TGGCCTGCCG ATGGGAGTGA GGAGTACGGG AACTTTCTGG TCACTCAGAA GAGTGTGCAA 3000
	GTGCTTGGCT ATTATACTGT GAGGAATTTT ACTCTAAGAA ACACAAAAAT AAAAAAGGGC 3060
70	TCCAGAAAG GAAGACCCAG TGGACGTGTG GTCAACAGT ATCACTACAC GCAGTGGCCT 3120
	GACATGGGAG TACCAGATTA CTCCTGCCA GTGCTGACCT TTGTGAGAAA GGCAGCCTAT 3180
	GCCAAGCGCC ATGCAGTGGG GCCTGTGTCT GTCCACTGCA GTGCTGGAGT TGAAGAACAA 3240
	GGCACATATA TTGTGCTAGA CAGTATGTTG CAGCAGATTC AACACGAAGG AACTGTCAAC 3300
	ATATTGGGCT TCTTAAACA CATCCGTTCA CAAAGAAATT ATTTGGTACA AACTGAGGAG 3360
75	CAATATGTCT TCATTATGTA TACACTGGTT GAGGCCATAC TTAGTAAAGA AACTGAGGTG 3420
	CTGGACAGTC ATATTATGTC CTATGTTAAT GCACCTCTCA TTCCTGGACC AGCAGGCAAA 3480
	ACAAAGCTAG AGAAACAATT CCAGCTCTCT AGCCAGTCAA ATATACAGCA GAGTGACTAT 3540
	TCGTGAGCCC TAAAGCAATG CAACAGGGAA AAGAATGAA CTTCTTCTAT CATCCCTGTG 3600
80	GAAAGATCAA GGGTTGGCAT TTCATCCCTG AGTGGAGAG GCACAGACTA CATCAATGCC 3660
	TCCTATATCA TGGGCTATTA CCAGAGCAAT GAATTCATCA TTACCCAGCA CCCTCTCCTT 3720
	CATACCATCA AGGATTTCTG GAGGATGATA TGGGACCATA ATGCCCAACT GGTGGTTATG 3780
	ATTCCTGATG GCCAAACAT GGCAGAAGAT GAATTTGTTT ACTGGCCAAA TAAAGATGAG 3840
	CCTATAAATT GTGAGAGCTT TAAGGTCACT CTTATGGCTG AAGAACAACA ATGTCTATCT 3900
	AATGAGGAAA AACTTATAAT TCAGGACTTT ATCTTAGAAG CTACACAGAG ATGGAGGAGT 3960
	GACGGCAGGA ACTTCTGTG CTCTGACAAC CCTTATGCAC CAACTAGAAA AAGAAATTC 4020

CGTGSATGTT TACCAGGTAG CCAAGATGAT CAATCTGATG AGGCCAGGAG TCTTTGCTGA 4080  
 CATTGAGCAG TATCAGTTTC TCTACAAAGT GATCCTCAGC CTGTGTAGCA CAAGGCAGGA 4140  
 AGAGAATCCA TCCACCTCTC TGGACAGTAA TGGTGCAGCA TTGCCTGATG GAAATATAGC 4200  
 TGAGAGCTTA GAGTCTTTAG 4220

Seq ID NO: C104 DNA Sequence  
 Nucleic Acid Accession #: XM\_002914.6  
 Coding sequence: 1..4314

10	1	11	21	31	41	51	
	ATGAAGGATA	TCGACATAGG	AAAAGAGTAT	ATCATCCCCA	GTCCTGGGTA	TAGAAGTGTG	60
	AGGGAGAGAA	CCAGCACTTC	TGGGACGCAC	AGAGACCGTG	AAGATTCCAA	GTTTCAGGAGA	120
	ACTCGACCGT	TGGAAATGCCA	AGATGCCTTG	GAACACAGCAG	CCCGAGCCGA	GGGCTCTCT	180
15	CTTGTAGCCT	CCATCTGATT	TCAGCTCAGA	ATCCTGGATG	AGGAGCATCC	CAAGGGAAAG	240
	TACCATCATG	GCTTGTAGTG	TCTGAAGCCC	ATCCGACTTA	CTTCCAAACA	CCAGCACCCA	300
	GTGGACAAATG	CTGGGCTTTT	TTCTGTATG	ACTTTTTCGT	GGCTTCTCTC	TCTGGCCCGT	360
	GTGGCCCAACA	AGAAAGGGGA	GCTCTCAATG	GAAGACGTGT	GGTCTCTGTC	CAAGCAACGAG	420
	TCTTCTGAGC	TGAAGTGCAG	AAGACTAGAG	AGACTGTGGC	AAGAAGAGCT	GAATGAAGTT	480
20	GGGCCAGAGC	CTGCTTCCCT	GCGAAGGGTT	GTGTGGATCT	TCTGCCGCAC	CAGGCTCATC	540
	CTGTCCATCG	TGTCCCTGAT	GATCACGCAG	CTGGCTGGCT	TCAGTGGACC	AGCCTTCATG	600
	GTGAAACACC	TCTTGGAGTA	TACCCAGGCA	ACAGAGTCTA	ACCTGCAGTA	CAGCTTGTGT	660
	TTAGTGTCTGG	GCCTCTCTCT	GACGGAATC	GTGCGGTCTT	GGTGCCTTGC	ACTGACTTGG	720
	GCATTGAATT	ACCGAACCGG	TGTCCGCTTG	CGGGGGGCCA	TCTAAACCAT	GGCATTTAAG	780
25	AAGATCCCTTA	AGTTAAAGAA	CATTAAAGAG	AAATCCCTGG	GTGAGCTCAT	CAACATTTCG	840
	TCCAACGATG	GGCAGAGAAT	GTTTGAGSCA	GCAGCCGTGG	GCAGCTGTCT	GGCTGGAGGA	900
	CCCGTTGTTG	CCAATCTTAGG	CATGATTAT	AATGTAATTA	TTCTGGGACC	AACAGGCTTC	960
	CTGGGATCAG	CTGTTTATAT	CCTCTTTTAC	CCAGCAATGA	TGTTTGATC	ACGGCTCACA	1020
	GCATATTTC	GGAGAAATG	CGTGGCCGCC	ACGGATGAAC	GTGTCCAGAA	GATGAATGAA	1080
30	GTTCTTACTT	ACATTAATAT	TATCAAAATG	TATGCTGGG	TCAAAGCAT	TTCTCAGAGT	1140
	GTTCAAAAA	TCCGCGAGGA	GGAGCGTCGG	ATATTGGAAA	AAGCTGGGTA	CTTCCAGAGC	1200
	ATCACTGTGG	GTGTGGCTCC	CATTGTGGTG	GTGATTGCCA	CGGTGGTGAC	CTTCTCTGTT	1260
	CATATGACC	TGGGCTTCGA	TCTGACAGCA	GCACAGGCTT	TCACAGTGGT	GACAGTCTTC	1320
	AATTCATGA	CTTTGTCTTT	GAAAGTAACA	CGGTTTTCAG	TAAAGTCCCT	CTCAGAAGCC	1380
35	TCAGTGGCTG	TTGACAGATT	TAAGAGTTTG	TTTCTAATGG	AAGAGTTTCA	CATGATAAAG	1440
	AACAAACCA	GAGTCTCTCA	CATCAAGATA	GAGATGAAAA	ATGCCACCTT	GGCATGGGAC	1500
	TCCTCCCACT	CCAGTATCCA	GAACTCGCCC	AAGCTGACCC	CCAAAATGAA	AAAAGACAG	1560
	AGGGCTTCCA	TGGGCAAGAA	AGAGAAGGTG	AGGCAGCTGC	AGCGCACTGA	GCATCAGGCG	1620
	GTGCTGGCAG	AGCAGAAAGG	CCACCTCCTC	CTGGACAGTG	ACGAGCGGCC	CAGTCCCGAA	1680
40	GAGGAAGAAG	GCAAGCACAT	CCACCTGGGC	CACCTGCGCT	TACAGAGGAC	ACTGCACAGC	1740
	ATCGATCTGG	AGATCCAAGA	GGGTAAACTG	GTGGAATCT	GCGGCAGTGT	GGGAAGTGA	1800
	AAAACCTCTC	TCATTTACAG	CATTTTAGGC	CAGATGACGC	TTCTAGAGGG	CAGCATTGCA	1860
	ATCAGTGGAA	CCTTCTGCTA	TGTGGCCAG	CAGGCCCTGA	TCCTCAATGC	TACTCTGAGA	1920
	GACAAATCC	TGTTTGGGAA	GGAATATGAT	GAAGAAAGAT	ACAACCTCTG	GCTGAACAGC	1980
45	TGCTGCTCTG	GGCCTGACCT	GGCCATTCTT	CCCAGCAGCG	ACCTGACCGA	GATTGGAGAG	2040
	CGAGGAGCCA	ACCTGAGCGG	TGGGCAGCGC	CAGAGGATCA	GCCTTGCCCG	GGCCTTGAT	2100
	AGTGACAGGA	GCATCTACAT	CCTGGACGAC	CCCCTCAGTG	CCTTAGATGC	CCATGTGGGC	2160
	AACCAATCT	TCATATAGTG	TATCCGGAAG	CATCTCAAGT	CCAAGACAGT	TCTGTTTGT	2220
	ACCCACCACT	TACAGTACCT	GGTGAAGTGT	GATGAAGTGA	TCTTCATGAA	AGAGGGCTGT	2280
50	ATTACGGAAA	GAGGCACCCA	TGAGGAATCT	ATGAATTTAA	ATGGTGACTA	TGCTACCAAT	2340
	TTTAATAACC	TGTTGCTGGG	AGAGACACCG	CCAGTTGAGA	TCAATTCAAA	AAAGGAAACC	2400
	AGTGGTTTAC	AGAAAGAGTC	ACAAGACAGG	GGTCTCAAAA	CAGGATCAGT	AAAGAAAGGA	2460
	AAAGCAGTAA	AGCCAGAGGA	AGGGCAGCTT	GTGCAGCTGG	AAGAAAAGGG	GCAGGGTTCA	2520
	GTGCCCTGGT	CAGTATATGG	TGTCTACATC	CAGGCTGCTG	GGGGCCCCCT	GGCATTCTCT	2580
55	GTTATTATGG	CCCTTTTCAT	GCTGAATGTA	GGCAGCACCG	CCTTCAGCAC	CTGGTGGTTG	2640
	AGTTACTGGA	TCAAAGCAAG	AAGCGGGAAC	ACCACTGTGA	CTCGAGGGAA	CGAGACCTCG	2700
	TGAGATGACA	GCATGAAGGA	CAATCTCAT	ATGCAGTACT	ATGCCAGCAT	CTACGCCCTC	2760
	TCCATGGGAG	TCATGCTGAT	CCTGAAAGCC	ATTGAGGAGG	TTGTCTTTGT	CAAGGGCAGC	2820
	CTCGAGGACT	CCTCCCGGCT	GCATGACGAG	CTTTCCGAA	GGATCCTCTG	AAGCCCTATG	2880
60	AAGTTTCTTG	ACACGACCCC	CACAGGGAGG	ATTCTCAACA	GGTTTTCCAA	AGACATGAT	2940
	GAAGTTGACG	TGCGGCTGCC	GTTCCAGGCC	GAGATGTTCA	TCCAGAACGT	TATCCTGGTG	3000
	TTCTTCTGTG	TGGGAATGAT	CGCAGGAGTC	TTCCGCTGGT	TCCTTGTGGC	AGTGGGCCCC	3060
	CTTGTCATCC	TCTTTTCAGT	CCTGCACATT	GTCTCCAGGG	TCTGATTTCG	GGAGCTGAAG	3120
	OGTCTGGACA	ATATACGCA	GTCACCTTTC	CTCTCCACA	TACGTCCAG	CATACAGGGC	3180
65	CTTGCCACCA	TCCACGCTTA	CAATAAAGGG	CAGGAGTTTC	TGCACAGATA	CCAGGAGCTG	3240
	CTGGATGACA	ACCAAGCTCC	TTTTTTTTTG	TTTACGTGTG	CGATGCGGTG	GCTGGCTGTG	3300
	CGGCTGGACC	TCATCAGCAT	CGCCCTCATC	ACCAACACGG	GGCTGATGAT	GGTTCTTATG	3360
	CACGGGCAGA	TCTCCCCAGC	CTATGCGGGT	CTGCGCATCT	CTTATGCTGT	CCAGTTAAAG	3420
	GGGCTGTCC	AGTTTACGGT	CAGACTGGCA	TCTGAGACAG	AAGCTCGATT	CACCTCGGTG	3480
70	GAGAGGATCA	ATCACTACAT	TAAGACTCTG	TCCTTGGAA	CACCTGCCAG	AATTAAGAAC	3540
	AAGGCTCCCT	CCCTGACTG	GCCCCAGGAG	GGAGAGGTGA	CCTTTGAGAA	CGCAGAGATG	3600
	AGGTACCGAG	AAAACCTCCC	TCTGCTCTTA	AAGAAAGTAT	CCTTCAAGAT	CAAACTTAA	3660
	GAGAAGATTG	TGGAGAAATG	GCGGACAGGA	TCAGGGAAAT	CCTGCTGGG	GATGGCCCTC	3720
	TTCCGCTGGG	TGGAGTTATC	TGGAGGCTGC	ATCAAGATTG	ATGGAGTGA	AATCAGTATG	3780
75	ATTGGCCTTG	CCGACCTCCG	AAGCAAACTC	TCTATCATTC	CTCAAGAGCC	GGTGTCTGTC	3840
	AGTGGCAGTG	TCAGATCAAA	TTTGGACCCC	TTCAACCACT	ACACTGAAGA	CCAGATTGTTG	3900
	GATGCCCTGG	AGAGGACACA	CATGAAAGAA	TGTATTGCTC	AGCTACCTCT	GAAACTTGAA	3960
	TCTGAAGTGA	TGGAGAAATG	GGATAACTTC	TCAGTGGGGG	AACGGCAGCT	CTTGTGCATA	4020
	GCTAGAGCCC	TGCTCCGACA	CTGTAAAGAT	CTGATTTTAG	ATGAAGCCAC	AGCTGCCATT	4080
80	GACACAGAGA	CAGACTTATT	GATTCAAGAG	ACCATCCGAG	AAGCATTTGC	AGACTGTACC	4140
	ATGCTGACCA	TTGCCCATCG	CCTGCACACG	GTTCTAGGCT	CCGATAGGAT	TATGGTGTCTG	4200
	GCCCAAGGAC	AGGTGGTTGA	GTTTGACACC	CCATCGGTCC	TTCTGTCCAA	CGACAGTTCC	4260
	CGATTCTATG	CCATGTTTGC	TGCTGCAGAG	AACAAGGTCC	CTGTCAAGGG	CTAG	4314

Seq ID NO: C105 DNA Sequence  
Nucleic Acid Accession #: NM\_005688.1  
Coding sequence: 126..4439

5	1	11	21	31	41	51	
	CGGGGAGGCT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTGGAGC	60
	AGGGGCGCAG	GAATTCCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCGCTCAG	120
10	AGAAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTC	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCCTCTCTGA	TGCTCTCAGT	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
15	ACCCAGTGGG	CAATGCTGGG	CTTTTTTCCT	GTATGACTTT	TTCGTGGCTT	TCCTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGGAAG	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCTCTGC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
20	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCTCT	CTCCTGACCG	AAATCGTGGC	GTCTTGGTCT	CTTGCACTGA	840
	CTTGGGCATT	GAATACCGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCCTA	ACCATGGCAT	900
	TTAAGAAAGT	CCTTAAGTTA	AAGAACAATA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGCTCCAA	CGATGGGCGC	AGAATGTTG	AGGCAGCAGC	CGTTGGCAGC	CTGTGGCTG	1020
25	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATCTCT	GGACCAACAG	1080
	GCTTCTCGGG	ATCAGCTGTT	TTTATCTCTT	TTTACCCAGC	AATGATGTTT	GCATCAGCGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGG	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
30	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTT	TGGTGGTGTG	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTCATAT	GACCCCTGGG	TTTCATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCCTCAATTC	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTTCAATAAG	TCCTCTCTAG	1500
	AAGCCTCAGT	GGCTGTGTAC	AGATTTAAGA	GTTTGTCTCT	AATGGAAGAG	GTTCACATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
35	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGGCGGTGCT	GACAGGAGCA	AAAGGCCACC	TCCTCTGGA	CAGTGACGAG	CGGCCACGTC	1800
	CCGAAGAGGA	AGAAGGCAAG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AATCTGGTGG	AATCTGGCGC	AGTGTGGGAA	1920
40	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCGT	GACCTGGCCA	TTCTTCCAGC	CAGCGACCTG	ACGAGATTG	2160
	GAGAGCGAGG	AGSCAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGCCCT	2220
45	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTT	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CTCTTCTAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTAA	TAACTGTGTT	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
50	AAACCAAGTG	TTACAGAAAG	AAGTCACAAG	ACAAGGGTCC	TAAAACAGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAGTGCC	CTGCTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCCTGGTTAT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAACCCAC	TGTGACTCGA	GGGAACGAGA	2820
55	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTAATATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCATG	CTGATCCTGA	AAGCCATTGG	AGGAGTTGTC	TTTGTCAAGG	2940
	GCAOCTGCGG	CTGCTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTGAAGGCC	3000
	CTATGAAGTT	TTTTGACAGC	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAGAGCA	3060
	TGGATGAAGT	TGACGTGCGG	CTGCGTTTCC	AGGCGGAGAT	GTTTATCCAG	AACGTTATCC	3120
60	TGGTGTCTCT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCTCTGT	CATCCTCTTT	TCAGTCTTGC	ACATTGTCTC	CAGGGTCTCT	ATTCCGGAGC	3240
	TGAAGCGTCT	GGACAATATC	ACGCAGTCAC	CTTTCCTCTC	CCACATCAGC	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCCAG	3360
	AGCTGCTGGA	TGACAACCAA	GCTCCTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
65	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCAAGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAAAGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTACCT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAAG	CTCTGTCTCT	GGAAGCACTT	GCCAGAAATTA	3660
	AGAACAAGGC	TCCCTCCCTT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCAG	3720
70	AGATGAGGTA	CCGAGAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAC	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGGCGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGGCGAC	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
	TGTTCACTGG	CACITGACGA	TCAAAATTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
75	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TGGAATCTGA	AGTGATGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTATAGTGA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGACAGAT	4260
	GTACCATGCT	GACCATTGCC	CATGCGCTGC	ACACGGTCTC	AGGCTCOGAT	AGGATTATGG	4320
80	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAACGACA	4380
	GTTCGCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCCGCTGC	AAGSGCTGAC	4440
	TCCTCCCTGT	TGACGAAGTC	TCTTTTCTTT	AGAGCAATTG	CATTCCCTCG	CTGGGGCGGG	4500
	CCCTCATATG	CGTCTCTCTA	CCGAAACCTT	GCCTTCTCTG	ATTTATCTCT	TGSCACAGCA	4560
	GTTCGGGATT	GGCTGTGTGG	TTTCACTTTT	AGGGAGAGTC	ATATTTGAT	TATTGTATT	4620
	ATTCCATATT	CATGTAACAA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGTTCA	4680



5	GGGAACCGTT ATTATAATTG TATCAGAGGC CTATAATGAA GCITTATACG TGTAAGCTATA 4740
	TCTATATATA ATTCTGTACA TAGCCTATAT TTACAGTGAA AATGTAAGCT GTTATATTTA 4800
	TATTAAATA AGCACTGTGC TAATAACAGT GCATATTCCT TTCTATCATT TTTGTACAGT 4860
	TTGCTGTACT AGAGATCTGG TTTTGTATT AGACTGTAGG AAGAGTAGCA TTTTATTCTT 4920
	CTCTAGCTGG TGGTTTACAG GTGCCAGGTT TTCTGGGTGT CCAAAGGAAG ACCTGTGGCA 4980
	ATAGTGGGCC CTCGACAGC CCCCTCTGCC GCCTCCCCAC AGCGCTCCA GGGGTGGCTG 5040
	GAGACGGGTG GGGCGCTGGA GACCATGCAG AGCGCGTGA GTTCTCAGG CTCCTGCCTT 5100
	CTGTCTGGT GTCACTTACT GTTCTGTCA GGAGAGCAGC GGGGCGAAGC CCAGGCCCTT 5160
	TTTCACTCCC TCCATCAAGA ATGGGGATCA CAGAGACATT CCTCCGAGCC GGGGAGTTTC 5220
10	TTTCTGCTCT TCTTCTTTT GCTGTGTTT CTAAACAAGA ATCAGTCTAT CCACAGAGAG 5280
	TCCCACTGCC TCAGGTTCCT ATGGCTGCC ACTGCACAGA GCTCTCCAGC TCCAAGACCT 5340
	GTGTGTTCCA AGCCCTGGAG CCAACTGCTG CTTTTGAGG TGGCACTTT TCAATTGCTT 5400
	ATTCCACAC CTCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCCTTT 5460
	CTCACGCGAG TCGTGCACA GTCTCTCTCT CTCTCTCCCC TCAAGTCTG CAACTTTAAG 5520
15	CAGCTCTGC TAATCTCTT GTCACACTGG CGTAGAAGT TTTGTACTGT AAAGAGACCT 5580
	ACCTCAGGTT GCTGGTGTCT GTGTGGTTTG GTGTGTTCCC GCAAAACCCC TTTGTGCTGT 5640
	GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCTAC AGTTGAATGG TCAGCGTTCG 5700
	ATGTCTGAC CACTAGACA TTCTGTGCC TTAGCATGTT TGCTGAACAC CTGTGGGAAG 5760
20	CAAAATCTG AAAATGTGAA TAAATTTAT TTGATTTTG TAAAAAATA AAAAAAATA 5820
	AAAAAATA AAAAAAATA 5838

Seq ID NO: C106 DNA Sequence  
Nucleic Acid Accession #: NM\_005562  
Coding sequence: 90..3671

25	1 11 21 31 41 51
	ACAGCGGAGC GCAGAGTGAG AACCAACAAC CGAGGCGCGG GGCAGCGACC CCTGCAGCGG 60
30	AGACAGAGAC TGAGCGGCCC GGCACCGCCA TGCCCTGCCT CTGGCTGGGC TGCTGCCTCT 120
	GCTTCTCGCT CCTCTGCCC GCAGCCCGGG CCACTCCAG GAGGGAAGTC TGTGATTGCA 180
	ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGAACATCA CAGACAACT GGTAATGGAT 240
	TCCGCTGCCT CACTGCAAT GACAACACTG ATGGCAITCA CTGCGAGAAG TGCAAGAATG 300
	GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT 360
35	CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCGACTG TAAACCAAGT GTGACAGGAG 420
	CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCAACCAAG 480
	ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
	ACGCGGGCGG CTGTGTCTGC AAGCCAGCTG TTACTGAGAG ACGCTGTGAT AGGTGTGAT 600
40	CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG 660
	GGCATTGAGC CAGCTGCGCG AGCTCTGCGA AATACAGTGT CCATAAGATC ACCTCTACTC 720
	TTCTATCAGA TCTTGTATGG TGGAAAGCTG TCCAACGAAA TGGGTCTCCT GCAAGCTCC 780
	AATGTCACA GGGCCATCAA GATGTGTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840
	TTGTGGCTCC TGCCAAATTT CTGCGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCT 900
	TTGACTACCG TGTGACAGA GGAGGCAGAC ACCCATCTCG CCATGATGTG AITCTGGAAG 960
45	GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTTGTGGGC 1020
	TCACCAAGAT TCACACATTC AGGTTAAATG AGCATCCAAG CAATAATTGG AGCCCCAGC 1080
	TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA 1140
	CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CTTGATTTCG GCGCGCCTG 1200
	TCTCTGGAGC CCCAGCACCC TGGGTGTAAC AGTGTATATG TCCTGTTGGG TACAAGGGGC 1260
50	AATTCTGCCA GGATGTGTCT TCTGCTTACA AGAGAGATTC AGCGAGACTG GGGCCTTTTG 1320
	GCACCTGATG TCTTGTATAC TGTCAGGGG GAGGGGCTGT TGATCCAGAC ACAGGAGATT 1380
	GTTATTGAGG GGATGAGAA CTGACATTG AGTGTGCTGA CTGCCCAATT GGTTCCTACA 1440
	ACGATCCGCA CGACCCCGC AGCTGCAAGC CATGTCCCTG TCATAACGGG TTCAGTGTCT 1500
	CAGTGATGCC GGAGACGGAG GAGGTGGTGT GCAATAACTG CCCTCCCGGG GTCAACGGTG 1560
55	CCCGCTGTGA GCTCTGTGCT GATGGCTACT TTGGGGACCC CTTTGTGTAA CATGGCCAG 1620
	TGAGGCTTGT TCAGCCCTGT CAATGCAACA ACAATGTGGA CCCCAGTGCC TCTGGGAATT 1680
	GTGACCGGCT GACAGGCGAG TGTTTGAAGT GTATCCACAA CACAGCCGCG ATCTACTGCG 1740
	ACCAAGTCAA AGCAGGCTAC TTGGGGACC CATTGGCTCC CAACCCAGCA GACAAGTGT 1800
	GAGCTTGCAA CTGTAACCCC ATGGGCTCAG AGCCTGTAGG ATGTGGAAGT GATGGCACT 1860
	GTGTTTGCAA GCCAGGATT GTTGGCCCCA ACTGTGAGCA TGGAGCAITC AGCTGTCCAG 1920
60	CTTGCTATAA TCAAGTGAAG AITCAGATGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG 1980
	AGGCCCTGAT TTCAAAGGCT CAGGCTGGTG ATGAGTAGT ACCTGATACA GAGCTGGAAG 2040
	GCAGGATGCA CGAGGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTCAG 2100
	AAGGTGCTAG CAGATCCCTT GGTCTCCAGT TGGCCAGGT GAGGAGCCAA GAGAACAGCT 2160
65	ACCAGAGCCG CCTGGATGAC CTCAAGATGA CTGTGGAAAG AGTTCCGGCT CTGGGAAGTC 2220
	AGTACCAGAA CCGAGTTCCG GATACTACA GGCTCATCAC TCAGATGCAG CTGAGCCTGC 2280
	CAGAAAGTGA AGCTTCTTGT GGAACAACATA ACATTCTGCT CTCAGACCAC TACGTGGGGC 2340
	CAATGGCTT TAAAGTCTG GCTCAGGAGG CCACAAGATT AGCAGAAAGC CACGTTGAGT 2400
	CAGCCAGTAA CATGGAGCAA CTGACAAGGG AAACCTGAGGA CTATTCCAAA CAAGCCCTCT 2460
70	CACTGTGCGC CAGGCGCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG 2520
	CTGTGGTGCA AGGCTTGTG GAAAAATTGG AGAAAAACCA GTCCCTGGCC CAGCAGTTGA 2580
	CAAGGGAGGC CACTCAAGCG GAAATTGAAG CAGATAGGTC TTATCAGCAC AGTCTCGGCC 2640
	TCCTGGATTG AGTGTCTCG CTTCAGGAG TCAGTGATCA GTCTTTTCA GTGGGAAGAG 2700
	CAAGAGGAT CAAACAAAA GCGGATTAC TCTCAACGCT GGTAAACAGG CATATGGATG 2760
75	AGTTCAAGCG TACACAAAAG AATCTGGGAA ACTGGAAAGA AGAAGCAGAG CAGCTCTTAC 2820
	AGAAATGAAA AAGTGGGAGA GAGAAATCAG ATCAGCTGCT TTCCCGTGCC AATCTTGCTA 2880
	AAAGCAGAGC ACAAAGAGCA CTGAGTATGG GCAATGCCAC TTTTATGAAA GTTGAGAGCA 2940
	TCCTTAAAAA CCAAGAGAG TTTGACCTGC AGGTGGACAA CAGAAAAGCA GAAGCTGAAG 3000
80	AAGCCATGAA GAGACTCTCC TACATCAGCC AGAAGGTTTC AGATGCCAGT GACAAGACCC 3060
	AGCAAGCAGA AAGAGCCCTG GGGAGCGCTG CTGCTGATGC ACAGAGGGCA AAGAAATGGG 3120
	CCGGGAGGCG TCGGAAATC TCCAGTGAGA TTGAACAGGA GATTGGGAGT CTGAACCTGG 3180
	AAGCCAAATG GACAGCAGAT GGAGCCTTGG CCATGGAAAA GGGACTGGCC TCTCTGAAGA 3240
	GTGAGATGAG GGAAGTGGAA GGAGAGCTGG AAAGGAAGGA GCTGGAGTTT GACACGAATA 3300
	TGGATGCACT ACAGATGGTG ATTACAGAAG CCCAGAAGGT TGATACCAGA GCCAAGAACG 3360
	CTGGGGTTAC AATCCAAGAC ACATCAACA CATTAGACGG CCTCTGCAT CTGATGGACC 3420



5 AGCCTCTCAG TGTAGATGAA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCGAGGCCA 3480  
 AGACCCAGAT CAACAGCCAA CTGGGGCCCA TGATGTGAGA GCTGGAAGAG AGGGCAGGTC 3540  
 AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATTCTG GCTGATGTGA 3600  
 AGAACTTGGG GAACATTAGG GACAACCTGC CCCCAGGCTG CTACAATACC CAGGCTCTTG 3660  
 AGCAACAGTG AAGCTGCCAT AATATTTCT CAACTGAGGT TCTTGGGATA CAGATCTCAG 3720  
 GGCCTGGGAG CCATGTGATG TGAGTGGGTG GATGGGGAC ATTTGAACAT GTTTAATGGG 3780  
 TATGCTCAGG TCAACTGACC TGACCCCATT CCTGATCCCA TGGCCAGGTG GTTGTCTTAT 3840  
 TGCAACATAC TCCTTGCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA 3900  
 ATGATCAAGG ATCTGGACCC CAAAGAATAG ACTGGATGGA AAGACAACT GCACAGGCAG 3960  
 ATGTTTGGCT CATATAGTCT GTAAGTGAG TCCTGGAATT TGGACAAGTG CTGTTGGGAT 4020  
 ATAGTCAACT TATTTCTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCCAGGC 4080  
 ATGAAATTTCT TCCTAATGTC AGAACAGAGT GCAACCCAGT CACACTGTGG CCAGTAAAAAT 4140  
 ACTATTGGCT CATATTGTCC TCTGCAAGCT TCTTGTGAT CAGAGTTCTT CCTACTTACA 4200  
 ACCCAGGGTG TGAACATGTT CTCCATTTC AAGCTGGAAG AAGTGAGCAG TGTGGAGTGT 4260  
 AGGACCTGTA AGCGAGGCC ATTACAGACT ATGGTGGCTG CTGGTGCCTG CCACCTTCAA 4320  
 GTTCTGGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC 4380  
 ATTTTATTTA AAGCATTTCC TACCAGCAAA GCAATATGTT GGAAGATATT TACTTTTTCG 4440  
 GTTTCAAAGT GATGAAAAAG TGTGGCTTGG GCATTGAAAG AGGTAAAAAT CTCTAGATTT 4500  
 ATTAGTCTTA ATTCATCTCT ACTTTTCGAA CACCAAAAAAT GATGCGCATC AATGTATTTT 4560  
 ATCTTATTTT CTCATCTCTC TCTCTCTTTC CTCCACCCAT AATAAGAGAA TGTCTCTACT 4620  
 CACACTTCAG TGGGTGACA TCCATCCCTC CATTATCCCT TCCATCCATC TTTCCATCCA 4680  
 TTACTCCCAT CCATCTCTCC AACATATATT TATTGATGAC CTACTGTGTG CCAGGGGGCTG 4740  
 GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA 4800  
 AGCATTTTAA AAAAATAAAT TTAACCTTAC AAACCTTGTT TGTCAACAAGT GGTGTTTATT 4860  
 GCAATAACCG CTGCTGTTGC AACCTCTTTG CTCACAGAA CATATGTTGC AAGACCTTCC 4920  
 CATGGGGGCA CTGAGTTTTT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTTCCTTG 4980  
 CATTCCAGCT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040  
 TAACACAGT GGAATTTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGAAGACTA 5100  
 TGGTCTGCC TTGCTCTGT ATTTCCCTGG ATTTTCCTGA AAGTGTTTTT AATAAAGAA 5160  
 CAATTGTTAG ATGCC 5175

Seq ID NO: C107 DNA Sequence  
 Nucleic Acid Accession #: NM\_021101  
 Coding sequence: 221..856

35 1 11 21 31 41 51  
 GAATTCGGCA CGAGGCTCTG TGCCGGGGAG CAACCTCAGC TTCTAGTATC CAGACTCCAG 60  
 CGCGCGCCCG GCGCGGGACC CCAACCCCGA CCCAGAGCTT CTCCAGCGGC GCGCAGCGA 120  
 CGAGGGCTCC CGCGCTTAAC TTCTCCGCG GGGCCAGCC ACCTTCGGA GTCCGGGTTG 180  
 CCCACCTGCA AACTCTCCGC CTCTGCACC TGCCACCCCT GAGCCAGGCG GGGCGCCCGA 240  
 GCGAGTCATG GCCAAGCGGG GGTCTGACCT GTTGGGCTTC ATTCTGCTCT TCTTGGGATG 300  
 GATCGGGGCC ATCGTCAGCA CTGCGCTGCC CCACTGGAGG ATTTACTCCT ATGCGCGCGA 360  
 CAACATCTGT ACCGCCAGG CATGTACGA GGGGCTGTGG ATGTCTCTCG TGTGCGCAG 420  
 CACCGGGCAG ATCCAGTGCA AAGTCCTTGA CTCTTCTGCT AATCTGAGCA GCACATTGCA 480  
 AGCAACCCGT GCCTTGATGG TGGTTGGCAT CCTCTGCGG GTGATAGCAA TCTTTGTGTC 540  
 CACCGTTGGC ATGAAGTGTA TGAAGTGCTT GGAAGACGAT GAGGTGCGAG AGATGAGGAT 600  
 GGCTGTCTAT GGGGGCGCGA TATTTCTTCT TGCAGGTCTG GCTATTTTAG TTGCCACAGC 660  
 ATGGTATGGC AATAGAATCG TTCAAGAATT CTATGACCCT ATGACCCCA TCAATGCCAG 720  
 GTAAGAAATT GGTCAAGGCT TCTTCACTGG CTGGGCTGCT GCTTCTCTCT GCCTTCTGGG 780  
 AGGTGCCCTA CTTTGTCTGT CTTGTCCCG AAAAACCAAC TCTTACCCAA CACCAAGGCC 840  
 CTATCCAAAA CTGCACTCTC CCAGCGGGAA AGACTACGTG TGACACAGAG GCAAAAGGAG 900  
 AAAATCAATT TGAAACAAAC CGAAATGGA CATTGAGATA CTATCTTAA CATTAGGACC 960  
 TTAGAAATTT GGGTATTGTA ATCTAAAGTA TGTATTACA AAACAAACAA ACAACAAAA 1020  
 AACCATCTGT TTAATACTCT CAGTGCTAAA CATGGCTTAA TCTTATTTTA TCTTCTTCC 1080  
 TCAATATAGG AGGGAAGATT TTTCCATTG TATTACTGCT TCCCATGAG TAATCATACT 1140  
 CAAATGGGGG AAGGGGTGCT CCTTAAATAT ATATAGATAT GTATATATAC ATGTTTTTCT 1200  
 ATTAANAATA GCCAGTAAAA AAAAAAAA 1237

Seq ID NO: C108 DNA Sequence  
 Nucleic Acid Accession #: AF508964.1  
 Coding sequence: 98..1531

65 1 11 21 31 41 51  
 CAGAGCCGCA AGCCGAGGGA AGGCCTCCCC GCAAGGTGGG GGAAGCGGCG CGGTGCAGCG 60  
 CGGGGACAGG CACTCGGGCT GGCAGTGGCT GCTAGGGATG TCGTCTCTGA TAAGTTGGCA 120  
 TGGAACCGCC ATGGGCGGCG TCTGGGGCTT CTGCTGGCTG GTTGTGGGCT TCTGGAGGGC 180  
 CGCTTTCGCG TGTCACAGT CCTGCAATG CAGTGCTCT CTGATCTGCT GCACGACCCC 240  
 TTCTCTGGC ATGCTGGCAT TTCCGAGATT GGAGCCTAAC AGTGTAGATC CTGAGAACAT 300  
 CACCGAAATT TTCATGCAAA ACCAGAAAAG GTTAGAAATC ATCAAAGAG ATGATGTTGA 360  
 AGCTTATGTG GGAAGTGAAT ATCTGCAAT TGTGGATTCT GGATTAATAA TTGTGGCTCA 420  
 TAAAGCATT CTGAAAAACA GCAACCTGCA GCACATCAAT TTTACCCGAA ACAAACTGAC 480  
 GAGTTGTCT GTGAACATTT TCGGTCACTT TGACTGTCT GAACTGATCC TGGTGGGCAA 540  
 TCCATTACA TGCTCTGTG ACATTATGTG GATCAAGACT CTCCAAGAGG CTAATCCAG 600  
 TCCAGACACT CAGGATTGTG ACTGCTGAA TGAAGCAGC AAGAATATTC CCCTGGCAAA 660  
 CCTGAGATA CCCAATTGTG GTTGGCCATC TGCAATCTG GCGCACCTA ACCTCACTGT 720  
 GGAGGAAGGA AAGTCTATCA CATTATCTG TAGTGTGGCA GGTGATCCGG TTCTAATAT 780  
 GTATTGGGAT GTTGGTAACC TGGTTTCCAA ACATATGAAT GAAACAAGCC ACACACAGGG 840  
 CTCTTAAAG ATAATAACA TTTCAATCGA GACAGTGGG AAGCAGATCT CTTGTGTGGC 900  
 GGAATATCTT GTAGGAGAAG ATCAAGATTC TGTCAACCTC ACTGTGCAAT TTGACCAAC 960  
 TATCATTATT CTCGAATCTC CAACCTCAGA CCACCACTGG TGCAATCCAT TCACTGTGAA 1020  
 AGGCAACCCC AAACCAAGGC TTCAGTGGT CTATAACGGG GCAATATTGA ATGAGTCCAA 1080  
 ATACATCTGT ACTAAATAC ATGTTACCAA TCACACGGAG TACCACGGCT GCCTCCAGCT 1140

	GGATAATCCC	ACTCACATGA	ACAATGGGGA	CTACACTCTA	ATAGCCAAGA	ATGAGTATGG	1200
	GAAGGATGAG	AAACAGATTT	CTGCTCAGTT	CATGGGCTGG	CCTGGAATTG	ACGATGGTGC	1260
	AAACCCAAAT	TATCCTGATG	TAATTTATGA	AGATTATGGA	ACTGCAGCGA	ATGACATCGG	1320
	GGACACCACG	AACAGAAATG	ATGAAATCCC	TTCCACAGAC	GTCAGTGATA	AAACCGGTGC	1380
5	GGAACATCTC	TCGGTCTATG	CTGTGGTGGT	GATTGCGTCT	GTGGTGGGAT	TTTGCCTTTT	1440
	GGTAATGCTG	TTTCTGCTTA	AGTTGGCAAG	ACACTCCAAG	TTTGGCATGA	AAGGTTTTGT	1500
	TTTGTTCAT	AAGATCCAC	TGGATGGGTA	GCTGAAATAA	AGGAAAGAC	AGAGAAAGGG	1560
	GCTGTGGTGC	TTGTGGTGTG	ATGCTGCCAT	GTAGCTGGA	CTCCTGGGAC	TGCTGTGGC	1620
10	TTATCCCGGG	AAGTGTCTGT	TATCTGGGGT	TTTCTGGTAG	ATGTGGGCGG	TGTTTGGAGG	1680
	CTGTACTATA	TGAAGCCTGC	ATATACTGTG	AGCTGTGATT	GGGGAACACC	AATGCAGAGG	1740
	TAACTCTCAG	GCAGCTAAGC	AGCACCTCAA	GAACACATGT	TAAATTAATG	CTTCTCTTCT	1800
	TACAGTAGTT	CAAAATACAA	ACTGAAATGA	AATCCCATTG	GATTGTACTT	CTCTCTTGAA	1860
	AAGTGTGCTT	TTTGACCTTA	CTGGACATTT	ATTGACTTAA	TTGCTTCTGT	TTATTAATAAT	1920
	TGACCTGCAG	AGTTAAATAA	AAATTAAGT	TGAGAACAGG	TATAAGTGCA	CACTGAATAG	1980
15	TCTAATCTAC	ATGTAACACA	TATTTTAGTA	TGATTTTCTA	TACTCTAATC	AGCACTGAAT	2040
	TCAGAGGGTT	TGACTTTTTT	ATCTATAACA	CAGTGACTAA	AAGAGTTAAG	GGTATATATA	2100
	CCATCACTTT	GGGACTTGGT	AGTATTATTA	AAAGGTTATT	TCCTTCACTG	TCAATAAAG	2160
	TTCCAAATGT	TATCTTAGGT	CTGAGAGTCA	AACAATGTTA	AGGATTGTCT	TAAAGTTCCCT	2220
20	TAGCCAGCAA	AACAAACCAA	AACAAACCAA	ACAAATGAAA	AACGTTTAAA	AAGAGAAGA	2280
	AGAAAAAA	CAAGAACAAG	CAGCAACAGC	TGTTTTGTTG	GGGCTATAGA	TTTAAGTTAG	2340
	GCATAGTCAA	TTTCAGAATA	ACTAAGAGTG	GAATATATGC	ATATGGTGAA	ATTATAACCT	2400
	TGCCCCTTTT	TATTTGCCCT	CTGCGATCCA	CCTGGCTTTT	TAGAAGTCTG	CCGAGTGAGA	2460
	AGGCCACAGT	ATCTCATGCT	GTTTGCAATTA	CAGAACTGCA	GCTTTTCTAC	TCTGAAAGG	2520
25	CCTGGGAGCA	GAATGCTGGG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTC	2580
	CCCCCTACAA	CATACTGTCA	TACTGCTGGG	TTTTCATGGG	TAGGAAGCT	TGTCCTGACC	2640
	CCAGCAGCAA	AGAGGTGGCA	GGTGGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	2700
	TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCATCC	CCCCCTGAGT	TGACCCATGG	2760
	ACACCTGTTT	CATCTCATTT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	2820
30	CAGGCAGTAT	GCTGTGCTGT	AAGAGAGGTT	TGGCTATCCC	CCACCCACCC	CACCCACCTT	2880
	GTTCCCTTTT	TATCAGGAGG	ACTTCAGAGC	CAGGCCCTGCA	GCATTTTGGT	TGAAAAACAA	2940
	ATCAGCTCTG	ACAGTTAGAC	ATGCACACAG	ACGCCATAGC	TGGATTGGAA	ACATTGATGT	3000
	TTTAAAAATT	TATTTTTTTT	GGAAATAGTT	GCACAAATGC	TGCAATTTAG	CTTTAAGGTT	3060
	CTATAGATTT	TTAACTAGTC	CAACACAGTC	AGAAACATTG	TTTTGAATCC	TCTGTAAACC	3120
	AAGGCATTAA	TCTTAATAAA	CCAGGATCCA	TTTAGGTACC	ACTTGATATA	AAAAGGATAT	3180
35	CCATAATGAA	TATTTTATAC	TGCATCCTTT	ACATTAGCCA	CTAAATACGT	TATTGCTTGA	3240
	TGAAGACCTT	TCACAGAAATC	CTATGGATTG	CAGCATTTC	CTTGGCTACT	TCATACCCAT	3300
	GCCTTAAAGA	GGGCGAGTTT	CTCAAAAGCA	GAACCATGCC	GCCAGTCTCT	AAGTTTTCTT	3360
	CCTAACTCCA	TTTGAATGTA	AGGGCAGCTG	GCCCCCAATG	TGGGGAGGTC	CGAACATTTT	3420
40	CTGAATTCCT	ATTTCTCTGT	TCGGGCTTAA	ATGACAGTTT	CTGTCAATAC	TTAGATTCCG	3480
	ATCTTTCCCA	AAGGTGTGTA	TTTACAAGA	GGCCAGCTAA	TAGCAGAAAT	CATGACCCCTG	3540
	AAAGAGAGAT	GAAATTCAGG	CTGTGAGCCA	GGCAGGAGCT	CAGTATGSCA	AAGGTTCTTG	3600
	AGAATCAGCC	ATTTGGTACA	AAAAAGATTT	TTAAAGCTTT	TATGTTATAC	CATGGAGCCA	3660
	TAGAAAGGCT	TTGGAATGTT	TAAAGACTAT	TTTAAAGTGT	TCCAGACCCA	AAAAGGAAAA	3720
45	ATAAAAAAAA	AGGAATATTT	GTACCAACAA	GCTAGAAGGA	TTGCAAGGTA	GATTTTGTGT	3780
	TTAAATGGA	GAGAAGTGA	CAGATAAGGC	CATTTAATAT	ATCAAGATC	AGTTGACATC	3840
	TCTAGGGAAT	GATGAACAG	CAGGCTATTA	GAAAAATATT	TCATATAGTT	CTOGTGTCTT	3900
	TTTCTTTTTT	TAAATCCCTG	AAGGGAGATC	AGTAACATAG	CTTCTCTTTT	CTGTACTCTA	3960
	GACCAACCTT	TTTCAATCAT	TTGCTTTTAA	TGCTCTCCAT	AAGAAATGTC	CTTTTATAGG	4020
50	CTTCTTAATG	CATGTGTGTC	ATTATTCAG	CATTAGAAAA	GGAGAGGTAG	CATTTTGTCT	4080
	GAAATCGGSC	CTGTCACTCT	CCAATAAAGG	TTCTGGCACT	TCAATGCCAG	GCAGGTCTCC	4140
	TAAATGACAA	GAATGATCTG	TGTGAGCCGA	TGCTGCCCTT	TCCAGAGGGG	CCACTGTCCC	4200
	CAGCCGAGC	CAACTGTGTC	CCACAGGAAT	GGGAGCCTAG	GTTTCCAAAT	CTTGTGATTC	4260
	TTTAGGAGCA	ACATGAAACC	TGGATTTCGT	GTGAAATGTC	CCGATTGTTA	AAAAGTTGGC	4320
55	TCAATTAATTT	TTAAACATTT	TTGTAAGCCA	ACAAAAGTCT	GTGGGCTGCC	AGTTTATTAC	4380
	TTTTGTCTTA	AAACATGATC	ATTGTTCTCT	CACGGTATCC	TTCTGTCTTC	CCGTTGCAAA	4440
	TTCACTTTTC	TTTCTCTCTG	ACATTGCCAT	TGAGGGCTTT	GTTACCACAA	GCTAAGAAAC	4500
	TGAGTTTAAC	AGCCCAAGTA	TCTGCAACAT	GTCAATTACC	TTTGTCTCTC	TCTGTGATT	4560
	CCCACCAATG	TGTGACCTTC	AGCTGTCTCC	CTTGTCTGGG	AATCTGAC	CAATGTCTTC	4620
60	CCCTCAACCC	ATTCCCTGGT	TGGTCTACT	CCCGTGTGGC	CAGAGACATC	CTAGCAATTC	4680
	CTTCTCTCTA	TTATATCTGA	CATTAATTTT	TTTTCAACAG	CGCTCATGTC	TCTTGGCCCA	4740
	GTACAGGTGCT	GCCAGGTTTA	GATAGGAAAG	TACATGTCCC	ATTTTCATGG	GTGCCCTTAA	4800
	TGTGGTCCAC	GTCTTATATC	TTATTATATT	TACTCATGGC	TCAATGGGGG	CCTCCAGAGA	4860
	CCCTCTCAGG	CTGCTGAGCT	AGACTAAGGA	ATGCATCCAC	TGTCATCACA	TGAGACACTG	4920
65	ACTCTGTGAC	GACAAAGTGA	CAACAGTCT	GAGGCTAAGA	AAGGTTCTAT	TCACACAGG	4980
	AAAAACAAAT	CTCAACACAC	ATTAGAGATA	ATTGATTCAG	GGGTTTTCTC	TCCAGTCTC	5040
	CCAGCAGGGA	CTGATTTTAT	TTCTGACCCA	CTAGGTTTTC	TTTCCAGAAA	TAGGTAGCAA	5100
	GGACAGAAAC	TAAACAATCC	CAGCCCCACC	CAGCAACACA	GAACACAGGA	GTTTGTCTTT	5160
	GGCTTCTCAC	TCTCCAAGTA	ACCCTGAATT	AGGCCAGAAA	TGGCTGAGGC	TGGAGCATC	5220
70	TCCTCAGAGA	GAGCAGAGGC	GACACCTCTT	CAGGGGTGTG	TGGAGTAAAT	AGCTCGAAGA	5280
	GCTGAAGACA	GAAGACCACT	TTCAAGCCAG	GTGCGAGAGA	GAGCATAATG	GAGGGAAGCC	5340
	CGCTTTCTCT	CTCCTCTTCT	TTTCTCTTTA	TTTCTTTAGA	GCATTGACT	TTTTTTTCTC	5400
	TCTCTCTCTA	GTATTCTAAA	CTGACCCCAT	GACCACTGA	GAATTTATTT	TTGTTTCAAT	5460
	GGTTGTTTCA	CAGAAATAGA	ACACACAGCA	CTTTTATTC	CTCCATTGCA	AAATGGAATC	5520
75	AAGATACTAC	ACAGACCTTG	TGCTTTCTTC	CTTTGCAATG	TTTACACCTC	CGCCTGTTTT	5580
	GGTGTAGCT	GTCTAGAATC	TCTCTCTTGG	TTTGAATCTG	ATTCTTCAAC	ACTACACTAG	5640
	AAGTTTATTT	CATCTGTGTT	TGCTAGACT	CCAGATACAG	AGGGACAGCT	GGACTGAGGA	5700
	CAAGCAATTC	CATCTAGCAT	AGGGTCTCTC	AGGGTTGGTG	CATCCAGCCA	CATGGGCAGG	5760
	GCCAGTACA	TCTAGTCTAT	GTCCCCAGAG	CCCTTGGAGT	TGGCGAGCTT	AGCTGACTTG	5820
	ACTCCAGAGA	AAATAGTACA	GAAGTAACCA	CTCTATTAAG	TGTGTTCTGC	TATGTTCAAC	5880
80	TGCTGTAGCT	ACCTGCAAACT	CATGCCAGGT	TCACTAAAG	ACATAGGGGA	AGATTAAAGGA	5940
	CTCTTTTGA	CAGACCATGA	ATTGAATTTG	CTGCCAGGTG	CTGCCAGACT	GAATTTGGCT	6000
	GACAGAACTC	CCAGCCACAG	AAAGTTCCAT	GACATGACT	GTCCGAGAAG	GAATTTTCCC	6060
	ACTAAAGTCA	GTCCATTTTC	AAGTTTTGGT	CTTCAGAGAC	AAAAAGAACT	CCGAGCCACC	6120
	TGATTTTGAT	GGTGAGGTAA	CTCTAAGTTG	AATTCAGGCT	AGTGTTCAG	TATAGCTTTG	6180

5  
10

```

GCATGTTTCAT GAGTGAGCAC CCAGAAATGTG TTGAACCAAC CCCCACCCCT AACTACTGAC 6240
TATGACTGCA GTGGGTTTTT ATGGGGAAAA AAAGTGTGAA AAGCAAAAAG AAAGGAACAG 6300
AGATTTTTTAT TCACCTTTAT TGTAAAGACAG TCCATTTATG AATTGAGTAT AAACACATAC 6360
AAAGTAACAA GAGATTCCCTA AGAAACGCAA ATCCTTGAGT TTCAACGCACT TCATGTTCAA 6420
CCATTTCGCTG TAATCCAGAG GCAGCCTGTG AATCATTCTC ATGCCCTGTT TTTTTTTTTT 6480
TTTTCTCTATA ATGTTCTGGG TTTAAAGCC ATCTTTTCCA CATTTTCTGT AAATAATGGA 6540
TAATCATTTT AAAAAGTTTT ATTTTATAGT CTGTTTTAAC AATGTAGATA GATCATAAAT 6600
GTACTTGCTG AATTCAATCA TTTTAAACAA GCCAATAAAG TTTGATAATT CAAAAAATAA 6660
AAAAAATAA AAAAAATAA 6679

```

Seq ID NO: C109 DNA Sequence  
Nucleic Acid Accession #: NM\_006180.1  
Coding sequence: 352..2820

15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
CCCCCATTCG CATCTAACAA GGAATCTGCG CCCCAGAGAG TCCCGGAGCG CGCCGGTTCGG 60
TGCCCGGCGC GCGCGGCCAT GCAGCGACGG CCGCGGCGGA GCTCCGAGCA GCGGTAGCGC 120
CCCCCTGTAA AGCGGTTTCG TATGCCGGGA CCACCTGTGA CCCTGCCGCC TGCCGGAACA 180
CTCTTGCTC CGACCCAGCT CAGCCTCTGA TAAGCTGGAC TCGGCAACGCC CGCAACAAGC 240
ACCGAGGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCCCT CCGGCACCGG TGGGGGAAAG 300
CGGCCGGTGC AGCGCGGGGA CAGGCACTCG GGCTGGCACT GGCTGCTAGG GATGTCGTCC 360
TGGATAAGGT GGCATGGACC CGCCATGGCG CGGCTCTGGG GCTTCTGCTG GCTGGTTGTG 420
GGCTTCTGGA GGGCGCTTT CGCCTGTCCC ACCTCCTGCA AATGCAGTGC CTCTCGGATC 480
TGGTGCAGCG ACCCTTCTCC TGGCATCGTG GCAATTCGGA GATTGGAGCC TAACAGTGTG 540
GATCCTGAGA ACATCAACGA AATTTTCATC GCAAAACAGA AAAGGTTAGA AATCATCAAC 600
GAAGATGATG TTGAAGCTTA TGTGGGACTG AGAAATCTGA CAATTGTGGA TTCTGGATTA 660
AAATTTGTGG CTCTATAAAG ATTTCTGAAA AACAGCAACC TGCAGCACAT CAATTTTACC 720
CGAAACAAAC TGACGAGTTT GTCTAGGAAA CATTTCCGTC ACCTTGACCT GTCTGAACTG 780
ATCCTGGTGG GCAATCCATT TACATGCTCC TGTGACATTA TGTGGATCAA GACTCTCCAA 840
GAGGTAAAT CCAATCCAGA CACTCAGGAT TTGTACTGCC TGAATGAAAG CAGCAAGAAT 900
ATTCCTCTGG CAAACCTGCA GATACCCAAT TGTGGTTTGC CATCTGCAAA TCTGGCCGCA 960
CCTAACTCA CTGTGGAGGA AGGAAAGTCT ATCACAATTAT CCTGTAGTGT GGCAGGTGAT 1020
CCGGTTCCTA ATATGTATTG GGAATGTTGGT AACCTGGTTT CCAACATAT GAATGAAACA 1080
AGCCACACAC AGGCTCTCTT AAGGATAACT AACATTTCAT CGATGACAG TGGGAAGCAG 1140
ATCTCTGTG TGGCGGAAAA TCTTGTAGGA GAAGATCAAG ATTCTGTCAA CCTCACTGTG 1200
CATTTTGCAC CAACTATCAC ATTTCTCGAA TCTCCAACT CAGACCACCA CTGGTGCAAT 1260
CCATTCACTG TGAAAGGCAA CCCCAAACCA GCGCTTCAGT GGTTCATATA CGGGCAATA 1320
TTGAATGAGT CCAATACAT CTGTACTAAA ATACATGTTA CCAATCACAC GGAGTACCAC 1380
GGCTGCCCTG AGCTGGATA TCCCACTCAC ATGAACAATG GGGACTACAC TCTAATAGCC 1440
AAGATGAGT ATGGGAAGGA TGAGAAACAG ATTTCTGCTC ACTTCATGGG CTGGCCTGGA 1500
ATTGACGATG GTGCAAAACC AAATTATCCT GATGTAATTT ATGAAGATTA TGGAACTGCA 1560
GCGAATGACA CTGGGGACAC CACGAACAGA AGTAATGAAA TCCCTTCCAC AGACGTCAC 1620
GATAAAACCG GTCCGGGACA TCTCTCGGTC TATGCTGTGG TGGTGAATGC GTCTGTGGTG 1680
GGATTTTGGC TTTTGGTAAT GCTGTTTCTG CTTAAGTTGG CAAGACACTC CAAGTTTGGC 1740
ATGAAAGGCC CAGCCTCCGT TATCAGCAAT GATGATGACT CTGCCAGCCC ACTCCATCAC 1800
ATCTCCAATG GGAGTAACAC TCCATCTTCT TCGGAAGGTG GCGCCAGATG TGTCAATTAT 1860
GGAAATGACA AGATCCCTGT CATTGAAAAT CCCCAGTACT TTGGCATCAC CAACAGTCAG 1920
CTCAAGCCAG ACACATTGTG TCAGCACATC AAGCGACATA ACATTGTCTT GAAAGGGGAG 1980
CTAGGCGAAG CACTCTTTGG AAAAGTGTTC CTAGCTGAAT GCTATAACCT CTGTCTGAG 2040
CAGGACAGAG TCTTGGTGGC AGTGAAGACC CTGAAGGATG CCAGTGACAA TGACGCAAG 2100
GACTTCCACC GTGAGGCGCA GCTCCTGACC AACCTCCAGC ATGAGCACAT CGTCAAGTTC 2160
TATGGCGTCT GCGTGGAGGG CGACCCCTCT ATCATGGTCT TTGATACAT GAAGCATGGG 2220
GACCTCAACA AGTTCCTCAG GGCACACGGC CTGATGCCG TGCTGATGGC TGAGGGCAAC 2280
CCGCCACCG AACTGAACGA GTGCGAGATG CTGCATATAG CCCAGCAGAT CGCCGCGGGC 2340
ATGCTCTACC TGGCGTCCCA GCACTTCGTG CACCGCGATT TGGCCACAG GAACCTGCTG 2400
GTCCGGGAGA ACTTGCTGGT GAAATCGGG GACTTTGGGA TGTCCCGGGA CGGTACAGC 2460
ACTGACTACT ACAGGGTCCG TGGCCACACA ATGCTGCCCA TTCCGTGGAT GCCTCCAGAG 2520
AGCATCATGT ACAGGAAATG CACGACGGAA AGCGACGCTT GGAGCCTGGG GGTCTGTGTT 2580
TGGGAGATTT TCACCTATGG CAACAGGCC TGGTACCAGC TGTCAAACA TGAGGTGATA 2640
GAGTGTATCA CTCAGGGCGG AGTCTCTGAG CGACCCCGCA CGTCCCGCCA GGAGGTGTAT 2700
GAGCTGATG TGGGGTCTG GCAGCGAGAG CCCCACATGA GGAAGAACAT CAAGGGCATC 2760
CATACCCTCC TTCAGAACTT GGCCAAGGCA TCTCCGGTCT ACCTGGACAT TCTAGGCTAG 2820
GGCCCTTTTC CCCAGCCGA TCCCTCCCAA CGTACTCCTC AGACGGGCTG AGAGGATGAA 2880
CATCTTTTAA CTGCGCTGAG AGGCCACCAA GCTGCTCTCC TTCCTCTGA CAGTATTAA 2940
ATCAAGACT CCGAGAAGCT CTCGAGGAAA GCAGTGTGTA CTCTCTATC CATAGACAA 3000
GTATTGACT CTCTTTGGCA TTATCTCTTT CTCTCTTTCC ATCTCCCTTG GTTGTCTCT 3060
TTTCTTTTTT TAAATTTTCT TTTCTTCTT TTTTCTGTC TTCCCTGCTT CACGATTCTT 3120
ACCTTTCTT TTGAATCAAT CTGGCTTCTG CATTACTATT AACTCTGCAT AGACAAAGGC 3180
CTTAACAAAC GTAATTTGTT ATATCAGCAG ACACTCCAGT TTGCCACCA CAACTAACAA 3240
TGCCCTGTGT TATTCCTGCC TTTGATGTGG ATGAAAAAAA GGGAAAAACA ATATTCACT 3300
TAAACTTTGT CACTTCTGCT GTACAGATAT CGAGAGTTTC TATGATTCA CTCTATTTA 3360
TTTATTATTA TTAGTGTCT TATTGTTTT GGATGGCTTA AGCCTGTGTA TAAAAAGAA 3420
AACTTGTGTT CAATCTGTGA AGCCTTTATC TATGGGAGAT TAAACCAGA GAGAAAGAA 3480
ATTTATTATG AACCGCAATA TGGGAGGAAC AAAGACAACC ACTGGGATCA GCTGGTGTCA 3540
GTCCCTACTT AGGAAATACT CAGCAACTGT TAGCTGGGAA GAATGTATTC GGCACCTTCC 3600
CTTAGGACCT TTTCTGAGGA GTAAAAAGAC TACTGGCCTC TGTGCCATGG ATGATTCTTT 3660
TCCCATCACC AGAAATGATA GGTGTCAGTA GAGAGCAAG ATGGCTT 3707

```

Seq ID NO: C110 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 939..2372

1 11 21 31 41 51

	AAGACGGATT	CTCAGACAAG	GCTTGCAAAT	GCCCCGCGAGC	CATCATTTAA	CTGCACCCGC	60
	AGAATAGTTA	CGGTTTGTCA	CCCGACCCCTC	COGGATCGCC	TAATTTGTCC	CTAGTGAGAC	120
	CCCAGGCTC	TGCCCGCGCC	TGGCTTCTTC	GTAGCTGGAT	GCATATCGTG	CTCCGGGCAG	180
5	CGCGGGCGCA	GGGCAACGCT	TGCGGCACAC	CCTAGCACAC	ATGAACACGC	GCAAGAGCTG	240
	AACCAAGCAC	GGTTTCCATT	TCAAAAAGGG	AGACAGCCCTC	TACCGCGATT	GTAGAAGAGA	300
	CTGTGGTGTG	AATTAGGGAC	CGGGAGGCGT	CGAACGGAGG	AACGGTTCAT	CTTAGAGACT	360
	AATTTTCTGG	AGTTTCTGCC	CCTGCTCTGC	GTACGCCCTC	ACGTCACTTC	GCCAGCAGTA	420
	GCAGAGGCGG	CGGCGGCGGC	TCCCGGAATT	GGGTTGGAGC	AGGAGCCTCG	CTGGCTGTCT	480
10	CGCTCGCGCT	CTACGCGCTC	AGTCCCCGGC	GGTAGCAGGA	GCCTGGACCC	AGGCGCCGCC	540
	GGCGGGCGGT	AGGCGCGCGA	GCCCCGCCCTC	GAGGTGCATA	CCGACCCCCC	ATTGCGCATCT	600
	AACAGGAAT	CTGCGCCCCA	GAGAGTCCCG	GGAGCGCCGC	CGGTGCGTGC	CCGGCGCGCC	660
	GGGCCATGCA	CGCAGCGCGC	CGCGGAGCT	CGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
	GGTTGCGTAT	GCGGGGCCA	CTGTGAACCC	TGCCCGCTGC	CGGAACACTC	TTGCTCCGG	780
15	ACCAGCTCAG	CCTCTGATA	GCTGGACTCG	GCACGCCCGC	AACAAGCACC	GAGGAGTTAA	840
	GAGAGCGCGA	AGGCGAGGGA	AGGCCCTCCC	GCACGGGTGG	GGGAAGCGCG	CCGGTCAGC	900
	GCGGGGACAC	GCATTCGGGC	TGGCACTGGC	TGCTAGGGAT	GTGCTCTGG	ATAAGGTGGC	960
	ATGGACCCGC	ATGGCGCGCG	CTCTGGGGCT	TCTGCTGGCT	GGTTGTGGGC	TTCTGGAGGG	1020
	CGCTTTCTGC	CTGTCCCAAG	TCTTGCAAA	GCACTGCCCTC	TGGATCTGG	TGCAGCGACC	1080
20	CTTCTCTGG	CATCGTGGCA	TTTCCGAGAT	TGGAGCCTAA	CAGTGTAGAT	CCTGAGAACA	1140
	TCACCGAAAT	TTTCATCGCA	AACCAAGAAA	GGTTAGAAAT	CATCAACGAA	GATGATGTGT	1200
	AAGCTTATGT	GGGACTGAGA	AATCTGACAA	TTGTGGATTC	TGGATTAAAA	TTTGTGGCTC	1260
	ATAAAGCATT	TCTGAAAAAC	AGCAACCTGC	AGCACATCAA	TTTTACCCGA	AACAAACTGA	1320
	CGAGTTTGTG	TAGGAACAT	TTCCGTCAAC	TTGACTTGTC	TGAACGTATC	CTGGTGGGCA	1380
25	ATCCATTAC	ATGCTCTGT	GACATTATGT	GGATCAAGAC	TCTCCAAGAG	GCTAAATCCA	1440
	GTCCAGACAC	TCAGGATTGT	TACTGCCCTGA	ATGAAGCAG	CAAGAAATAT	CCCTGGCAA	1500
	ACCTCGAGAT	ACCCAAATGT	GGTTTGCCAT	CTGCAAACTC	GGCGGCACCT	AACCTCACTG	1560
	TGGAGGAAG	AAAGTCTATC	ACATTATCCT	GTAGTGTGGC	AGGTGATCCG	GTTCCTAATA	1620
	TGTATTGGGA	TGTTGGTAA	CTGGTTTCCA	AACATATGAA	TGAACAAGC	CACACACAGG	1680
30	GCTCCTTAAG	GATACTAAC	ATTTTCATCC	ATGACAGTGG	GAAAGCAGATC	TCTTGTGTGG	1740
	CGGAAATCT	TGTAGGAGAA	GATCAAGATT	CTGTCAACCT	CACGTGTGAT	TTTGACCCAA	1800
	CTATCACATT	TCTCGAATCT	CCAACTCAG	ACCACCACTG	GTGATTCCA	TTCACTGTGA	1860
	AAGGCAACCC	CAAAACGCGC	CTTCAGTGGT	TCTATAACGG	GGCAATATTG	AATGAGTCCA	1920
	AATACATCTG	TACTAAAATA	CATGTTACCA	ATCACACGGA	GTACCACGGC	TGCTCCAGC	1980
35	TGGATAATCC	CACCTCACATG	AACAATGGGG	ACTACACTCT	AATAGCCAAG	AATGAGTATG	2040
	GGAAGGATGA	GAAACAGATT	TCTGCTCACT	TCATGGGCTG	GCCTGGAATT	GACGATGGTG	2100
	CAAAACCAAA	TTATCCTGAT	GTAATTTATG	AAGATTATGG	AACGTGACGC	AATGACATCG	2160
	GGGACACAGC	AAGTGAAGAT	AATGAAATCC	CTTCCACAGA	CGTCACTGAT	AAACCGGTC	2220
	GGGAACATCT	CTCGTCTAT	GCTGTGGTGG	TGATTGCTC	TGTTGGTGGG	TTTGTCCCTT	2280
40	TGGTAATGCT	GTTCCTGCTT	AAGTTGGCAA	GACACTCCAA	GTITGGCATG	AAAGGTTTGG	2340
	TTTTGTTTCA	TAAGATCCCA	CTGGATGGGT	AGCTGAAATA	AAGGAAAAGA	CAGAGAAAGG	2400
	GGCTGTGGTG	CTTGTGTGTT	GATGCTGCCA	TGTAAGCTGG	ACTCCTGGGA	CTGCTGTGG	2460
	CTTATCCCGG	GAAAGTCTGC	TTATCTGGGG	TTTTCTGGTA	GATGTGGGCG	GTGTTGGAG	2520
	GCTGTACTAT	ATGAAGCCTG	CATATACTGT	GAGCTGTGAT	TGGGGAACAC	CAATGCAGAG	2580
45	GTAACCTCA	GGCAGCTAAG	CAGCACCTCA	AGAAAACATG	TTAAATTAAT	GCTTCTCTTC	2640
	TTACAGTAGT	TCAAAATCAA	AACGTAAATG	AAATCCCAT	GGATTGTACT	TCTCTCTGA	2700
	AAAGTGTGCT	TTTGACCCCT	ACTGGACATT	TATTGACTTA	ATTGCTTCTG	TTTATTAAAA	2760
	TTGACCTGCA	AAGTTAAAAA	AAAATTAAAG	TTGAGAACAG	GTATAAGTGC	ACACTGAATA	2820
	GTCTAATCTA	CATGTAAAC	ATATTTTAGT	GTGATTTTCT	ATACTCTAAT	CAGCACTGAA	2880
50	TTGAGAGGCT	TTGACTTTTT	CATCTATAAC	ACAGTGACTA	AAAGAGTTAA	GGGTATATAT	2940
	ACCATCACTT	TGGGACTGGG	TAGTATTATT	AAAAGGTTAT	TTCTTCACT	GTCAATAAAA	3000
	GTCCAAATGT	TTAGCTTAGG	TCTGAGAGTC	AAACAATGTT	AAGGATTGTC	TTAAAGTTCC	3060
	TTAGCCAGCA	AAACAAAAACA	AAACAAATGAA	AAAGCTTTAA	AAAGAAGAAG		3120
	AAGAAAAACA	ACAGCAACAA	GCAGCAACAG	CTGTTTGTIT	GGGGCTATAG	ATTAAAGTTA	3180
55	GGCATAGTCA	ATTTAGAAAT	AACTAAGAGT	GGAATATATG	CATATGGTGA	AATTATAACC	3240
	TTGCCCTTTT	TTATTTGCC	TCTGCGATCC	ACCTGCTTTT	TAGAAGTCTG	CCGAGTGAGA	3300
	AGGCCACAGT	ATCTCATGCT	GTITGACATTA	CAGAACTGCA	GCTTTCTAC	TCTGAAAAGG	3360
	CTGGGAGGCA	GAAATGGCTGG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTC	3420
	CCCCCTACAA	CATACCTGCA	TACTGCTGGG	TTTTCATGGG	TAGGAAAGCT	TGTCCTGACC	3480
60	CCAGCAGCAA	AGAGGTGGCA	GSTGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	3540
	TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TCTGCTATCC	CCCCTGAGTC	TGACCCATGG	3600
	ACACCTGTTT	CATTCACTTT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	3660
	CAGGCAATAT	GCTTGTCCCTG	AAGAGAGGTT	TGGCTATCCC	CACCCCCACC	CACCCCCACC	3720
	TGTTCTCTTT	TTATCAGGAG	GACTTCAGAG	CCAGGCTGCG	AGCATTTTGT	TTGAAAACAC	3780
65	AATCAGCTCT	GACAGTTAGA	CATGCACACA	GCAGCCATAG	CTGGATTGGA	AACATTGATG	3840
	TTTTAAAAAT	TTATTTTTTT	TGGAAATAGT	TGCACAAATG	CTGCAATTTA	GCTTTAAGGT	3900
	TCTATAGATT	TTTAACTAGT	CCAACACAGT	CAGAAACATT	GTITTTGAATC	CTCTGTAAC	3960
	CAAGGCATTA	ATCTTAATAA	ACCAGGATCC	ATTAGGTAC	CACTTGATAT	AAAAAGGATA	4020
	TCCATAATGA	ATATTTTATA	CTGCATCCTT	TACATTAGCC	ACTAAATACG	TTATTGCTTG	4080
70	ATGAAGACCT	TTCAAGAAAT	CCTATGGATT	GCAGCATTTT	ACTTGGCTAC	TTTATACCCA	4140
	TGCTTAAGAG	AGGGGCGATT	TCTCAAAAGC	AGAAACATGC	CGCCAGTTCT	CAAGTTTTC	4200
	TCCTAACTCC	ATTGTAATGT	AAGGGCAGCT	GGCCCCCAAT	GTGGGGAGGT	CCGAACATT	4260
	TCGTAATCCC	CACTTTCTTG	TTCCGGGCTA	AATGACAGTT	TCTGTCTTAA	CTTAGATTCC	4320
	GATCTTTCCC	AAAGGTGTTG	ATTTACAAAG	AGGCCAGCTA	ATAGCAGAAA	TCTAGACCTT	4380
75	GAAAGAGAGA	TGAATTTCAA	GCTGTGAGCC	AGGCAGGAGC	TGAGTATGGC	AAAGGTTCTT	4440
	GAGAATCAGC	CATTTGGTAC	AAAAAGATT	TTTAAAGCTT	TTATGTTATA	CCATGGAGCC	4500
	ATAGAAAGGC	TATGGATTGT	TTAAGAACTA	TTTAAAGGTG	TTCCAGACCC	AAAAAGGAAA	4560
	AATAAAAAAA	AAGGAATATT	TGTACCCAAC	AGCTAGAAGG	ATTGCAAGGT	AGATTTTTGT	4620
	TTTAAATGAG	AGAGAGTGG	ACAGATAAGG	CCATTTAATA	TATCAAGATG	CAGTTGACAT	4680
80	CTCCTAGGGA	ATGATGAAA	CAGCAGGCTA	T			4711

Seq ID NO: C111 DNA Sequence  
Nucleic Acid Accession #: NM\_130830.1  
Coding sequence: 1..1746

```

1      11      21      31      41      51
|      |      |      |      |      |
5  ATGCCACTGA AGCATTATCT CCTTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG 60
   GCCTACCATG GCTGCCCTAG CGAGTGTAAC TGCTCCAGGG CCTCCAGGT GGAGTGCACC 120
   GGGGCACGCA TTGTGGCGGT GCCACCCCTC CTGCCCTGGA ACGCCATGAG CCTGCAGATC 180
   CTCAACACGC ACATCACTGA ACTCAATGAG TCCCGTTCC TCAATATCTC AGCCCTCATC 240
   GCCCTGAGGA TTGAGAAGAA TGAGCTGTGG CGCATCACGC CTGGGGCCTT CCGAAACCTG 300
10  GGCTCGCTGC GCTATCTCAG CCTCGCCAAAC AACAGCTGCG AGGTTCTGCC CATCGGCCTC 360
   TTCCAGGGCC TGGACAGGCT TGAGTCTCTC CTCTGTCCA GTAAACAGCT GTTGAGATC 420
   CAGCCGGCCC ACTTCTCCCA GTGCAGCAAC CTCAGGAGC TGCAATTGCA CGGCAACCAC 480
   CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG 540
   GGCAAGAATA GCCTCACCCA CATCTCACCC AGGGTCTTCC AGCACCTGGG CAATCTCCAG 600
   GTCCCTCGGC TGTATGAGAA CAGGCTCACG GATATCCCCA TGGGCACTTT TGTAGGGCTT 660
15  GTTAACTGTC AGGAACCTGGC TCTACAGCAG AACAGATTG GACTGCTCTC CCCTGGTCTC 720
   TTCCACAACA ACCACAAGCT CCAGAGACTC TACCTGTCCA ACAACCACAT CTCCAGCTG 780
   CCACCCAGCA TCTTCATGCA GCTGCCCCAG CTCACCCGTC TTACTCTCTT TGGGAATTCC 840
   CTGAAGGAGC TCTCTCTGGG GATCTTCGGG CCGATGCCCA ACCTGGGGGA GCTTTGGCTC 900
   TATGACAACC ACATCTCTTC TCTACCCGAC AATGTCTTCA GCAACCTCCG CCAAGTTGCAG 960
20  GTCTGTATTG TTAGCCGCAA TCAGATCAGC TTCACTCTCC CGGGTGCCTT CAACGGGCTA 1020
   ACGGAGCTTC GGGAGCTGTC CCTCCACACC AACGCACTGC AGGACCTGGA CGGGAATGTC 1080
   TTCCGATGTT TGGCCAACCT GCAGAACATC TCCCTGCAGA ACAATGGCCT CAGACAGCTC 1140
   CCAGGGAATA TCTTCGCCAA CGTCAATGGC CTCATGGCCA TCCAGCTGCA GAACAACAG 1200
   CTGGAGAACT TGCCCTCGG CATCTTCGAT CACCTGGGGA AACTGTGTGA GCTCGCGCTG 1260
25  TATGACAATC CCGGAGGCTG TGACTCAGC ATCCTTCGCG TCCGCAACTT GCTCCTGCTC 1320
   AACCAGCCTA GGTTAGGGAC GGACACTGTA CTGTGTGTT TCAGCCACAG CAATGTCCGA 1380
   GGCCAGTCCC TCATTATCAT CAATGTCAAC GTTGTGTGTC CAAGCGTCCA TGTCCCTGAG 1440
   GTGCCTAGTT ACCCGAAGAC ACCATGGTAC CCAGACACAC CCAGTTACCC TGACACCACA 1500
   TCCGTCTCTT CTACCACTGA GCTAACACAG CCTGTGGAAG ACTACACTGA TCTGACTACC 1560
30  ATTCAAGGTA CTGAGTACCG CAGCGTTTGG GGCATGACCC AGGCCAGAGC CGGCTGGGCC 1620
   ATTGCCGCCA TTGTAATTGG CATTTGCGCC CTGGCTGCTC CCCTGGCTGC CTGCGTGGC 1680
   TGTGCTGCTC GCAAGAAGAG GAGCCAGCT GTCTGTATGC AGATGAAGGC ACCCAATGAG 1740
   TGTAA

```

Seq ID NO: C112 DNA Sequence  
Nucleic Acid Accession #: NM\_002658.1  
Coding sequence: 77..1372

```

1      11      21      31      41      51
|      |      |      |      |      |
40  GTCCCGCAG CGCCGTCGGG CCTCTCTGCC GCAGGCCACC GAGGCCGCG CCGTCTAGCG 60
   CCGGAGCTTC GCGACCATGA GAGCCCTGCT GCGCGGCTG CTCTCTGCG TCCTGGTCTG 120
   GAGCGACTCC AAAGGCAGCA ATGAAGTTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
   TGGAGGACCA TTGTGTCCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA 240
45  GAAATTCGGA GGCAGCACTC GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
   TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCTGGAA 360
   CTCTGCCACT GTCTCTCAGC AAAGTACCA TGCCCAAGA TCTGATGCTC TTCAGCTGGG 420
   CCTGGGGAAG CATATTAATC CGAGGAACCC AGACAACCGG AGGCGACCCG GGTGCTATGT 480
   CAGAGTGGCC CTAAAGCGCG TTGTCCAAGA GTGCATGGTG CATGACTCGC CAGATGGAAA 540
50  AAAGCCCTCC TCTCCTCCAG AAGAATTAAA ATTTCACTGT GGCCAAAAGA CTCTGAGGCC 600
   CGCTTTAAG ATTATTGGGG GAGAATTAC CACCATCGAG AACAGCCCTT GGTTTGGGGC 660
   CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTC TGTGGAGGCA GCCTCATCAG 720
   CCTTGCTGGG GTGATCAGCG CCACACACTG CTTCATTGAT TACCCAAAGA AGGAGGACTA 780
   CATCGTCTAC CTGGGTGCGT CAAGGCTTAA CTCCAACAGC CAAGGGGAGA TGAAGTTTGA 840
55  GGTGGAAGAA CTCACTCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
   CATTTGCTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGACTAT 960
   ACAGACCATC TGCTCTGCCCT CGATGTATAA CGATCCCGAG TTTGGCACAA GCTGTGAGAT 1020
   CACTGGCTTT GGAAGAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAGATGAC 1080
   TGTGTGAAG CTGATTTCCT ACCGGGAGTG TCAGCAGCCC CACTACTAGC GCTCTGAAGT 1140
60  CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200
   CTGAGGGGGA CCCCTGCTCT GTTCCCTCCA AGGCCGATG ACTTTGACTG GAATTGTGAG 1260
   CTGGGCGCGT GGAATGTGCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
   CTTACCCCTG ATCCGCGAGT ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
   AGGGAGGAAA CGGGCACCAC CCGCTTCTCT GCTGGTTGTC ATTTTTCGAG TAGAGTCACT 1440
65  TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCTGTGG 1500
   CACCACCAAG GTGAACGACA ATAGCTTTAC CCTCAGGAT AGGCCTGGGT GCTGGCTGCC 1560
   CAGACCTCTC GGCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620
   TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAAGAGGGG CAGGGCATCT CCTGTGATG 1680
   GGCTCGAAGG GAGAGCCAGC TCCCCGACCC GGTGGGCATT TGTGAGGCC ATGGTTGAGA 1740
70  AATGAATAAT TTCCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800
   AATGTGGGAG CAGCGTTTGG GGGAGCAGAG ACACTAACGA CTTGAGGCA GGGCTCTGAT 1860
   ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTGG 1920
   GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT 1980
   AAAGTGTGTG GACTGTGATG CCACACAGAG TGCTCTTCTT GGAGAGGTTA TAGGTCACCT 2040
75  CTGGGCGCTC TTGGGTCCCC CACGTGACAG TGCCCTGGGA TGTACTTATT CTGCAGCATG 2100
   ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCATAGTA TGTCCCTTTC TTGGCCAGTT 2160
   ATCCCTCTCT TTTAGCTAG TTTATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
   AACTGAATA TTTATATTTT ACTATTTTAA TTTATATTTT TGTAAATTTA AATAAAGTG 2280
80  ATCAATAAAA TGTGATTTT CTGA 2304

```

Seq ID NO: C113 DNA Sequence  
Nucleic Acid Accession #: XM\_087254.1  
Coding sequence: 47..2332

	1	11	21	31	41	51	
	AGAGTACGTG	TTTACAGATA	AAACTGGTAC	ACTGACAGAA	AATGAGATGC	AGTTTCGGGA	60
	ATGTTCAATT	AATGGCATGA	AATACCAAGA	AATTAATGGT	AGACTTGTAC	COGAAGGACC	120
5	AACACCAGAC	TCTTCAGAAG	GAAACTTATC	TTATCTTAGT	AGTTTATCCC	ATCTTAACAA	180
	CTTATCCCAT	CTTACACCA	GTTCTCTTT	CAGAACCACT	CCTGAAAATG	AAACTGAACT	240
	AATTAAAGAA	CATGATCTCT	TCTTTAAAGC	AGTCAGTCTC	TGTCACTCTG	TACAGATTAG	300
	CAATGTTCAA	ACTGACTGCA	CTGGTATGG	TCCCTGGCAA	TCCAACCTGG	CACCATCGCA	360
	GTTGGAGTAC	TATGCATCTT	CACCAGATGA	AAAGGCTCTA	GTAGAAGCTG	CTGCAAGGAT	420
10	TGGTATTGTG	TTTATTGGCA	ATTCTGAAGA	AACTATGGAG	GTTAAAACCT	TTGGAAGAACT	480
	GGAACGGTAC	AAACTGCTTC	ATATTCTGGA	ATTGATTCA	GATCGTAGGA	GAATGAGTGT	540
	AATTGTTTCA	GCACCTTCAG	GTGAGAAAGT	ATTATTGGCT	AAAGGAGCTG	AGTCATCAAT	600
	TCTCCCTAAA	TGTATAGGTG	GAGAAATAGA	AAAAACCAGA	ATTCATGTAG	ATGAATTTGC	660
	TTTGAAGGG	CTAAGAACTC	TGTGTATAGC	ATATAGAAAA	TTTACATCAA	AAGAGTATGA	720
15	GGAAATAGAT	AAACGCATAT	TTGAAGCCAG	GACTGCCTTG	CAGCAGCGGG	AAGAGAAATT	780
	GGCAGCTGTT	TTCCAGTTCA	TAGAGAAAGA	CCTGATATTA	CTTGGAGCCA	CAGCAGTAGA	840
	AGACAGACAT	CAAGATAAAG	TTGAGAAAC	TATTGAAGCA	TTGAGAAATG	CTGGTATCAA	900
	AGTATGGGTA	CTTACTGGGG	ATAAACATGA	AACAGCTGTT	AGTGTGAGTT	TATCATGTGG	960
20	CCATTTTCAT	AGAACCATGA	ACATCCTTGA	ACTTATAAAC	CAGAAATCAG	ACAGCGAGTG	1020
	TGCTGAACAA	TTGAGGCAGC	TTGCCAGAAG	AATTACAGAG	GATCATGTGA	TTGAGCATGG	1080
	GCTGGTAGTG	GATGGGACCA	GCCTATCTCT	TGCACTCAGG	GAGCATGAAA	AACTATTAT	1140
	GGAAAGTTTC	CAAGAAATGTT	CAGCTGTATT	ATGCTGTCTG	ATGGCTCCAC	TGCAGAAAGC	1200
	AAAAGTAATA	AGACTAATAA	AAATATCACC	TGAGAAACCT	ATAACATTGG	CTGTGGGTGA	1260
	TGGTGCTAAT	GACGTAAAGCA	TGATACAAGA	AGCCCATGTT	GGCATAGGAA	TCATGGGTAA	1320
25	AGAAGGAAGA	CAGGCTGCAA	GAAACAGTGA	CTATGCAATA	GCCAGATTTA	AGTTCCTCTC	1380
	CAAAATGCTT	TTTGTTTCATG	GTCATTTTAA	TTATATTAGA	ATAGCTACCC	TTGTACAGTA	1440
	TTTTTTTAT	AAGAATGTGT	GCTTTATCAC	ACCCAGTTT	TTATATCAGT	TCTACTGTTT	1500
	GTTTTCTCAG	CAAACTTGT	ATGACAGCGT	GTACCTGACT	TTATACATA	TTTGTTTTAC	1560
	TTCCCTACCT	ATTCGATAT	ATAGTCTTTT	GGAACAGCAT	GTAGACCTTC	ATGTGTTTAC	1620
30	AAATAAGCCC	ACCCCTTATC	GAGACATTAG	TAAAAACGCG	CTCTTAAGTA	TTAAAAACAT	1680
	TCTTTATTGG	ACCATCTCGG	GCTTCAGTCA	TGCCCTTATT	TTCTTTTGTG	GATCCTATT	1740
	ACTAATAGGG	AAAGATACAT	CTCTGCTTGG	AAATGGCCAG	ATGTTTGGAA	ACTGGACATT	1800
	TGGCACTTGG	GCTCTCACAG	TCATGGTTAT	TACAGTCAAC	GTAAAGATGG	CTCTGGAAC	1860
	TCATTTTGG	ACTTGGATCA	ACCATCTCGT	TACCTGGGGA	TCTATTATAT	TTTATTITGT	1920
35	ATTTTCTTGG	TTTTATGGAG	GGATTCTCTG	GCCATTTTGG	GGCTCCGAGA	ATATGTATTT	1980
	TGTGTTTATT	CAGCTCTCTG	CAAGTGGTTC	TGCTTGGTTT	GCCATAATCC	TCATGGTTGT	2040
	TACATGTCTA	TTTCTGTATA	TCATAAAGAA	GGTCTTTGAC	CGACACCTCC	ACCCCTACAAG	2100
	TACTGAAAAG	GCACAGCTTA	CTGAAACAAA	TGCAGGTATC	AAGTGCTTGG	ACTCCATGTG	2160
	CTGTTTCCCG	GAAGGAGAAG	CAGCGTGTGC	ATCTGTTGGA	AGAATGCTGG	AACGAGTTAT	2220
40	AGGAAGATGT	AGTCCAACCC	ACATCAGCAG	ATCATGGAGT	GCATCGGATC	CTTTCTATAC	2280
	CAAGCAGCAG	AGCATCTTGA	CTCTCTCCAC	AATGGACTCA	TCTACTTGT	AAAGGGGCGAG	2340
	TAGTACTTTG	TGGGAGCCAG	TTCACTCCCT	TTCTTAAAT	TCAGTGTGAT	CACCTGTITA	2400
	ATGGCCACAC	TAGCTCTGAA	ATTAATTTCC	AAAACTTTTG	TAGTAGTTCA	TACCCACTCA	2460
	GAGTTATAAT	GGCAACAAA	CAGAAAGCAT	TAGTACAAGC	CCCTCCCAAC	ACCCCTAATT	2520
45	TGAATCTGAA	CATGTTAAAA	TTTGAGAATA	AAGAGACATT	TTTCATCTCT	TTGCTCGGTT	2580
	TGTCCTTGT	GCTTATGGGA	CTCTTAATGG	CAITTCAGTC	TGTTGCTGAG	GCCATTATAT	2640
	TTTAATATAA	ATGTAGAAAA	AAGAGAGAAA	TCTTAGTAAA	GAGTATTTT	TAGTATTAGC	2700
	TTGATTATTG	ACTCTTCTAT	TTAAATCTGC	TTCTGTAAT	TATGCTGAAA	GTTTGCTTGT	2760
	AGAACTCTAT	TTTTTTATTA	GAGTTATATT	TAAAGCTTTT	CATGGGAAAA	GTTAATGTGA	2820
50	ATACCTGAGG	ATTTTGGTCC	CTCAGTGACC	TGTTGTGTTA	ATTCAATTAAT	GCATCTGAG	2880
	TTACAGAGCA	AAATTAGGAG	AATCATTTCC	AACCAATTAT	TACTGCACTA	TGGGGAGTAA	2940
	ATTTATACCA	ATTCCTCTAA	CTGTACTGTA	ACACAGCCTG	TAAAGTTAGC	CATATAAATG	3000
	CAAGGGTATA	TCATATATAC	AAATCAGGAA	TCAGGTCCGT	TCACCGAACT	TCAAATTGAT	3060
	GTTTACTAAT	ATTTTGTGGA	CAGAGTATAA	AGACCCCTATA	GTGGGTAAAT	TAGATACTAT	3120
55	TAGCATATTA	TAAATTTAAT	GTCCTTATCA	TGGATCTTT	TGCATGCTTT	AATCTGGTTA	3180
	ACATATTTAA	ATTTGCTTTT	TTTCTCTTTA	CCTGAAGGCT	CTGTGTATAG	TATTTCTATGA	3240
	CATCGTTGTA	CAGTTTAACT	ATATCAATAA	AAAGTTTGGG	CAGTATTTAA	ATATTGCAAA	3300
	TATGTTTAAAT	TATACAAATC	AGAATAGTAT	GGGTAATTTA	ATGAATACAA	AAAGAAGAGC	3360
	CTCTTCTGCG	AGCCGACTTA	GACATGCTCT	TCCCTTTCTA	TAAGCTAGAT	TTTGAATAAA	3420
60	AGGGTTTCAG	TAAATTAATCT	TATTTTCAGG	TTATGTCATC	TAACCTATAG	CAAACTACCA	3480
	CAATACAGTG	AGTCTGCGCA	GTGTCGCCAGT	ACAGGCATTA	TTTCAGGTGT	GGCTGTGGAA	3540
	TGTAAAAATG	CTCAACTTGT	ATCAGGTAAT	GTTAGCAATA	AATTAAATGC	TAAGAATGAT	3600
	TAATCGGGTA	CATGTTACTG	TAATTAATCT	ATTGCACTTC	AAAACCTAAC	TTCCATCTCG	3660
	AAITTTATCAA	GTAGTTTCACT	ATTGTCAATT	GTTTTTGT	TATTGAAAAG	TAAATGTTGT	3720
65	TTAAGATTTA	GAAGTGATTA	TTAGCTTGAG	AACTATTACC	CAGCTCTAAG	CAAAATATGA	3780
	TTGTATACAT	ATTAAGATAA	TGGTTAAATG	CGGTTTACC	AAGTTTCCC	TTGAAAATGT	3840
	AAITTCCTTTA	TGGAGATTTA	TTGTGACGCC	CTAAGCTTCC	TTCCCATTTT	ATGAATATAA	3900
	GGCTTCTAGA	ATTGSACTGG	CAGGGGAAAG	AATGTTAGAG	ACAGAAATTA	AGACTTTATC	3960
70	CTTGTGTTGCT	TGTAAACTAT	TATTTTCTTG	CTAATGTAAC	ATTGCTCTGT	TCCAGTGATG	4020
	TAAGGATATT	AAGTTATTAA	GCTAAATATT	AATTTTCAAA	AATAGTCTCT	CTTTAACTTA	4080
	GATATTTTCA	AGCTGGAATT	AGGAAGATCT	GTTATTCTGG	AAGTACTAAA	AAGAATAATA	4140
	CAACGTACAA	TGCTCACTAT	CACTAATTCA	TGTTCCAGAA	GAGGAAATAA	TGAAGATATA	4200
	CTCAGTAGAG	TACTAGGTGG	GAGGATATGG	AAATTTGCTC	ATAAAATCTC	TTATAAAACG	4260
	TGCATATAAC	AAAATGACAC	CCAGTAGGCC	TGCATTACAT	TTACATGACC	GTGTTTATTT	4320
75	GCCATCAAAT	AAACTGAGTA	CTGACACCG	ACAAAGACTC	CAAAAGTCATA	AAATAGCCTA	4380
	TGACCAACTG	CAGCAAGACA	GGAGGTGAGC	TGCGCTATAA	TGGTGCTTAA	AGTGTGATTT	4440
	ATGTAATTTT	CTGTACTCAC	CAITTTGAAGT	TAGTTAAGGA	GAACCTTTAT	TTTTTAAAAA	4500
	AAGTAAATGG	CAACCACTAG	TGTGCTCATC	CTGAACCTGT	ACTCCAAATC	CACTCOGTTT	4560
80	TTAAAGCAAA	ATTATCTTGT	GATTTTAAAG	AAAGAGTTTT	CTATTATTAT	AAGAAGTAA	4620
	CAATGCAGTC	TGCAAGCTTT	CAGTAGTTTT	CTAGTGCTAT	ATTCTATCTG	TAAACTCTT	4680
	ACTACGTAAC	CAGTAATCAC	AAGGAAAGTG	TCCCTTTTGC	ATATTCTCTT	AAAAATCTTT	4740
	CTTTGGAAG	TATGATGTTG	ATAATTAAC	TACCTTTATC	TGCCAAAACC	AGAGCAAAAT	4800
	GCTAAATACG	TTATGCTTAA	TCAGTGGTCT	CAAAATCGATT	TGCTCTCCCT	TGCTCTGCTC	4860
	GAGGGCTGTA	AGCCTGAAGA	TAGTGGCAAG	CACCAAGTCA	GTTTCCAAAA	TTGCCCTCTA	4920

5  
10  
15

```

GCTGCTTTAA GTGACTCAGC ACCCTGCCTC AGCTTCAGCA GGCCTAGGCT CACCCCTGGGC 4980
GGAGCAAAGT ATGGGCCAGG GAGAACTACA GCTACGAAGA CCTGCTGTCT AGTTGAGAAA 5040
AGGGGAGAA TTTAGGTCTG AATTTTCTAA CTGTCTCTTT TCTTGGGTCT AAAGCTCATA 5100
ATACACAAAG GCTTCAGAC CTGAGCCACA CCCAGGCCCT ATCCTGAACA GGAGACTAAA 5160
CAGAGGCAAA TCAACCTAG GAAATACCTG CATTCTGCC TACGGTTAGT ACCAGGACTG 5220
AGGTCATTTC TACTGGAAAA GATTGTGAGA TTGAACCTAT CTGATCGCTT GAGACTCCTA 5280
ATAGGCAGGA GTCAAGGCCA CTAGAAAATT GACAGTTAAG AGCCAAAAGT TTTTAAAAA 5340
TGCTACTCTG AAAAATCTCG TGAAGGCTGT AGGAAAAGGG AGAATCTTCC ATGTTGGTGT 5400
TTTTCTCTGA AAGATCAGTT TGGGGTATGA TATAAGCAGG TATTAATAAA AATAACACAC 5460
CAAGAAGTTA GCTAAAACAT GTTTTATTAA TTTTGGTCCC CAGTACAGA CATTTTATTT 5520
CTATTTTGAA ATGAGTTATC TATTTTCATA AAAGTAAAC ACTATTAAAG TGCTGTTTTA 5580
TGTGAAATAA CTGGAATGTT GTTCTATATA AAAATAGATC ATAACCTATG ATATGTTTGT 5640
AATCATGGTA ATTTAGATTT TTATGAGGAA TGAGTATCTG GAAATATTGT AGCAATACTT 5700
GGTTTAAAT TTTGACCTG AGACACTGTG GCTGTCTAAT GTAATCCTTT AAAAATCTCT 5760
TGCAATTGTC GTAAATGTAG TATATTATTG TACAGTACT CATATTTTTT TAAAGTTTAT 5820
GAAGTTATAT TTATCAATA AAAACTTTCC TATAT 5855

```

20

Seq ID NO: C114 DNA Sequence  
Nucleic Acid Accession #: XM\_087461.1  
Coding sequence: 236..1138

25  
30  
35  
40  
45  
50  
55

```

1 11 21 31 41 51
| | | | |
COGGCGCGCG GGGCGGGGGG GAACCCCAAA CGCAACCGGG TCTGGAGGGA TCCCGCGCGC 60
GAGCCAGCGG CGGTACCGCG CTCCGCGCGG CCCCTGCGGG CTGGCAGGC GCCCGGCGCG 120
CCCGCACTGC GCCCGGCGCG CGGCTCCCGC GGTCCACCGG TGAGCTCGCC GGCCCGTGGC 180
CGCTCTGCCA TGCAACCGCC CGCGGCTCGG CGCGGCTAGG CGCCCGCGCG AGGCCATGCT 240
GCCCTCTGCT GACCGGCTCC TGCGCGCGCG CTGCCCGCTG CGCCCGCTCC GCGCGCGGGC 300
CGCGGAGCGG CCGCGGCTCC TCGGGGTGCC CTCCAATGCT TCAGTCAACG CGTCTCCCGC 360
GGCGAGCCCA TCGCCCGCGG GCTGCTGGCC TCGCGGGCCC CGGGGCCCC CGAGCGCCCG 420
GGCCCGGAGG AGGCGCGCGG GCGCGCGCGG CCTGTGCAAC ATCAGCGTGC AGCGGCAGAT 480
GCTGAGCTCG CTGCTCGTGC GCTGGGGCGG CCGCGGGGGG TTCCAGTGGC ACCTACTGCT 540
CTTCTCCACC AACCGGCAAG GCGCGCTTT CTTCGCGCGG GCCTTCCACC GCGTCGGGCC 600
GCGCTGCTCT ATCGAGCACC TGGGGCTGGC GCGCGGCGCG GCGCAGCAGG ACCTGCGCCT 660
CTGCGTGGGC TCGCGCTGGG TGCGCGGTGC CGCAACCGGC CGCTCGCGC CGCGCGCGCG 720
CCCCAGCGCC GCGCGCGCCA CCGCGGGGGC GCCCACCGCG CTGCCAGCCT ACCCGCGCGC 780
CGAGCGCGCC GGGCGCTGT GGTGCGAGGG CGAGCGCGCT CATTTCTGCT GCCTAGACTT 840
CAGCTAGTAG GAGCTGCAGG GCGAGCCGGG CTGGCGGCTG AACCGTAAGC CCATTGAGTC 900
CAGCTGTGTG GCTGCTTCA TGACCTGGT CATCGTGGT TGGAGCGTGG CCGCCCTCAT 960
CTGCGCGGTG CCGCTATCG CTGCTTCTCT GCCCAACGCG ATGGAACAGC GCGGACCAAC 1020
CGCCAGCACC ACCGCGCCA CCGCGCGCG AGTGCCCGCA GGGACCAACG CAGCGCGCGC 1080
CGCCCGCGCC GCTGCGCGCG CCGCGCGCGG CGTCACTTGG GGGGTGGCGA CCAAGTGACC 1140
CGCTCGCTCT CTCCCTGTGT CGCTCTGTGT TCGCGCGCGG CGGCTGCCCT TCCCGCGGCA 1200
GACTCGGCGG GTGTGCTTGG TGCTGTAGTT ATCGTTAGTT CCTCTTCCCG AGATGGGGCC 1260
GCGGAGAGAC CCGAGCGCCT TTGAAAAGCA AGGTTTGTGC TCGCTTCCA GTTCCGAAAA 1320
GCAGATGTTT AAGCCCTTGG ACTGAGGGTG GGATCGCAGC TCCGAAGACG GAGAGGAGGG 1380
AAATGGGGCC CTTTCCCTTC TATTGCTACC CCTGCGCGA CTCTTCCCC GCACCAACGT 1440
GCGCTAGATT CATGGCAGAA AATGACCAAA TCGTGTGTAT TTGTTTATA TATTTAATAA 1500
CTGTTTAAAG TGAAGTTTAT AGTAAAAAAA ATACAAAACA AAAAGATTAA ATTGCTATTG 1560
CTGTAGTAAG AGAAGCTCTT TGTATCTGAA CATAGTTGTA TTTGAAATTT GTGGTTTTTT 1620
AATTTATTTA AATTTGGGGG GAGGGCATGG GAAGGATTTA ACACCGATAT ATTGTTACCG 1680
CTGAAAATGA ACTTTATGAA CCTTTTCCAA GTTGATCTAT CCAGTGACGT GGCCTGGGTG 1740
GCGTTTCTTC TTGTACTTAT GTGGTTTTTT GGCTTTTAAT ACAGACATT TCCCTCC 1796

```

55

Seq ID NO: C115 DNA Sequence  
Nucleic Acid Accession #: XM\_051522.4  
Coding sequence: 127..1215

60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ACAGTTGTTG CAAAGTGCTC AGCACTAAGG GAGCCAGCGC ACAGCACAGC CAGGAAGGCG 60
AGCGAGCCCA GCCAGCCAGC CCAGCCAGCG CAGCCCGGAG GTCATTGAT TGCCCGCCTC 120
AGAACGATGG ATCTGCATCT CTTCGACTAC TCAGAGCCAG GGAACCTTCT GGACATCAGC 180
TGCCCATGCA CATGCGAGCA CTGCATGCTG GTGACACCGG TGATGTGTCC CAACATGCCC 240
AACAAAGAGG TCCTGCTCTA CAOGCTCTCC TTCAATTACA TTTTCATCTT CGTCATGGCC 300
ATGATTGCCA ACTCCGTGGT GGTCTGGGTG AATATCCAGG CCAAGACCAC AGGCTATGAC 360
ACGCACGTCT ACATCTTGAA CCTGGCCATT GCCGACCTGT GGGTTGTCTT CACCATCCCA 420
GTCTGGGTGG TCAGTCTCGT GCAGCACAAC CAGTGGCCCA TGGCGAGCT CAOGTGCAAA 480
GTACACAAC TCATCTTCTC CATCAACCTC TTCCGACGCA TTTTCTTCTT CAOGTGCAAT 540
AGCGTGGACC GCTACCTCTC CATCACTTAC TTCAACAACA CCCCAGCAG CAGGAAGAG 600
ATGGTACGCC GTGTCTCTG CATCTGTGTG TGGCTGTGG CCTTCTCGGT GTCTCTGCTT 660
GACACCTACT ACCTGAAGAC CGTCACTGCT GCGTCCAACA ATGAGACCTA CTGCGGTGCT 720
TTCTACCCCG AGCAGAGCAT CAAGGAGTGG CTGATCGGCA TGGAGCTGGT CTCCGTTGTC 780
TTGGGCTTTG CCGTTCCTCT CTCCATTATC GCTGTCTTCT ACTTCTGTCT GGCCAGAGCC 840
ATCTCGCGGT CCACTGACCA GGAGAAGCAC AGCAGCGGGA AGATCATCTT CTCTCAAGTG 900
GTGTCTTCTC TTGTCTGCTG GCTGCCCTAC CAGTGGCGGG TGCTGTGGA CATCTTCTCC 960
ATCTTGCACT ACATCCCTTT CACTGCGCG CTGGAGCACG CCTCTTTCAC GGCCCTGCAT 1020
GTACACAGT GCTGTGCGCT GTTGCACTGC TCGTCAACC CTGTCTCTCA CAGCTTCTAT 1080
AATCGCAACT ACAGGTACGA GCTGATGAAG GCCTTCACTT TCAAGTACTT GGCCAAAACA 1140
GGGCTCACCA AGCTATCGA TGCTCCAGA GTCTCAGAGA CGGAGTACTT TGCTTGGAG 1200
CAGAGCACCA AATGATCTGC CCGTGGAGGG CTCTGGGAGG GGTTTACTTG TTTTGAACA 1260
GGGTGATGGG CCCTATGGTT TTCTAGAGCA AAGCAAAGTA GCTTGGGGTC TTGATGCTTG 1320
AGTAGAGTGA AGAGGGGAGC ACGTGCCCC TGCTATCCAT CTCTCTTCTT CTGATGACG 1380
CAGCTGTCAT TTGGCTGTGC GTGCTGACAG TTTTGCAACA GGCAGAGCTG TGTGACAG 1440

```



5	CAGTGCTGTG	CGTCAGAGCC	AGCTGAGGAC	AGGCTTGCCT	GGACTTCTGT	AAGATAGGAT	1500
	TTTCTGTGTT	TCCTGAATTT	TTTATATGGT	GATTGTGATT	TAAATTTTAA	GACTTTATTT	1560
	TCTCACTATT	GGGTACCTT	ATAAATGTAT	TTGAAAGTTA	AATATATTTT	AAATATTGTT	1620
	TGGGAGGCAT	AGTGCTGACA	TATATTGAGA	GTGTTGTAGT	TTTAAGGTTA	CGGTGACTTC	1680
	AGTTTTGACT	ARGGATGACA	CTAATTGTTA	GCTGTTTGA	AATTATATAT	ATATAAATAT	1740
	ATATAAATAT	ATAAATATAT	GCCAGTCTTG	GCTGAAATGT	TTTATTTACC	ATAGTTTTAT	1800
	ATCTGTGTGG	TGTTTTGTAC	CGGCACGGGA	TATGGAAACGA	AAACTGCTTT	GTAATGCAGT	1860
	TTGTGACATT	AATAGTATTG	TAAAGTTACA	TTTTAAATA	AACAAAAAAC	TGTTCTGGAC	1920
10	TGCAATCTCG	CACACACAAC	GAACAGTTGC	ATTTGAGAGA	GTTCTCTCAA	TTTGTAAGTT	1980
	ATTTTTTTTT	AATAAAGATT	TTTGTTTCCT				2010

Seq ID NO: C116 DNA Sequence  
Nucleic Acid Accession #: NM\_000350.1  
Coding sequence: 82..6903

15	1	11	21	31	41	51	
	CTGGCTCTTA	ACGGCGTTTA	TGTCCTTTGC	TGTCGAGGG	GCCTCAGCTC	TGACCAATCT	60
20	GGTCTTCGTG	TGCTCATTAG	CATGGGCTTC	GTGAGACAGA	TACAGCTTTT	GCTCTGGAAG	120
	AACCTGGACCC	TGGCGAAAAG	GCAAAAGATT	CGCTTTGTGG	TGGAACCTCGT	GTGGCCTTTA	180
	TCCTTATTTT	TGGTCTTGAT	CTGTTTAAAG	AATGCCAACCC	CGCTCTACAG	CCATCATGAA	240
	TGCCATTTC	CCAACAAGGC	GATGCCCTCA	GCAGGAATGC	TGCCGTGGCT	CCAGGGGATC	300
	TTCTGCAATG	TGAACAATCC	CTGTTTTCAA	AGCCCCACCC	CAGGAGAATC	TCTTGGAAAT	360
25	GTGTCAAAC	ATAACAATCT	CATCTTGSCA	AGGGTATATC	GAGATTTTCA	AGAATCTCTC	420
	ATGAATGCAC	CAGAGAGCCA	GCACCTTGGC	CGTATTTGGA	CAGAGCTACA	CATCTTGTC	480
	CAATTCATGG	ACACCCCTCG	GACTACCCCG	GAGAGAATTG	CAGGAAGAGG	AATACGAATA	540
	AGGGATATCT	TGAAGAATGA	AGAAACACTG	ACACTATTTC	TCAATAAAAA	CATCGGCCTG	600
	TCTGATCAG	TGGTCTACCT	TCTGATCAAC	TCTCAAGTCC	GTCCAGAGCA	GTTGCTCAT	660
30	GGAGTCCCGG	ACCTGGCGCT	GAAGGACATC	GCCTGCACGG	AGGCCCTCCT	GGAGCGCTTC	720
	ATCATCTTCA	GCCAGAGAGC	CGGGGCAAG	ACGGTGCCTG	ATGCCCTGTG	CTCCCTCTCC	780
	CAGGGCACCC	TACAGTGGAT	AGAAGACACT	CTGTATGCCA	ACGTGGACTT	CTTCAAGCTC	840
	TTCCGTGTGC	TTCCCACTCT	CCTAGACAGC	CGTTCTCAAG	GTATCAATCT	GAGATCTTGG	900
	GGAGGAATAT	TATCTGATAT	GTCAACCAAG	ATTCAAGAGT	TTATCCATCG	GCCGAGTATG	960
35	CAGGACTTGC	TGTGGGTGAC	CAGGCCCTCT	ATGCAGAAATG	GTGGTCCAGA	GACCTTTACA	1020
	AAGCTGATGG	GCATCTCTGC	TGACCTCTCT	TGTGGCTACC	CCGAGGGAGG	TGGCTCTGG	1080
	GTGCTCTCCT	TCAACTGGTA	TGAAGACAAT	AACTATAAGG	CCTTTCTGGG	GATTGACTCC	1140
	ACAAGGAAGG	ATCCTATCTA	TTCTTATGAC	AGAAGAACA	CATCTTTTGG	TAATGCATTG	1200
	ATCCAGAGCC	TGGAGTCAAA	TCCTTTAACC	AAAATCGCTT	GGAGGGCGGC	AAAGCCTTTG	1260
40	CTGATGGGAA	AAATCTGTGA	CACTCCTGAT	TCACCTGCAG	CACGAAGGAT	ACTGAAGAAT	1320
	GCCAACTCAA	CTTTTGAAGA	ACTGGAACAC	GTTAGGAAGT	TGGTCAAAGC	CTGGGAAGAA	1380
	GTAGGGCCCC	AGATCTGGTA	CTTCTTTGAC	AACAGCACAC	AGATGAACAT	GATCAGAGAT	1440
	ACCCCTGGGG	ACCCCAACAGT	AAAAGACTTT	TTGAATAGGC	AGCTTGGTGA	AGAAGGTATT	1500
	ACTGCTGAAG	TGATCTAATA	CTTCTCTAC	AAGGGCCCTC	GGGAAGGCCA	GGCTGACGAC	1560
45	ATGGCCAACT	TGCACTGGAG	GGACATATTT	AACATCACTG	ATGCCACCTT	CCGCTCTGTC	1620
	AATCAATACC	TGGAGTGCTT	GGTCTCTGAT	AAGTTTGAAA	GCTACAATGA	TGAAATCTAG	1680
	CTCACCCAAC	GTGCCCTCTC	TCTACTGGAG	GAAACATGTT	TCTGGGCGGG	AGTGGTATTC	1740
	CCTGACATGT	ATCCCTGGAC	CAGCTCTCTA	CCACCCCAAG	TGAAGTATAA	GATCCGAATG	1800
	GACATAGAGC	TGGTGGAGAA	AACCAATAAG	ATTAAAGACA	GGTATTGGGA	TTCTGGTCCC	1860
50	AGAGCTGATC	CCGTGGGAAG	TTTCCGGTAC	ATCTGGGGCG	GGTTTGCCCTA	TCTGCAGGAC	1920
	ATGGTTGAAC	AGGGGATCAC	AAGGAGCCAG	GTGCAGGCGG	AGGCTCCAGT	TGGAATCTAC	1980
	CTCCAGCAGA	TCGCCATCCC	CTGCTTCGTG	GACGATTCTT	TCATGATCAT	CCTGAACGCG	2040
	TGTTTCCCTA	TCTTCTAGGT	GCTGGCATGG	ATCTACTCTG	TCTCCATGAC	TGTGAAGAGC	2100
	ATGCTCTTGG	AGAAGGAGTT	GCGACTGAAG	GAGACCTTGA	AAAATCAGGG	TGCTCTCAAT	2160
55	GCAGTGATTT	GGTGTACCTG	GTCTCTGGAC	AGCTTCTCCA	TCATGTGATG	GAGCATCTTC	2220
	CTCCTGACGA	TATTCATCAT	GCATGGAAGA	ATCCTACATT	ACAGCGACCC	ATTCATCTTC	2280
	TTCTGTCTCT	TGTTGGCTTT	CTCCACTGCC	ACCATCATGC	TGTGCTTTCT	GCTCAGCAC	2340
	TTCTTCTCCA	AGGCCAGTCT	GGCAGCAGCC	TGTAGTGGTG	TCATCTATTT	CACCTCTACT	2400
	CTGCCACACA	TCTCTGTGCT	CGCTTGGCAG	GACCCGATGA	CCGCTGAGCT	GAGAAGGGCT	2460
60	GTGAGCTTAC	TGCTCTCGGT	GGCATTTGGA	TTTGGCAGTG	AGTACCTGGT	TGCTTTTGAA	2520
	GAGCAAGGCC	TGGGGCTGCA	GTGAGCAAC	ATCGGGAACA	GTCCCAAGGA	AGGGGACGAA	2580
	TTACGCTTCC	TGCTGTCCAT	GCAGATGATG	CTCCTTGATG	CTGCGTGCTA	TGGCTTACTC	2640
	GCTTGGTACC	TTGATCAGGT	GTTTCCAGGA	GACTATGGAA	CCCCACTTCC	TTGTTACTTT	2700
	CTTCTACAAG	AGTCTGATTG	GCTTAGCGGT	GAAGGGTGT	CAACCAAGGA	AGAAAGAGCC	2760
65	CTGGAAAAGA	CCGAGCCCTC	AACAGAGGAA	ACGGAGGATC	CAGAGCACCC	AGAAGGAATA	2820
	CACGACTCCT	TCTTTGAAGC	TGAGCATCCA	GGGTGGGTTT	CTGGGGTATG	CGTGAAGAAT	2880
	CTGGTAAAGA	TTTTTGAGCC	CTGTGGCCGG	CCAGCTGTGG	ACCGTCTGAA	CATCACCTTC	2940
	TACGAGAACC	AGATCACCGC	ATTCCCTGGC	CACAATGGAG	CTGGGAAAAC	CACCACCTTG	3000
	TCCATCTCTGA	CGGGTCTGTT	GCCACCAACC	TCTGGGACTG	TGCTCGTTGG	GGGAAGGGAC	3060
70	ATTGAACCA	GCCTGGATGC	AGTCCGGCAG	AGCCTTGGCA	TGTTCCACA	GCACAACTAC	3120
	CTGTTCCACC	ACCTCACGGT	GGCTGAGCAC	ATGCTGTTCT	ATGCCAGCT	GAAAGGAAAG	3180
	TCCAGGAGG	AGGCCAGACT	GGAGATGGAA	GCCATGTTGG	AGGACACAGG	CCTCCACCCAC	3240
	AAGCGGAATG	AAGAGGCTCA	GGACCTATCA	GGTGGCATGC	AGAGAAGACT	GTGCGTTGCC	3300
	ATTGCTTTTG	TGGGAGATGC	CAAGGTGGTG	ATTCTGGAGC	AACCCACCTC	TGGGGTGGAC	3360
75	CCTTACTCGA	GAGCTCAAT	CTGGGATCTG	CTCTGAAAT	ATGCTCAGG	CAGAACCATC	3420
	ATCATGCCCA	CTCACCATAT	GGACGAGGCC	GACCACCAAG	GGGACCGCAT	TGCCATCAT	3480
	GCCAGGGAA	GGCTCTACTG	CTCAGGCACC	CCACTCTTCC	TGAAGAAGCT	CTTTGGCACA	3540
	GGCTGTACT	TAACTTGGT	GCGCAAGATG	AAAAACATCC	AGAGCCAAAG	GAAAGGCAGT	3600
	GAGGGGACCT	GCAAGCTGCTC	GTCTAAGGGT	TTCTCCACCA	CGTGTCCAGC	CCACGTGAT	3660
80	GACCTAATCT	CAGAACAGT	CCTGGATGGG	GATGTAAATG	AGCTGATGGA	TGTAGTTCTC	3720
	CACCATGTTT	CAGAGGCAAA	GCTGGTGGAG	TGCATTGGTG	AAGAACITAT	CTTCTTCTT	3780
	CCAAATAAGA	ACTTCAAGCA	CAGAGCATAT	GCCAGCCTTT	TCAGAGAGCT	GGAGGAGAGC	3840
	CTGGCTGACC	TTGGTCTCAG	CAGTTTGGTA	ATTTCTGACA	CTCCCTCGGA	AGAGATTTTT	3900
	CTGAAGGTA	CGGAGGATTC	TGATTGAGGA	CCTCTGTTTG	CGGGTGGCGC	TCAGCAGAAA	3960
	AGAGAAAACG	TCAACCCCGC	ACACCCCTGC	TTGGGTCCCA	GAGAGAAGGC	TGGAACAGAA	4020



	CCCCAGGACT	CCAATGTCTG	CTCCCCAGGG	GCGCCGGCTG	CTCACCAGCA	GGGCCAGCCT	4080
	CCCCAGAGCC	CAGAGTGCCC	AGGCCCGCAG	CTCAACAACG	GGACACAGCT	GGTCTCCAG	4140
	CATGTGCAGG	CGCTGTCTGGT	CAAGAGATTC	CAACACACCA	TCCGAGGCCA	CAAGGACTTC	4200
5	CTGGCGCAGA	TGCTGTCTCCC	GGCTACCTTT	GTGTTTTTGG	CTCTGATGCT	TTCTATTGTT	4260
	ATCCTTCCCT	TTGGCGCAATA	CCCCGCTTTG	ACCCTTCACC	CCTGGATATA	TGGGCAGCAG	4320
	TACACCTTCT	TCAGCATGGA	TGAACCAAGG	AGTGAGCAGT	TCACGGTACT	TGCAGACGTC	4380
	CTCCTGAATA	AGCCAGGCTT	TGGCAACCGC	TGCCTGAAGG	AAGGGTGGCT	TCCGGAGTAC	4440
	CCCTGTGGCA	ACTCAACACC	CTGGAAGACT	CCTTCTGTGT	CCCCAAACAT	CACCCAGCTG	4500
10	TTCCAGAAGC	AGAAATGGAC	ACAGGTCAAC	CCTTCCACAT	CCTGCAGGTG	CAGCACCAGG	4560
	GAGAAGCTCA	CCATGTCTGCC	AGAGTGTCCC	GAGGGTGGCG	GGGGCCTCCC	GCCCCCCAG	4620
	AGAACACAGC	GCAGCAGCGA	AATTCTACAA	GACCTGACGG	ACAGGAACAT	CTCCGACTTC	4680
	TTGGTAAAGA	CGTATCTCTG	TCTTATAAGA	AGCAGCTTAA	AGAGCAAATT	CTGGGTCAAT	4740
	GAACAGAGGT	ATGGAGGAAT	TTCCATTGGA	GGAAGCTCC	CAGTGTCTCC	CATCACGGGG	4800
15	GAAGCACTTG	TTGGGTTTTT	AAGCGACCTT	GGCCGGATCA	TGAATGTGAG	CGGGGGCCCT	4860
	ATCACTAGAG	AGGCCTCTAA	AGAAATACCT	GATTTCTTAA	AACATCTAGA	AACTCAAGAC	4920
	AACATTAAAG	TGTGGTTTAA	TAAACAAAGG	TGGCATGCCC	TGGTCAGCTT	TCTCAATGTG	4980
	GCCCAACAAG	CCATCTTACG	GGCCAGCCTG	CCTAAGGACA	GGAGCCCGCA	GGAGTATGGA	5040
	ATCACCGTCA	TTAGCCCAACC	CCTGAACCTG	ACCAAGGAGC	AGCTCTCAGA	GATTACAGTG	5100
20	CTGACCACTT	CAGTGGATGC	TGTGGTTGCC	ATCTGCGTGA	TTTCTCCAT	GTCCCTCGTC	5160
	CCAGCCAGCT	TTGTCTCTTA	TTTGATCCAG	GAGCGGGTGA	ACAAATCCAA	GCACCTCCAG	5220
	TTTATCAGTG	GAGTGAGCCC	CACCACCTAC	TGGGTGACCA	ACTTCTCTG	GGACATCATG	5280
	AATTATTCCG	TGAGTGTCTG	GCTGGTGGTG	GGCATCTTCA	TGGGTCTTCA	GAAGAAAGCC	5340
	TACACTTCTC	CAGAAACCTT	TCCTGCCCTT	GTGGCACTGC	TCCTGCTGTA	TGGATGGGG	5400
25	GTCAATCCCA	TGAGTATACC	AGCATCCTTC	CTGTTTGATG	TCCCCAGCAC	AGCCTATGTG	5460
	GCTTTATCTT	GTGCTAATCT	GTTCATCGGC	ATCAACAGCA	GTGCTATTAC	CTTCATCTTG	5520
	GAATTATTGT	ATAATAACCG	GACGCTGCTC	AGGTTCAACG	CCGTGCTGAG	GAAGCTGCTC	5580
	ATTGTCTTCC	CCCACTTCTG	CCTGGGCGGG	GGCCTCATTG	ACCTTGCACT	GAGCCAGGCT	5640
	GTGACAGATG	TCTATGCCCG	GTTTGGTGAG	GAGCACTCTG	CAAAATCCGT	CCACTGGGAC	5700
30	CTGATTGGGA	AGAACTGTGT	TGCCATGGTG	GTGGAAAGGG	TGGTGTACTT	CCTCTGACC	5760
	CTGCTGGTCC	AGGCCCACTT	CTTCTCTCC	CAATGGATTG	CCGAGCCAC	TAAGGAGCCC	5820
	ATTGTTGATG	AAGATGATGA	TGTGGCTGAA	GAAAGACAAA	GAATTATTAC	TGGTGGAAAT	5880
	AAAACCTGCA	TCTTAAGGCT	ACATGAACCT	ACCAAGATTT	ATCTGGGCAC	CTCCAGCCCA	5940
	GCAGTGGACA	GGCTGTGTGT	CGGAGTTCGC	CCTGGAGAGT	GCTTTGGCCT	CCTGGGAGTG	6000
35	AATGGTGGCG	GCAAAACAAC	CACATTCAAG	ATGCTCACTG	GGGACACCAC	AGTGACCTCA	6060
	GGGGATGCCA	CCGTAGCAGG	CAAGAGTATT	TTAACCAATA	TTTCTGAAGT	CCATCAAAAT	6120
	ATGGGCTACT	GTCTCAGTTT	TGATGCAATC	GATGAGCTGC	TCACAGGACG	AGAACATCTT	6180
	TACCTTTATG	CCCGGCTTGG	AGGTGTACCA	GCAGAAAGAA	TGAAAGAGT	TGCAAACTGG	6240
	AGTATTAAAG	GCCTGGGCTC	GACTGTCTAC	CGCGACTGCC	TGGCTGGCAC	GTACAGTGGG	6300
40	GGCAACAAGC	GGAACTCTC	CACAGCCATC	GCATCACTTG	GCTGCCACCC	GCTGGTGTCT	6360
	CTGGATGAGC	CCACCACAGG	GATGGACCCC	CAGGCACGCC	GCATGCTGTG	GAACGTCATC	6420
	GTGAGCATCA	TCAGAAAGGG	GAGGGCTGTG	GTCTCTCAT	CCCAACGAT	GGAAGATGTT	6480
	GAGGCACTGT	GTACCCGGCT	GGCCATCATG	GTAAAGGGCG	CCTTTCGATG	TATGGGCGCC	6540
	ATTGAGCATC	TCAAGTCCAA	ATTGGAGAT	GGCTATATCG	TCACAATGAA	GATCAAAATC	6600
45	CGGAAGGACG	ACCTGCTTCC	TGACCTGAAC	CCTGTGGAGC	AGTTCTTCCA	GGGGAACTTC	6660
	CCAGGCAGTG	TGCAGAGGGA	GAGGCACTAC	AACATGCTCC	AGTTCCAGGT	CTCTCTCTCC	6720
	TCCTTGGCGA	GGATCTTCCA	GCTCCTCTC	TCCCAACAAG	ACAGCCTGCT	CATCGAGGAG	6780
	TACTCAGTCA	CACAGACCC	ACTGGACCC	GTGTTTGTAA	ATTITGCTAA	ACAGCAGACT	6840
	GAAGTTCATG	ACCTCCTCTG	GCACCTCGA	GCTGCTGGAG	CCAGTCCGAC	AGCCAGGAC	6900
50	TGATCTTTCA	CACCGTCTGT	TCCTGCAGCC	AGAAAGGAAC	TCTGGGCAGC	TGGAGGGCGA	6960
	GGAGCCTGTG	CCCATATGGT	CATCCAAATG	GACTGGCCCA	CGCTAAATGA	CCCACTGCA	7020
	GCAGAAACCA	AACACACGAG	GAGCATGCAG	CGAATTGAGA	AAGAGGTCTT	TCAGAAAGGAA	7080
	ACCGAAATCG	ACTTGTCTAC	CTGGAACACC	TGATGGTGAA	ACCAACAAAT	TACAAATATC	7140
	TTCTCCAGAC	CCCAAGACTA	GAAACCCCGG	GCCATCCAC	TAGCAGCTTT	GGCCTCCATA	7200
55	TTGCTCTCAT	TTCAAGCAGA	TCTGCTTTTC	TGCTATGTTG	TCTGTGTGTC	TGGCTTGTGT	7260
	GTGATTTTCA	TGGAATAATA	AAATGCAAAAT	GCATCATCA	CAAAAAAATA	AAAAAATA	7318

Seq ID NO: C117 DNA Sequence  
Nucleic Acid Accession #: NM\_006671.2  
Coding sequence: 138..1820

60	1	11	21	31	41	51	
	GGCACGAGGC	TGGTGTTTAG	CAACTCCGAC	CACCTGCTCT	CTGAGGGGCT	AGAGCCCTCA	60
65	GCCACAGACC	TGTGCCCCCG	GCGGGGCTCT	CATGCGTGGA	ATGGTGTCTG	GCCCCCTGCC	120
	AGCAGGCCAG	GCTCACCATG	GTGCCGATG	CCATCTTGGC	ACGGGGGAGG	GACGTGTGCA	180
	GGCGGAATGG	ACTCCTCATC	CTGTCTGTGC	TGCTGTCTAT	CGTGGGCTGC	CTCCTCGGCT	240
	TCTTCTTGAG	GACCCGGGCG	CTCTCACCAC	AGGAAATTAG	TTACTTCCAG	TTCCCTGGAG	300
	AGCTCTCTGAT	GAGGATGCTG	AAGATGATGA	TCCTGCCACT	GGTGGTCTCC	AGCTTGATGT	360
70	CGGACTTGGC	GCTCCTGGAT	GCCAAGACCT	CTAGCCGCTT	GGGCGTCTTC	ACCGTGGGCT	420
	ACTACCTGTG	GACCACCTTC	ATGGCTGTCA	TCGTGGGCAT	CTTCATGGTC	TCCATCATCC	480
	ACCCAGGCAG	CGCGGCCGAG	AAGGAGACCA	CGGAGCAGAG	TGGGAAGCCC	ATCATGAGCT	540
	CAGCGGATGC	CCTGTGTGGAC	CTCATCCGGA	ACATGTTCCC	AGCCAACTTA	GTAGAAGCCA	600
	CATTCAAAAC	GTACCGCACC	AAGACCACCC	CAGTTGTCAA	GTCCCCCAAG	GTGGCACCAG	660
75	AGGAGGCCCC	TCCTCGGCGG	ATCCTCATCT	ACGCGGTCCA	GGAGGAGAAT	GGCTCCCATG	720
	TGCAGAACTT	CGCCCTGGAC	CTGACCCCGC	CGCCGAGGTT	CGTTTACAAG	TCAGAGCCGG	780
	GCACAGCGGA	TGGCATGAAT	GTGCTGGGCA	TGCTCTTCTT	CTCTGCCACC	ATGGGCATCA	840
	TGCTGGGCGG	CCTGTGTGAC	AGCGGGGCCG	CCCTGGTCTG	CTTCTGCCAG	TGCTCAATG	900
	AGTGGGTCAT	GAAGATCGTG	GCGTGGCTGT	TGTGGTATT	CCCCTTGGGC	ATTGTGTTC	960
80	TCATTGCGGG	TAAGATCCTG	GAGATGGACG	ACCCAGGGC	CGTGGGCAAG	AAGCTGGGCT	1020
	TCTACTCAGT	CACCGTGGTG	TGCGGGCTGG	TGCTCCACGG	GCTCTTTATC	CTGCCCTGTC	1080
	TCTACTTCTT	CATCACCAAG	AAGAAATCCA	TGCTCTTCAT	CCGCGGCATC	CTGCAGGCTC	1140
	TGCTCATGCG	GCTGGCCACG	TCCTCCAGCT	CAGCCACACT	GCCCATCACC	TTCAAGTGCC	1200
	TGCTGGAGAA	CAACCAATC	GACCGGCGCA	TGCTCGCTT	CGTGTGCCCC	GTGGGTGCCA	1260
	CCATCAACAT	GGACGGCACT	GCGCTCTACG	AGGCTGTGGC	CGCCATCTTC	ATGCCCCAGG	1320

TCAACAACCTA CGAGCTGGAC TTTGGCCAGA TCATCACCAT CAGTATCACA GCCACTGCAG 1380  
 CCAGCATTTGG GGCAGCTGGC ATCCCCCAGG CCGGCTCGT CACCATGGTC ATCGTGTCTCA 1440  
 CCTCCGTGGG ACTGCCACC GATGACATCA CCTCATCAT TGCCGTGAC TGGGCTCTGG 1500  
 ACGTTTCCG CACCATGATT AAGTGTCTGG GTGATGCGCT GGCAGCGGG ATCATGGCCC 1560  
 5 ATATATGTCG GAAGGATTTT GCCCGGGACA CAGGCACCGA GAACTGCTG CCTGCGAGA 1620  
 CCAAGCCAGT GAGCCTCCAG GAGATCGTGG CAGCCAGCA GAATGGCTGT GTGAAGAGTG 1680  
 TAGCCAGGCG CTCGAGCTC ACCCTGGGCC CCACTGCCCC CCACCCAGTC CCCGTTCAAG 1740  
 TGGAGCGGGA TGAGGAGCTG CCCGCTGCGA GTCTGAACCA CTGACCATC CAGATCAGCG 1800  
 AGCTGGAGAC CAATGTCTGA GCCTGCGGAG CTGACGGGGC AGGCGAGGCC TCCAGGGGCA 1860  
 10 GGGTCTCTGAG GCAGGAACCT GACTCTCCAA CCTCCTGAG CAGCCGGCAG GGGCCAGGAT 1920  
 CACACATTTCT TCTCACCTTT GAGAGGCTGG AATTAACCCC GCTTGACGGA AAATGTATCT 1980  
 CAGAGAAGGG AAAGGCTGCA TGGGGGAGCC CCATCCAGGG AGTGTAGGG CCGGCATTGC 2040  
 CTGAGGGCCC GCTGTGACAG TTCCCGCGT GTGAGCCCGG TGAGGGCGGC AGGCAGGGGT 2100  
 15 TATCCGCCCC CACTTCTCG ATGACAGACT TGAGGCTCTG AGAGCTGAAA ACCTTGTCC 2160  
 AAGGTCTCAC GTTAAGGTCA AGACACTAAC TCAATCTTT CAAGCCCGC CTCTCTCTT 2220  
 GGAGGACAGG GCAGCCTGCA GCTGTGTCCA GGGCCAGGCC CCACCCCAT AAGAGTGGCC 2280  
 TCAGCCACAC AGTTCTCCCC AAGGGGAGCA GCCCAGGGCC AAGCCCGCT GCCTTCCCA 2340  
 GGCCACAGT GCTCCAGTCT CCTGTCTGTC CAGCTGTCTT TTGCAAGCT CCTTGGATGT 2400  
 20 GGAGACAGAT GTCTTTACTA GAGCTGAAAG GCCCCTTGA CACATCCAGG CCAACCTCCC 2460  
 ATGGAATAGG TAGGCAAGCC AGGACTCCGG GAAGGAGGTG CAGCCAGGAT GCTCTGGTGG 2520  
 AGCTGCCGAT GGGGCCCTGG TGTGAGAACT CCCAAAGGC CTGTGCGTCC AAGTGGAGTC 2580  
 AGGTTTCTA TTCTTTCTG TGTTTGCAAA TTCAGTGTTA ACTAAATAAA GGTATTTTGT 2640  
 TTTTCAAAA AAAAAAAA AAA 2663

25 Seq ID NO: C118 DNA Sequence  
 Nucleic Acid Accession #: NM\_005689  
 Coding sequence: 278..2806

30 1 11 21 31 41 51  
 GGGCCTGCAG TTGGCAGAAG GGTCCCGGGC CCAGAGCCAG CGGGGCGCTG CTGAGACGGC 60  
 GTACGTGCCC TGCGTGAAGT CGTGGCGCGC GCGCGTGGCC TAGGGGAGTG GCGGTGAGG 120  
 CTGTGTCCAC GTGCGTCCCT TCCCGGGACC CCGCAGCTT GCGGCCAGC GGCTACGTGA 180  
 35 GCGAAGGCAC CCGGATGTCC GCGCCCTCT CCGAGTGACA AGTCCCGCC TCCGGTCCCG 240  
 CAGTGCCCGC AGCCTCGGCC GCGCTCCAGC CATGCGCATG GTGACTGTGG GCAACTACTG 300  
 CGAGGCCGAA GGGCCCGTGG GTCCGCGCTG GATGAGGAT GGCCTGAGTC CCTGCTCTT 360  
 CTTACGCTC GTGCCCTCGA CGCGGATGGC TTAGGGACT CTGCGCTTGG TGCTGGCTCT 420  
 TCCCTCCAGA CGCCCGGAGC GCGCCGCTGG TGCTGATTGG CTGTCTTGGG GGGCGGCGCC 480  
 40 TCGCATCTCT CCTACGTGTC TGCACTGCT TCTGGCCACA CTTAGGCGG CGCTGCCCT 540  
 GGCCTGCTTC GCTGGCGCGG TGGGCACTGC CCGGGGCGCC CCACTGCCAA GCTATCTACT 600  
 TCTGGCTTCC GTGCTGGAGA GTCTGGCGGG CGCTGTGGC CTGTGCTGTC TTGTCGTGGA 660  
 GCGAGGCCAG GCACGGCAGC GTCTGGCAAT GGCATCTGG ATCAAGTTCA GGCACAGCCC 720  
 TGGTCTCTCG TCCCTCTGGA CTGTGGCGTT TGCACTGAG AACTTGGCCC TGCTGTCTTG 780  
 45 GAACAGCCCA CAGTGTGTGT GGGCAAGGGC AGACTTGGGC CAACAGGTTT AGTTTAGCCT 840  
 GTGGGTGCTG CGTATGTGT TCTCTGGAGG GCTGTTTGT CTGGGTCTCT GGGCCCTGG 900  
 ACTTGTCTCC CAGTCTCTATA CATTCAGGT TCATGAAGAG GACCAAGATG TGGAAAGGAG 960  
 CCAAGTTTCCG TCAGCAGCCC AACAGTCTAC CTGGCGAGAT TTTGGCAGGA AGCTCCGCT 1020  
 CCTGAGTGGC TACCTGTGGC CTCGAGGGAG TCCAGCTCTG CAGCTGTGTG TGCTCATCTG 1080  
 50 CCTGGGGCTC ATGGGTTTGG AACGGGCAT CAATGTGTGG GTGCTATAT TCTATAGGAA 1140  
 CATTTGTAAC TTGCTGACTG AGAAGGCACC TTGAACTCT CTGGCTGGA CTGTTACCAG 1200  
 TTAGCTCTTC CTCAAGTTCC TCCAGGGGGG TGGCACTGGC AGTACAGGCT TGTGAGCAA 1260  
 CCTGGCACC TTCTGTGGA TCCGGGTGCA GCAGTTCAOG TCTCGGCGGG TGGAGTGTCT 1320  
 CATCTCTCC CACCTGCAAG AGCTCTCACT GCGCTGGCAC CTGGGGCGCC GCACAGGGGA 1380  
 55 GGTGCTGCGG ATCGCGGATC GGGGCACATC CAGTGTACA GGGCTGTCTA GCTACCTGGT 1440  
 GTTCAATGTC ATCCCCAGC TGGCCGACAT CATCAITGGC ATCAITACT TCAGCATGTT 1500  
 CTTCAAGGCC TGGTTTGGCC TCATTGTGTT CCTGTGATG AGTCTTTACC TCACCCTGAC 1560  
 CATTTGTGTC ACTGAGTGA GAACCAAGTT TGTGTGTGCT ATGAACACAC AGGAGAACGC 1620  
 TACCOCGGCA CAGCAGTGG ACTCTCTGCT AAACCTCGAG ACGGTGAAGT ATTACAAGC 1680  
 60 CGAGAGTTAC GAAGTGAAC GCTATCGAGA GGCCATCATC AAATATCAGG GTTTGAGATG 1740  
 GAAGTCGAGC GCTTCACTGG TTTTACTAAA TCAGACCCAG AACCTGGTGA TTGGGCTCGG 1800  
 GCTCTCGCC GGCTCCCTGC TTTGCGCATA CTTGTCACT GAGCAGAAGC TACAGTTGG 1860  
 GGACTATGTG CTCTTTGGCA CCTACATAT CCAGCTGTAC ATGCCCTCA ATTGGTTTGG 1920  
 65 GAAAGAGGAG ACAGAAGTGA AGGACCTTCC TGGAGCAGGG CCCCTTGCCT TTCAGAAAGG 2040  
 CCGTATTGAG TTTGAGAACG TGCACCTCAG CTATGCCGAT GGGCGGAGA CTCTGCAGGA 2100  
 CGTGTCTTTC ACTGTGATGC CTGGACAGAC ACTTGCCTG GTGGGCCCAT CTGGGCGAGG 2160  
 GAAGAGCAGA ATTTTGGGCC TGCTGTTTGG CTCTACGAC ATCAGCTCTG GCTGCAATCG 2220  
 AATAGATGGG CAGGACATTT CACAGGTGAC CCAGGCTCT CTCCGTCTC ACATTGGAGT 2280  
 70 TGTGCCCAA GACACTGTCC TCTTTAATGA CACCATCGCC GACAATATCC GTTACGGCCG 2340  
 TGTCAAGCT GGGAAATGAT AGGTGGAGGC TGCTGTCTAG GCTGCAGGCA TCCATGATGC 2400  
 CATTTAGGCT TTCCCTGAAG GGTACAGGAC ACAGGTGGGC GAGCGGGAGC TGAAGCTGAG 2460  
 CGGCGGGGAG AAGCAGCGCG TCGCATATGC CCGCACCATC CTCAGGCTC CGGGCATCAT 2520  
 TCTGCTGGAT GAGGCAAGCT CAGCGCTGGA TACATCTAAT GAGAGGGCCA TCCAGGCTTC 2580  
 75 TCTGGCCAAA GTCTGTGCCA ACCGCACCA CATCGTAGTG GCACACAGGC TCTCAACTGT 2640  
 GGTCAATGCT GACCAATGCC TCGTCTCAAA GGATGGCTGC ATCGTGAGA GGGGACGACA 2700  
 CGAGGCTCTG TTGTCCCGAG GTGGGCTGTA TGCTGACATG TGGCAGCTGC AGCAGGGACA 2760  
 GGAAGAAACC TCTGAAGACA CTAAGCTTCA GACCATGGAA CGGTGACAAA AGTTTGGCCA 2820  
 CTTCCTCTC AAAGACTAAC CCAGAGGGA ATAAGATGTG TCTCCTTTC CTGGCTTATT 2880  
 80 TCATCTGCT CTGCGGTAT GGTGCTAGCT ATGGTAAGGG AAAGGGACCT TTCGAAAAA 2940  
 CATCTTTTGG GGAATAAAA ATGTGGAGTG TGAATAAAA AAAAAAAA AAA 2993

Seq ID NO: C119 DNA Sequence  
 Nucleic Acid Accession #: NM\_000676  
 Coding sequence: 333..1331

```

1      11      21      31      41      51
|      |      |      |      |      |
5  GGGCAATTG TTAGTTATCC GCGGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG 60
   CCCCGCGCG GCGCGAACTT TGGGCTGGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA 120
   CGGCGCGGCG CGCGGCCCAA TGGGTGCGGC CTCTTGGCCG CGGGGGGCCC CGACCCGTGG 180
   GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG 240
   GGGCTATGCG CCATGCCCCG GGGGTCTCAC GCGGCTGCCC CTGCCCCGCG GCGCCTTCGG 300
10 TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT 360
   ACGTGGCGCT GGAGCGGCTC ATGCGCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGGC 420
   CCGCGGTGGG CACGCGGAAC ACTCTGCAGA GCGCCACCAA CTACTTCTG GTGTCCCTGG 480
   CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCTTT TGCCATCACC ATCAGCCTGG 540
   GCTTCTGCAC TGACTTCTAC GGTGCGCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCAOCG 600
   AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC 660
15 CGCTCAGGTA TAAAGTTTGG GTACGCGGGA CCGAGCAAG AGGGGTCAAT GCTGTCTCT 720
   GGGTCTTGTC CTTTGGCATC GGATTGACTC CATTCTCTGG GTGGAACAGT AAAGACAGTG 780
   CCACCAACAA CTCACAGAA CCCTGGGATG GAACCAAGAA TGAAGCTGCG TGCCCTTGTA 840
   AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT 900
   GTGTCTGCGC CCCACTGCTT ATAATGTCTG TGATCTACAT TAAGATCTTC CTGTGGCGCT 960
20 GCAGGCAGCT TCAGCGCAGT GAGCTGATGG ACCACTCGAG GACCACCCCT CAGCGGAGA 1020
   TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG 1080
   TGCATGCTGT TAAGTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT 1140
   GGGCAATGAA TATGGCCATT CTCTGTGCAC ATGCCAATTC AGTGTCAAT CCCATTGTCT 1200
   ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTCT 1260
25 TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTGAGGCTGG GGTACAGCCT GCTCTCGGTG 1320
   TGGGCTATG ATCTAGGCTC TCGCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA 1380
   AGAGGACAGC GCTGTTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGAGCTGC 1440
   CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAAGTAG 1500
   AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTGAG CTGCTTTTAC TGTGTGGATT 1560
30 ATGCCAACAG CTGAATGGA TTCTAACAGA CTCTTTTGT TTTAAAGTCT GCTCTGTTT 1620
   ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA 1680
   TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG 1733

```

Seq ID NO: C120 DNA Sequence  
Nucleic Acid Accession #: NM\_052932  
Coding sequence: 217..786

```

1      11      21      31      41      51
|      |      |      |      |      |
40 CCCAGCCCCG CCCCGCCGCC CGGGCTGGGC ACGCGAGGCC CCTCCAGGC CCGCTCCTG 60
   CGCCCTATT TGGTCAATCG GGGGCAAGCG GCGGAGGGG AAAAGTGGCG GCGCGAAGCG 120
   GAAGCGGAGC CGCGCGCGGC TGCGCAGAGG AGCGCTCTC GCGCGGCCA CCTCGGCTGG 180
   GAGCCACAGA GCGTGCAGCA TCCTGCCCTC GGAACAATGG GACTCGGCGC GCGAGGTGCT 240
   TGGGCGCGCG TGCTCCTGGG GAGCTGCGAG GTGCTAGCGC TGCTGGGGGC CGCCCATGAA 300
45 AGCGCAGCCA TGGCGGAGAC TCTCCAACAT GTGCCTTCTG ACCATACAAA TGAACCTTCC 360
   AACAGTACTG TGAACACACC AACTTCAGTT GCCTCAGACT CCAATATAC AACGCTCACC 420
   ACCATGAACC CTACAGCGGC ATCTAATACA ACAACACCAG GGATGGTCTC AACAAATATG 480
   ACTTCTACCA CCTTAAGTCT TACACCCAAA ACAACAAGTG TTTACAGAAA CACATCTCAG 540
   ATATCAACAT CCACAATGAC CGTAACCCAC AATAGTTCAG TGACATCTGC TGCTTCATCA 600
50 GTAAACATCA CAACAACATAT GCATTCTGAA GCAAGAAAGG GATCAAAATT TGATCTGGG 660
   AGCTTTGTTG GTGGTATGTT ATTAACGCTG GAGATTITAT CTATTCTTTA CATTGGATGC 720
   AAAATGTATT ACTCAAGAAG AGGCATTGGG TATCGAAGCA TAGATGAACA TGATGCCATC 780
   ATTTAAGGAA AATCATGGAC CAAGGATGGA ATACAGATTG ATGCTGCCCT ATCAATTTAT 840
   TTTGGTTTAT TAATAGTTTA AAACAATATT CTCTTTTGA AAATAGTATA AACAGGCCAT 900
55 GCATATATAT TACGTGTAT TACGTAAATA TGTAAAGATT CTTCAAGTGA ACAAGGGTTT 960
   GGGTTTGAAT ATAAACATCT GGATCTTATA GACCGTTCAT ACAATGGTTT TAGCAAGTTT 1020
   ATAGTAAGAC AAACAAGTCC TATCTTTTTT TTTTGGCTG GGGTGGGGGC ATTGGTCACA 1080
   TATGACCAGT AATGAAGAGA CGTCATCACT GAAAGACAGA ATGCCATCTG GGCATACAAA 1140
   TAAGAAGTTT GTCACAGCAC TCAGGATTTT GGGTATCTTT TGATGCTCAC ATAAAGAACT 1200
60 TCAGTGCTTT TCAGAGCTGG ATATATCTTA ATTACTAATG CCACACAGAA ATTATACAA 1260
   CAACTAGAT CTGAAGCATA ATTAAGAAA AACATCAACA TTTTGTGTC TTTAACTGT 1320
   AGTAGTTGGT CTAGAAACAA AATCTCCAA GAAAAAGAAA ATTTTCAAT AAAACCCAAA 1380
   ATAATAGCTT TGCTTAGCCC TGTTAGGGAT CCATTGGAGC ATTAAGGAGC ACATATTTTT 1440
   ATTAACCTCT TTTAGCTTT CAATGTGAT GTAATTTTTG TTCTCTGTGT AATTTAGGTA 1500
65 AACTGCAGTG TTTAACATAA TAATGTTTTA AAGACTTAGT TGTGATATT AAATAATCCT 1560
   GGCATTATAG GGAACAAACC TCCTAGAAGT TAGATTATTT GCTACTGTGA GAATATTGTC 1620
   ACCACTGGAA GTTACTTTAG TTCAATTAAT TTTAATTTTA TATTTTGTGA ATATTTTAA 1680
   AACTGTAGAG CTGCTTTCAA TATCTAGAAA TTTTAATTTG AGTGAACAA CACCTAACTT 1740
   TAAGAAAAAG AACCGCTGT ATGATTTTCA AAAGAACATT TAGAATCTTA TAGAGTCAAA 1800
70 ACTATAGCGT AATGCTGTGT TTATTAAGCC AGGGATTGTG GGAATCCGCC CAGGCAACTA 1860
   AACCTGCAGG ATGAAATGCG TATATTTTCT TTCATGCACT GTGATATTA CTCAGATTGT 1920
   GGGAAATGAC ATTTTATATC TAAACAAAC ACCAAATAT TTTAGAATAA ATCTTAGAAA 1980
   AGTTTTGAGA GGAATTTTTA GAGAGGACAT TTCCTCTTC CTGATTGGGA TATTCCTCA 2040
   AATCCCTCCT CTACTCCAT GCTGAAGGAG AAGTACTCTC AGATGCATTA TGTAAATGGA 2100
75 GAGAAAAAGC ACAGTATTGT AGAGACACCA ATATTAGCTA ATGATTTTGG GAGTGTTTTC 2160
   CATTTTACAG TTTATATTCC AGCACTCAAA ACTCAGGGTC AAGTTTAAAC AAAAGAGGTA 2220
   TGTAGTCACA GTAAATACTA AGATGGCATT TCTATCTCAG AGGSCCAAAG TGAATCACAC 2280
   CAGTTTCTGA AGGTCTCTAA AATAGCTCAG ATGTCTCAAT GAACATGCAC CTACATTTAA 2340
   TAGGAGTACA ATAAACTGCT TGTCAGCTTT TGTTTTACAG AGAACGCTAG ATATTAGAAA 2400
80 TTTGAAATG AATGCTTTCT ACTTGCTGTG CATTTTAACC AATAATCTGA TGAATATAGA 2460
   AAAAAATGAT CCAAAATATG GATATGATTG GATGTATGTA ACACATACAT GGAGTATGGA 2520
   GCAATTTTTC TGAATAATAC ATTTAGATTA GTTTAGTTTG AAGGAGAGGT GGGCTGATGG 2580
   CTGAGTTGTA TGTACTAAC TTGGCCCTGA CTGGTTGTGC AACCATTGCT TCATTTCTTT 2640
   GCAAAATGTA GTTAAGATAT ACTTTATTCT AATGAAGGCC TTTTAAATTT GTCCACTGCA 2700

```

5 TTCTTGGTAT TTCACTACTT CAAGTCAGTC AGAACTTGGT AGACCGACCT GAAGTTTCTT 2760  
 TTTGAATACT TGTTCCTTTA GCACCTTTGAA GATAGAAAAA CCACTTTTAA AGTACTAAGT 2820  
 CATCATTTCG CTGGAAGATT TCCTCTGCAT TGGGTTTGAA GTAGTTTAGT TATGTCTTTT 2880  
 TCTCTGTATG TAAGTAGTAT AATTGTGTAC TTTCAAATAC CGTACTTTTG AATGTAGGTT 2940  
 TTTTGTGTGT TGTATCTAT AAAAATTGAG GGAAATGGTT ATGCAAAAAA ATATTTTGCT 3000  
 TTGGACCATA TTTCTTAAGC ATAAAAAAT GCTCAGTTTT GCTTGCAATC CTTGAGAATG 3060  
 TATTTATCTG AAGATCAAAA CAAACAATCC AGATGTATAA GTACTAGGCA GAAGCCAATT 3120  
 TTAATAATTC CTGGAATAAT CCATGAAAGG AATAATTCAA ATACAGATAA ACAGAGTTGG 3180  
 CAGTATATTA TAGTGATAAT TTTGTATTTT CAAMAAAAAA AAAGTTAAAC TCTCTTTTTC 3240  
 10 TTTTATTAT AATGACCAGC TTTTGGTATT TCATTGTTAC CAAGTCTCAT TTTTAGATAA 3300  
 AATTGTTCTC CTTCTAAAAA AAAAAAATAA AAAAAAAA 3338

Seq ID NO: C121 DNA Sequence  
 Nucleic Acid Accession #: NM\_004195  
 Coding sequence: 1..726

1 11 21 31 41 51  
 20 ATGGCACAGC ACGGGGCGAT GGGGCGGTTT CGGGCCCTGT GCGGCCTGGC GCTGCTGTGC 60  
 GCGCTCAGCC TGGGTACGGG CCCCACCGGG GGTCCCGGTT GCGGCCCTGG GCGCCTCCTG 120  
 CTTGGGACGG GAACGGGACG GCGCTGTGTC CGGGTTCACA CGACGGCGTG CTGCCGCGAT 180  
 TACCGGGGCG AGGAGTGCTG TTCCGAGTGG GACTGCATGT GTGTCCAGCC TGAATTCCAC 240  
 TCGGGAGACC CTGTCTGCAC GACCTGCGCG CACCAACCTT GTCCCCCAGG CCAGGGGGTA 300  
 25 CAGTCCGAGG GGAATTCAG TTTTGGCTTC CAGTGTATCG ACTGTGCTTC GGGGACCTTC 360  
 TCCGGGGGCC ACGAAGGCCA CTGCAAACTT TGGACAGACT GCACCCAGTT CGGGTTTCTC 420  
 ACTGTGTTC CTTGGGAACA GACCCACAAC GCTGTGTGCG TCCAGGGGTC CCGCCGGGCA 480  
 GAGCGCTTG GGTGCTGAC CGTCTGCTC CTGGCCGTGG CCGCCTGCGT CCTCCTCCTG 540  
 ACCTCGGCC AGCTTGGACT GCACATCTGG CAGCTGAGGA GTCACTGCAT GTGGCCCGCA 600  
 30 GAGACCAGC TGCTGCTGGA GGTGCGCGCG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC 660  
 CCGAGGAAG AGCGGGGCGA GCGATCGGCA GAGGAGAAGG GCGGCTGGG AGACCTGTGG 720  
 GTGTGA 726

Seq ID NO: C122 DNA Sequence  
 Nucleic Acid Accession #: AK091896.1  
 Coding sequence: 28..1572

1 11 21 31 41 51  
 40 AGATCCGGGA GCCCGTCAGC CTGCGCCATG GGCTGCGAGC GCGCGTGTGC GGGGCTGCTC 60  
 CCGCGCAACC TGCAGCCAC GCTCACCTAC TGGAGGCTCT TCTTCAGCTT CCGCCTGTGC 120  
 ATCGCCTTCC TGGGGCCAC GCTGCTGGAC CTGCGCTGTC AGACGCACAG CTCGCTGCCC 180  
 CAGATCTCCT GGGTCTTCTT CTGCGAGCAG CTCTGCTCC TGCTGGGCGG CCGCCTCGGC 240  
 GCGGTCTTCA AAAGGACCTT GGCCCACTCA CTATGGGCCC TGTTCACCTC CTCTCTGGCC 300  
 45 ATCTCCCTGG TGTGTGCGT CATCCCTTTC TGCGCGGAGG TGAAGGTGCT GGCCTCAGTC 360  
 ATGGGCGTGG CCGGCTTGGC CATGGGCTGC ATGACACCG TGGCCAACAT GCAGCTGGTA 420  
 AGGATGTACC AGAAGGACTC GCGCGTCTTC CTCCAGGTGC TCCATTCTCT CGTGGGCTTT 480  
 GGTGCTCTGC TGAGCCCTCT TATTGTGAC CCTTCTCTGT CTGAGGCCAA CTGCTTGCCT 540  
 GCGAATAGCA CGGCCAACAC CACCTCCCGA GGCCACCTGT TCCATGTCTC CAGGGTGTCT 600  
 50 GGCCAGCACC ACGTAGATGC CAAGCCTTGG TCCAACCGA CGTTCGAGG GCTGACTCCA 660  
 AAGGACGGGG CAGGACCGG AGTGTCTTAT GCCTTCTGGA TCATGGCCCT CATGATCTT 720  
 CCAGTGCCCA TGGCTGTGCT GATGCTGCTG TCCAAGGAGC GGCTGCTGAC CTGCTGTCCC 780  
 CAGAGGAGGC CCTCTGCTCT GTCTGTGAT GAGCTTGCTT TGGAGACACA GCCTCCTGAG 840  
 AAGGAAGATG CCGCTCTACT GCGCCCAAAG TTTCACTCAC ACCTAGGGCA TGAGGACCTG 900  
 55 TTAAGTCTCT GCCAAAGGAA GAACCTCAGA GGAGCCCTTT ATTCTTCTT TGCCATCCAC 960  
 ATCAGCGGG CCGTGTACT GTTCATGACG GATGGGTGGA CGGGTGCTTA TTCCGCTTC 1020  
 GTGTACAGCT ATGCTGTGGA GAAGCCCTCT TCTGTGGGAC ACAAGGTGGC TGGCTACCTC 1080  
 CCCAGCCTCT TCTGGGGCTT CATCACACTG GCGCGGCTCC TCTCCATTCC CATATCTCTA 1140  
 AGAATGAGC CGGCCACCAT GGTTTTCATC AACGTGGTTG GCGTGGTGGT GACGTTCTCT 1200  
 60 GTGCTGCTTA TTTTCTCTTA CAACGTGCTC TTCTGTGCTG TGGGGACGGC AAGCCTGGGC 1260  
 CTGTTCTTCA GCAGCACTT CCCCAGCATG CTGGCTTACA CGGAGGACTC GCTGCAGTAC 1320  
 AAAGGCTGTG CAACACAGT GCTGTGACA GGGGCGAGG TTGGCGAGAT GGTGCTGCAG 1380  
 ATGCTGGTGG GTTCGATATT CCAGGCTCAG GGCAGCTATA GTTTCCTGGT CTGTGGCGTG 1440  
 65 ATCTTTGGTT GTCTGGCTTT TACCTTCTAT ATCTTGTCTC TGTTTTCCA CAGGATGCAC 1500  
 CCTGAGCTCC CATCAGTTC TACCAAGAC AGATCAATTG GAATGGAATA CTCTGAGTGC 1560  
 TACCAGAGGT AAACTGGGT GAAGAAGGCA AGAGAAGACT TTCAGCCTCT TGATCACCAG 1620  
 CACGACCATA CTGTTTCAGA AAGCTGGGTG GTGGTGGAGG CGCTCTCTCA ATGGCTATTC 1680  
 AAGTCTTCTC CACTAAACTT TGGTTGGGTA GAGGAAATTA AATTGAGTCC TGGTACCTGG 1740  
 TCAAAATCAT TAGAAGTTTA CCTGGCTTCT CAAGTTATCT TCTCCCTGGG TTCAGACTGT 1800  
 70 TGGTAAGAGC TGTCAGATA CCCAGATGGG AAGGAAGGAG ACAGCCGCGC GCTTCACTCC 1860  
 ATTTGTCACC TCATGCAATG ACCATCTCT GGGTTTGAGA TCATTCTTCA TTGAAGTTTG 1920  
 TAAAAATAGG TTGAATTTGT AAAGCTCCAT GATCACTGCT ATATGTAGAT ATATTTCAT 1980  
 TTAAGCAAAA CAAGCTGCAA GTTATTCCTT GGCATGCTCA AAGGATTTTC GTGCTTTTCA 2040  
 CTTAATAGTC CAAGTCTCT TAAATTCCTG CTGCAGATAT CAATAGCTTA TCTATATTCT 2100  
 75 CAACACCCAA AAGGAAAGT TGAATCTTGC TCTCTTGGT ATACTAATGT AGTGGTATGC 2160  
 TAAGCTGGCT CATACCACT TAGAAAAGCT GATTGTAAAA TTTTCATTTT GACAGCTGGT 2220  
 TATTAATATG AGCCATTATT AAAAATCAAA TCATACAAAC TTATAATTAA ATCAATTACA 2280  
 TTTAAACAAA AGGTAAATAA TATTCAAAGC ATATCACTTC CT 2322

Seq ID NO: C123 DNA Sequence  
 Nucleic Acid Accession #: NM\_002203.2  
 Coding sequence: 43..3588

1 11 21 31 41 51  
 | | | | |

	CTGCAAAACC	AGCGCAACTA	CGGTCCCCCG	GTCAGACCCA	GGATGGGGCC	AGAAACGGACA	60
	GGGGCCGGCC	CGCTGCCGCT	GCTGCTGGTG	TTAGCGCTCA	GTCAGAGCAT	TTTAAATTGT	120
	TGTTTTGGCT	ACAATGTTGG	TCTCCAGAA	GCAAAATAT	TTTCCGGTCC	TTCAAGTGAA	180
5	CAGTTTGGGT	ATGCAGTGCA	GCAGTTTATA	AATCCAAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCTGGGA	GTGGCTTTCC	TGAGAACCGA	ATGGGAGATG	TGTATAAATG	TCCTGTTGAC	300
	CTATCCACTG	CCACATGTGA	AAAACATAAT	TTGCAAACTT	CAACAAGCAT	TCCAAATGTT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCCTCA	CCAGGAACAT	GGGAACATGA	420
	GGTTTTCTCA	CATGTGGTCC	TCTGTGGGCA	CAGCAATGTG	GGAATCAGTA	TTACACAACG	480
10	GGTGTGTGTT	CTGCATCAG	TCCTGATTTT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
	CAGCCCTGCC	CTTCCCTCAT	AGATGTTGTG	GTTGTGTGTG	ATGAATCAAA	TAGTATTAT	600
	CCTTGGGATG	CAGTAAAGAA	TTTTTTGGAA	AAATTTGTAC	AAGGCCTTGA	TATAGGCCCC	660
	ACAAAGACAC	AGGTGGGGTT	AAATTCAGTAT	GCCAATAATC	CAAGAGTTGT	GTTTAACTTG	720
	AACACATATA	AAACCAAGA	AGAAATGATT	GTAGCAACAT	CCAGACATC	CCAATATGTT	780
15	GGGACCTCA	CAACACATT	CGGAGCAATT	CAATATGCAA	GAAATATGTC	CTATTACGCA	840
	GCTTCTAGTG	GGCAGCGAAG	TGCTACGAAA	GTAATGGTAG	TTGTAACCTGA	CGGTGAATCA	900
	CATGATGGTT	CAATGTTGAA	AGCTGTGATT	GATCAATGCA	ACCATGACAA	TATACTGAGG	960
	TTTGGCATAG	CAGTCTCTGG	GTACTTAAAC	AGAAACGCCC	TTGATACTAA	AAATTTAATA	1020
	AAAGAAATAA	AAGCGATGCG	TAGTATTCCA	ACAGAAAGAT	ACTTTTTCAA	TGTGTCGTAT	1080
20	GAAGCAGCTC	TACTAGAAAA	GGCTGGGACA	TTAGGAGAAC	AAATTTTCAG	CATTGAAGGT	1140
	ACTGTTCAAG	GAGGAGACAA	CTTTCAGATG	GAAATGTCA	AAGTGGGATT	CAGTGCAGAT	1200
	TACTCTTCTC	AAAATGATAT	TCTGATGCTG	GGTGCAGTGG	GAGCTTTTGG	CTGGAGTGGG	1260
	ACCATTGTCC	AGAAGACATC	TCATGGCCAT	TTGATCTTTC	CTAAACAAGC	CTTTGACCAA	1320
	ATTCTGCAGG	ACAGTAATCA	CAGTTCATAT	TTAGGTTACT	CTGTGGCTGC	AATTTCTACT	1380
25	GGAGAAAGCA	CTCACTTTGT	TGCTGGTGCT	CCTCGGGCAA	ATTATACCGG	CCAGATAGTG	1440
	CTATATAGTG	TGAAATGAGAA	TGGCAATATC	ACGGTTTATC	AGGCTCACCG	AGGTGAACAG	1500
	ATTGGCTCCT	ATTTTGGTAG	TGTGCTGTGT	TCAGTTGATG	TGGATAAAGA	CACCATTACA	1560
	GAGCTGCTCT	TGATAGGTGC	ACCAATGTAC	ATGAGTGACC	TAAAGAAAGA	GGAAGGAAGA	1620
	GTCTACTCTG	TACTATCAA	AAAGGGCAAT	TTGGGTGAGC	ACCAATTCTT	TGAAGGCCCC	1680
30	GAGGGCATTG	AAAACACTCG	ATTTGGTTCA	GCAATTGCAG	CTCTTTCAGA	CATCAACATG	1740
	GATGGCTTTA	ATGATGTGAT	TGTTGGTTCA	CCACTAGAAA	ATCAGAATTC	TGGAGCTGTA	1800
	TACATTTACA	ATGCTCATCA	GGGCACTATC	CGCACAAGT	ATTCCAGAA	AATCTTGGGA	1860
	TCCGATGGAG	CCCTTAGGAG	CCATCTCCAG	TACTTTGGGA	GGTCTTGGGA	TGGCTATGGA	1920
	GATTTAAATG	GGGATTCAT	CACCGATGTG	TCTATTGGTG	CCTTTGGACA	AGTGGTTCAA	1980
35	CTCTGGTCA	AAAGTATGCT	TGATGTAGCT	ATAGAAGCTT	CATTACACAC	AGAAAAATC	2040
	ACTTTGGTCA	ACAAGATGTC	TCAGATAATT	CTCAAACTCT	GCTTCAGTGC	AAAGTTTCAG	2100
	CCTACTAAGC	AAAACAATCA	AGTGGCCATT	GTATATAACA	TCACACTTGA	TGCAGATGGA	2160
	TTTTCAATCA	GAGTAACCTC	CAGGGGGTTA	TTTAAAGAAA	ACAATGAAG	GTGCTGTCAG	2220
	AAGAATATGG	TAGTAAATCA	AGCACAGAGT	TGCCCGAGC	ACATCAITTA	TATACAGGAG	2280
40	CCCTCTGATG	TTGCAACTC	TTTGGATTG	CGTGTGGACA	TCAGTCTGGA	AAACCTGGC	2340
	ACTAGCCCTG	CTATTGAAGC	CTATTCTGAG	ACTGCCAAGG	TCTTCAGTAT	TCCTTTCCAC	2400
	AAAGACTGTG	GTGAGGATGG	ACTTTGCATT	TCTGATCTAG	TCCTAGATGT	CCGACAAATA	2460
	CCAGCTGCTC	AAGAACAACC	CTTTATTGTC	AGCAACCAAA	ACAAAAGGTT	AACATTTTCA	2520
	GTAACTACTG	AATAATAAAG	GGAAAGTGCA	TACAACACTG	GAATTGTTGT	TGATTTTTCA	2580
45	GAAACTTGT	TTTTTGATC	ATTCTCCCTA	CCGGTTGATG	GGACAGAAGT	AACATGCCAG	2640
	GTGGCTGCAT	CTCAAGATGC	TGTTGCCTGC	GATGTAGGCT	ACCCTGCTTT	AAAGAGAGAA	2700
	CAACAGGTGA	CTTTTACTAT	TAACTTTGAC	TTCAATCTTC	AAAACCTTCA	GAATCAGGCG	2760
	TCTCTCAGTT	TCCAGCCCTT	AAGTGAAAGC	CAAGAAGAAA	ACAAGGCTGA	TAATTTGGTC	2820
	AACTCAAAA	TTCTCTCTCT	GTATGATGCT	GAAATTCAC	TAAACAAGATC	TACCAACATA	2880
50	AAATTTTATG	AAATCTCTCT	GGATGGGAAT	GTTCCTTCAA	TCGTGCACAG	TTTTGAAGAT	2940
	GTGGTCCCAA	AATTCATCTT	CTCCCTGAAG	GTAACAACAG	GAAGTGTTC	AGTAAGCATG	3000
	GCAACTGTAA	TCATCCACAT	CCCTCAGTAT	ACCAAAGAAA	AGAACCCTCT	GATGTACCTA	3060
	ACTGGGTGTC	AAACAGACAA	GGCTGGTGAC	ATCAGTTGTA	ATGCAGATAT	CAATCCACTG	3120
	AAAATAGGAC	TACCACATCTC	TTCTGTATCT	TTCAAAAGTG	AAAATTTACG	GCACACCAAA	3180
55	GAATTGAATC	GCAGAACTGC	TTCTGTAGT	AATGTTACCT	GCTGTTTGAA	AGACGTTTAC	3240
	ATGAAAGGAG	ATACTTTTGT	TAATGTGACT	ACCAGAAAT	GGAACGGGAC	TTTCGCATCA	3300
	TCAACGTTCC	AGACAGTACA	GCTAACGGCA	GCTGCAGAAA	TCAACACCTA	TAACCTGAG	3360
	ATATATGTGA	TGAAAGATAA	CAGTGTACG	ATTCCTCTGA	TGATAATGAA	ACCTGATGAG	3420
60	AAAGCCGAAG	TACCACAGAG	AGTTATAATA	GGAAGTATAA	TTGCTGGAAT	CCTTTGTCTG	3480
	TTAGCTCTGG	TTGCAATTTT	ATGGAAGCTC	GGCTTCTTCA	AAAGAAAATG	TGAAAAGATG	3540
	ACCAAAAATC	CAGATGAGAT	TGATGAGACC	ACAGAGCTCA	GTAGCTGAAC	CAGCAGACCT	3600
	ACCTGCAGTG	GGAACCGGCA	GCATCCAGC	CAGGTTTTCG	TGTTTGGGTG	CATGGATTTC	3660
	TTTTTAAATC	CCATATTTTT	TTTATCATGT	CGTAGGTAAA	CTAACCTGGT	ATTTTAAAGAG	3720
	AAAACCTGAG	GTCAAGTTTG	ATGAAGAAAT	TGTGGGGGGT	GGGGGAGGTG	CGGGGGGCG	3780
65	GTAGGGAAT	AATAGGGAAT	ATACCTATTT	TATATGATGG	GGGAAAAAAA	GTAATCTTTA	3840
	AACTGGCTGG	CCAGAGTTT	ACATTCTAAT	TTGCATTGTG	TCAGAAACAT	GAAATGCTTC	3900
	CAAGCATGAC	AATCTTTTAA	GAAAAATATG	ATACTCTCAG	ATTTTAAAGG	GGAAAACTGT	3960
	TCTCTTTAAA	ATATTTGTCT	TTAAACAGCA	ACTACAGAG	TGGAAGTGCT	TGATATGTAA	4020
70	GTACTTCCAC	TTGTGTATAT	TTTAATGAAT	ATTGATGTTA	ACAAGAGGGG	AAAACAAAAC	4080
	ACAGGTTTTT	TCAATTTATG	CTGCTCATCC	AAAGTTGCCA	CAGATGATAC	TTCCAAGTGA	4140
	TAATTTTAT	TATAAACTAG	GTAAATTTG	TTGTGGTTTC	CTTTTATACC	ACGGCTGCCC	4200
	CTTCCACACC	CCATCTGTCT	CTAATGATCA	AAACATGCTT	GAATAACTGA	GCTTAGAGTA	4260
	TACCTCCTAT	ATGTCCATTT	AAGTTAGGAG	AGGGGGCGAT	ATAGAGACTA	AGGCACAAAA	4320
75	TTTGTTTTAA	AACCTCAGAT	ATAACATTTA	TGTAATAATC	CATCTGCTAG	AAGCCCATCC	4380
	TGTGCCAGAG	GAGGAAAGAG	GAGGAAATTT	CCTTCTCTCT	TTAGGAGGCA	CAACAGTTCT	4440
	CTTCTAGGAT	TTGTTTGGCT	GACTGGCAGT	AACCTAGTGA	ATTTTGAAGA	GATGAGTAAT	4500
	TTCTTTGGCA	ACCTTCTCTC	TCCTTACTG	AACCACTCTC	CCACCTCTCT	GTGGTACCAT	4560
	TATTATAGAA	GGCCTCTACA	GCCTGACTTT	CTCTCCAGCG	GTCCAAAGTT	ATCCCTCTCT	4620
80	TTACCCCTCA	TCCAAAGTTC	CCACTCCTTC	AGGACAGCTG	CTGTGCATTA	GATATTAGGG	4680
	GGGAAAGTCA	TCTGTTTAA	TTACACACTT	GCATGAATTA	CTGTATATAA	ACTCCTTAAC	4740
	TTCAAGGAGC	TATTTTCATT	TAGTGCTAAA	CAAGTAAGAA	AAATAAGCTA	GAGTGAATTT	4800
	CTAAATGTTG	GAATGTTATG	GGATGTAAAC	AATGTAAAGT	AAAACACTCT	CAGGATTTC	4860
	CCAGAAGTTA	CAGATGAGGC	ACTGGAAACC	ACCACCAAT	TAGCAGGTGC	ACCTTCTGTG	4920
	GCTGTCTTGT	TTCTGAAGTA	CTTTTCTTTC	CACAAGAGTG	AATTTGACCT	AGGCAAGTTT	4980
	GTTCAAAAGG	TAGATCTCTGA	GATGATTGCG	TCAGATTGGG	ATAAGGCCCA	GCAATCTGCA	5040

5  
 TTTTAACAAG CACCCAGCTC ACTAGGATGC AGATGGACCA CACTTTGAGA AACACCACCC 5100  
 ATTTCTACTT TTTCACCTT ATTTTCTCTG TTCCTGAGCC CCCACATTCT CTAGGAGAAA 5160  
 CTTAGATTAA AATTACAGA CACTACATAT CTAAAGCTTT GACAAGTCCT TGACCTCTAT 5220  
 AAACCTTCAGA GTCCTCATTA TAAATGGGA AGACTGAGCT GGAGTTCAGC AGTGATGCTT 5280  
 TTTAGTTTAA AAAGTCTATG ATCTGATCTG GACTTCCTAT AATACAAATA CACAATCCTC 5340  
 CAAGAATTGG ACTTGGAAAA G 5361

10  
 Seq ID NO: C124 DNA Sequence  
 Nucleic Acid Accession #: NM\_031460  
 Coding sequence: 103..1101

15  
 20  
 25  
 30  
 35  
 40  
 1 11 21 31 41 51  
 AGCAGGCGTT TGCGAGAGGA GATACGAGCT GGACGCGCTGG CCTTCCCTC CCACCGGGTC 60  
 CTAGTCCACC GCTCCCGGCG CGGCTCCCC GCCTCTCCCG CTATGTACC ACCCGAGGCC 120  
 CGGGCGGCTC CGGAGGGCAG GGTCCGGGGC TGCGCGGTGC CCAGCACCGT GCTCCTGCTG 180  
 CTCGCTTACC TGGCTTACTT GCGCTTGGG ACCGCGGTGT TCTGGACGCT GGAGGGCGGC 240  
 GGGGCGCAGG ACTCCAGCCG CAGCTTCCAG CGGACCAAGT GGGAGCTGTT GCAGAACTTC 300  
 ACGTGTCTGG ACGCCCGGCG GCTGGACTCG CTGATCCGGG ATGTCTGCCA AGCATACAAA 360  
 AACCGAGCCA GCCTCTCAG CAACACCACC AGCATGGGCG GCTGGGAGCT CGTGGGCTCC 420  
 TTCTTCTTTT CTGTGTCCAC CATCACCACC ATTGGCTATG GCAACCTGAG CCCCAACACG 480  
 ATGGCTGCCC GCCTCTCTCG CATCTTCTTT GCCTTGTGG GATCCCACT CAACCTCGTG 540  
 GTGCTCAACC GACTGGGGCA TCTCATGCAG CAGGGAGTAA ACCACTGGGC CAGCAGGCTG 600  
 GGGGGCAGCT GGCAAGATCC TGACAAGGCG CGGTGGCTGG CGGGCTCTGG CGCCTCTCTC 660  
 TCGGCGCTCC TGCTCTTCTT GCTGTGCCA CGCTGCTCT TCTCCCATAT GGAGGGCTGG 720  
 AGCTACACAG AGGGCTTCTA CTTGCGCTTC ATCACCCTCA GCACCGTGGG CTTGGGCGAC 780  
 TACGTGATTG GAATGAACCC CTCACAGAGG TACCCACTGT GGTACAAGAA CATGGTGTCC 840  
 CTGTGGATCC TCTTTGGGAT GGCATGGCTG GCCTTGATCA TCAAACTCAT CCTCTCCAG 900  
 CTGGAGAGCG CAGGGAGGGT ATGTTCTCTG TGCCACCACA GCTCTAAGGA AGACTTCAAG 960  
 TCCCAAGCTC GGAGACAGG ACCTGACCGG GAGCCAGAGT CCACTCCCC ACAGCAAGGA 1020  
 TGCTATCCAG AGGGACCCAT GGAATCATA CAGCATCTGG AACCTTCTGC TCACGCTGCA 1080  
 GGCTGTGGCA AGGACAGCTA GTTATACTCC ATTCTTTGGT CGTCCGCTCT GGTAGCAAGA 1140  
 CCGCTGATT TAAGCTTTGC ACATGTCCAC CCAAACTAAA GACTACATT TCCATCCACC 1200  
 CTAGAGGCTG GGTGACGTA TATGATTAA TCTGCCAAT AGGGTATACA GAGACATGTC 1260  
 CTGGGTGACA TGGGATGTGA CTTTGGGGTG TCGGGGAGC ATGCCCTTCT CCCCCACTTC 1320  
 CTTACTTTAG CGGGCTGCAA TGCGCGGAT ATGATGGCTG GGAGCTCTGG CAGCCATACG 1380  
 GCACCATGAA GTAGCGGCAA TGTTTGAGCG GCACAATTAG ATAGGAAGAG TCTGGATCTC 1440  
 TGATGATCAC AGAGCCATCC TAACAAACGG AATATCACCG ACCCTCCTTT ATGTGAGAGA 1500  
 GAAATAAACA TCTATGAAA 1519

Seq ID NO: C125 DNA Sequence  
 Nucleic Acid Accession #: NM\_004154  
 Coding sequence: 309..1295

45  
 50  
 55  
 60  
 65  
 70  
 75  
 80  
 1 11 21 31 41 51  
 AAGGACAGAG GAGGGGCCCT TCCTGTGAGC TGGCTGGGAG CAGAGGTGGC TTTGTCTTTT 60  
 CGGAAGAACT GGTTCGTGGG AATTGTGCT TATTCCCAT CAAGGATCAA GGACCTGCTC 120  
 TGGGGCTACC TCAGGGCCCC ACAGGATGAG GGGCTGGTTT TCAGATGAGT TTTCTGCTTG 180  
 CTTGTACTCT GGATATGTCT TAAAAATTG CAAACTGCCT TCTGTGCTAG GTCTGTCTCA 240  
 TTCTTCTATG CACTCTGAT ATGTCTCTCA GTTTCCTCAT CTGTGCTCTC TCCAGACTTC 300  
 TGCCAGAACA TTGACGCGCA CAGTTTCAGG CACAGAACTG ACTGGCAGCA GGGGCTGCTC 360  
 CACGATGGGG AAATTGTCTCC AGCACTTCAC GGACTGCAAG CGAGGCACCT GCTAACTCTT 420  
 GGATAACAGG ACCTCTGCCA GAAGAACCAT GGCTTTGGAA GGGCGAGTTC AGGCTGAGGA 480  
 GATGGGTGGG TCCTCTAGTG AGCCCCGCTC TCCCTGAACA TAGGAAACCC ACCTGGGCAG 540  
 CCATGGAATG GGACAAATGG ACAGGCCAGG CTCTGGGCTT GCCACCCACC ACCTGTGTCT 600  
 ACCCGAGAAA CTTCAAGCAA CTGTGCTGTC CACTGTGTA TTCGGCGGTG CTGGCGGCTG 660  
 GCCTGCGCTG GAACATCTGT GTCAATACCC AGATCTGCAC GTCCCGCCGG GCCCTGACCC 720  
 GCACGCGCGT GTACACCTTA AACCTTGCTC TGGCTGACCT GCTATATGCC TGCTCCCTGC 780  
 CCGTGTCTAT CTACAACTAT GCCCAAGGTG ATCACTGGCC CTTTGGCGAG TTGCGCTGCC 840  
 GCCTGTGTCG CTTCTCTTTC TATGCCAACC TGCAOAGCAG CATCTCTTTC CTCACCTGCA 900  
 TCAGCTTCCA GCGCTACCTG GGCATCTGCC ACCCGTGGC CCCCTGGCAC AAACGTGGGG 960  
 GCGCGCGGCG TGCCCTGGCTA GTGTGTGTAG CCGTGTGGCT GGCCGTGACA ACCCAATGCC 1020  
 TGCCCAAGCG CATCTTGGCT GCCACAGGCA TCCAGCGTAA CCGCACTGTC TGCTATGACC 1080  
 TCAGCCCGCC TGCCCTGGCC ACCCACTATA TGCCCTATGG CATGGCTCTC ACTGTATCG 1140  
 GCTTCTGCTG GCCCTTGGCT GCCCTGCTGG CTTGCTACTG TCTCTGGGCC TGCCGCTGCT 1200  
 GCGCCGAGGA TGGCCCGGCA GAGCGTGTGG CCCAGGAGCG GCGTGGCAAG GCGGCCGCA 1260  
 TGGCCGTGCT GGTGGCTGCT GCCTTGGCCA TCAGCTTCTT GCCTTTTACG ATCACCAGA 1320  
 CAGCCTACCT GGCAGTGGCG TCGAOCGCGG GCGTCCCTCG CACTGTATTG GAGGCGTTTG 1380  
 CAGCGGCTTA CAAAGGCAGG CGGCGGTTTG CAGTGCCAA CAGCGTGTCT GACCCCATCC 1440  
 TCTTCTACTT CACCCAGAAG AAGTTCCGCC GCGCAACACA TGAGCTCTTA CAGAACTCA 1500  
 CAGCCAAATG GCAAGGCGAG GGTGCTGTAG TCCTCCAGGT CCTGGGCGAG CTTCAATATT 1560  
 GCCATTGTGT CCGGGGCACC AGGAGCCCCA CCAACCCCAA ACCATGCGGA GAATTAGATT 1620  
 TTAGCTCAGC TGGGCATGGA GTTAAGATCC CTCACAGGAC CCAGAAGCTC ACCAAAACT 1680  
 ATTTCTCAG CCCCTTCTCT GGGCCAGACC CTGTGGGCTG GGAGATGGAC AGACCTGGGC 1740  
 CTGGCTCTTG AGAGGTCCCA GTCAGCCATG GAGAGCTGGG GAAACCATAT TAAGGTGCTC 1800  
 AAAAAATAC AGTGTGACGT GTACTGTCAA AA 1832

Seq ID NO: C126 DNA Sequence  
 Nucleic Acid Accession #: NM\_007197  
 Coding sequence: 18..1763

1 11 21 31 41 51  
 | | | | |

5  
10  
15  
20  
25  
30  
35  
40  
45

```

ACACGTCCAA CGCCAGCATG CAGCGCCCGG GCGCCCGCCT GTGGCTGGTC CTGCAGGTGA 60
TGGGCTCGTG CGCCGCCATC AGCTCCATGG ACATGGAGGG CCGGGGCGAC GGCAAATGCC 120
AGCCCATCGA GATCCCGATG TGCAAGGACA TCGGCTACAA CATGACTCGT ATGCCCAACC 180
TGATGGGCCA CGAGAACAGG CGCGAGGCGG CCATCCAGTT GCACGAGTTC GCGCCGCTGG 240
TGGAGTACGG CTGCCACGGC CACCTCGGCT TCTTCTGTG CTGCTGTATC GCGCGATGT 300
GCACCGAGCA GGTCTCTACC CCCATCCCGG CCGTCCCGGT CATGTGCGAG CAGGCCCGGC 360
TCAAGTGTCT CCGCATTTATG GAGCAGTTCA ACTTCAAGTG GCGCGACTCC CTGGACTGCC 420
GGAAACTCCC CAACAAGAAC GACCCCACT ACCTGTGCAT GGAGGCGGCC AACCAACGGCT 480
CGGACGAGCC CAGCCGGGGG TCGGGCCTGT TCCGCGCGCT GTTCCGCGCG CAGCGGCCCC 540
ACAGCGGGCA GGAGCACCCG CTGAAGGACG GGGGCCCGGG GCGCGCGGCG TGCGACAACC 600
CGGGCAAGTT CCACCACGTG GAGAAGAGCG CGTCGTGCGC GCGGCTCTGC ACGCCCGGCG 660
TGGACGTGTA CTGGAGCGCG GAGGACAAGC GCTTCGCGAT GGTCTGGCTG GCCATCTGGG 720
CGGTGCTGTG CTCTCTCTCC AGCGCCTTCA CCGTGCTCAC CTTCCTCATC GACCCGGCCC 780
GCTTCCGCTA CCGCGAGCGC CCCATCATCT TCCTCTCCAT GTGCTACTGC GTCTACTCCG 840
TGGGCTACCT TCCCGGCTCT TTCCGCGCGC CCGAGAGCAT CGCTCGCAC CGGGACAGCG 900
GCCAGCTCTA TGTCTATCCG GAGGAGCTGG AGAGCACCGG CTGCACGCTG GTCTTCTCTG 960
TCCTCTACTA CTTCGCGATG GCCAGCTCGC TGTGGTGGGT GGTCTCTCAG CTCACCTGGT 1020
TCCTGGCGCG CGGCAAGAAC TGGGGCCACG AGGCCATCGA AGCCAAACAG AGCTACTTCC 1080
ACCTGGCAGC CTGGGCGATC CCGGCGGTGA AGACCATCCT GATCCTGGTC ATGCGCAGGG 1140
TGGCGGGCGA CGACAGTTCG GGGGTCTGCT ACGTGGGCG CATGGACGTC AACCGCTCA 1200
CCGGCTTCGT GCTCATTTCC CTGGCCTGCT ACCTGGTCAT CGGCACGTCC TTCATCTCT 1260
CGGGCTTCGT GGGCCTGTTC CACATCCGGA GGGTGATGAA GACGGGCGCG GAGAACACGG 1320
ACAAGCTGGA GAAGCTCATG GTGCGTATCG GGCTCTTCTC TGTGCTGTAC ACCGTGCGCG 1380
CCACCTGTGT GATCGGCTGC TACTTTTACG AACGCTCAA CATGGATTAC TGAAGATCC 1440
TGGCGCGGCA GCACAAGTGC AAAATGAACA ACCAGACTAA AACGCTGGAC TGCCTGATG 1500
CGGCTCCAT CCCGCGCGTG GAGATCTTCA TGGTGAAGAT CTTTATGCTG CTGGTGGTGG 1560
GGATCACCA GCGGATGTGG ATTTGGACCT CCAAGACTCT GCAGTCTCTG CAGCAGGTGT 1620
CGAGCGGTAG GTTAAAGAA GAGAGCCGGA GAAACCGCGC CAGCGTGATC ACCAGCGGTG 1680
GGATTACAA AAAAGCCGAG CATCCCGAGA AAACCTACCA CGGGAATAT GAGATCCCTG 1740
CCAGTCCGCG CACCTGCGTG TSAACAGGGC TGGAGGGGAG GGCACAGGGG CGCCCGGAGC 1800
TAAGATGTGG TGCTTTTCTT GGTGTGTTT TTCTTTCTTC TTCTTCTTTT TTTTTTTTTT 1860
ATAAAGCAA AAGAGAAATA CATAAAAAG TGTTTACCTT GAAATTCAGG ATGCTGTGAT 1920
ACACTGAAG GAAAAATGTA CTAAAGGGT TTTGTTTTGT TTTGGTTTTT CAGCGAAGGG 1980
AAGCTCTCC AGTGAAGTAG CCTCTTGTGT AACTAATTG TGGTAAAGTA GTTGATTGAG 2040
CCCTCAGAG AAAACTTTTG TTTAGAGCCC TCGTAAATA TACATCTGTG TATTGAGTT 2100
GGCTTTGCTA CCCATTTACA AATAAGAGGA CAGATAACTG CTTTGCAAT TCAAGACCT 2160
CCCTTGGGTT AACAAATGAG CCATCCCGAG GGGCCACCCC CAGGAAGGCC ACAGTGTCTG 2220
GGGCGATCCC TGCAGAGGAA AGACAGGACC CGGGGCCCGC CTCACACCCC AGTGGATTG 2280
GAGTTGCTTA AAATAGACTC TGGCCTTAC CAATAGTCTC TCTGCAAGAC AGAAACCTCC 2340
ATCAAAAGCA CACTTTGTGA ACTCAACGTA TGTGCAATAC ATTTTCTTCT CTTTCTTGA 2400
AAATAAAAG AGAAACAAGT ATTTTGCTAT ATATAAGAC AACAAAGAA ATCTCCTAAC 2460
AAAAGAACTA AGAGGCCGAG CCCTCAGAAA CCCTTCAGTG CTACATTTTG TGGCTTTTTA 2520
ATGGAACCA GAAACAATGTT ATAGACGTTT GGAAGTATT GTGGAAGGA GGGGGGAAGA 2580
GGGAGAAGGA TCATTCAAAA GTTACCCAAA GGGCTTATG ACTCTTCTA TTGTTAAACA 2640
AATGATTAGC AAAACAGAT CAGGAAGCAC TAGGTTGGCA GAGACACTT GTCTAGTGA 2700
TTCTCTTAC AGTGCCAGGA AAGAGTGGTT TCTGCGTGTG TATATTGTA ATATATGATA 2760
TTTTTCATGC TCCACTATTT TATTAATAAT AAAATATGTT CTTTAAAAAA A 2811

```

50 Seq ID NO: C127 DNA Sequence  
Nucleic Acid Accession #: NM\_005761.1  
Coding sequence: 250..4956

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
GCGAGGAGGA AACGGTGGCG GAGCGCGCAG GGCTTGCTGC CGCCACCGCC GCTGCACAGG 60
CTGCGCGAGC GAGCCTGCCG CGCGCGCGCC TCCCGCTCT CTCTCTCGGG CGAGCTGCGG 120
GGATGGGGCG CGCGCGGGAG CCGAGGCGCG CGCAGGAACC GCGCGCGCGG CCGCCCGCGT 180
CTCGTATCCC GCGCGGCTGA GCGCGCGTGC CGCGCGCGCG CCTGCGCGGG GGGCGGCGCC 240
CCAGGCCCCA TGGAGGTCTC CCGGAGGAAG GCGCGCGCGC GCGCGCGCGG CCGCGCAGCG 300
CACTGCCCCC TGCTCGCTCA TCTGCTGGCA CTGGCGGCTC CCGCGCGGGG CGCGGACGAG 360
CCGCTGTGGC GGTGCGAGCA AGCCATCGGA GCCATCGCGG CGAGCCAGGA GGACGCGGTG 420
TTTGTGGGGA GCGGCGAGCT CCGGAGCCAG CTGGACTACA GCCTGGAGCA CAGCCTCTCG 480
CGCCTGTACC GGAACCAAGC GGGCAACTGC ACAGAGCCGG TCTCGTGGC GCGCCCGCGG 540
CGGCCCCGGC CCGGAGCAG CTTCAGCAAG CTGCTGCTGC CCTACCGCGA GGGGGCGGCC 600
GGCTCGGGG GGTGCTGCTC CACCGGCTGG ACCTTGGACC GGGGGCGCTG CGAGGTGCGG 660
CCCTTGGGCA ACCTGAGCGG CAACTCCCTG CGCAACGGCA CGAGGTGGT GTGCTGCCAC 720
CGCAGGGCT CGACGGCGGG CGTGGTGTAC CGCGCGGGCC GGAACAACCG CTGTACCTG 780
GCGGTGGCGG CCACCTACGT GCTGCCTGAG CGGAGACGG CGAGCGCTG CAACCCCGG 840
GCATCCGACC ACACACCGCG CATCGCGCTC AAGGACACGG AGGGGCGCAG CCTGGCCACG 900
CAGGAGCTGG GCGCGCTCAA GCTGTGCGAG GCGCGGGGCA GCCTGCATT CTGGGACGCC 960
TTTCTCTGGA ACGGCAGCAT CTACTTCCCC TACTACCCCT ACAACTATAC GAGCGCGGCT 1020
GCCACCGGCT GGCACGATG GCGCGGCTAT GCGCAGAGCA CCGAGGTGCT GTTCCAGGGC 1080
CAGGCATCCC TCGACTGCGG CCGCGGCCAC CCGCGGCTGCT CCTCTCTCC 1140
AGCCTAGTGG AGGCCCTGGA CGTCTGGGCG GAGGTGTTCA GCGCGCGCGG TGGAGAGGGC 1200
CAGGAGCGGG GCTTCCCCAC CACCAAGGCG CTCTGCTCTC TCAGAAATGAG TGAGATCCAG 1260
GCGCGCGCCA AGAGGCTCAG CTGGGACTTC AAGACGCGCG AGAGCCACTG CAAAGAGGGG 1320
GATCAACCTG AAAGAGTCCA ACCAATCGCA TCATCTACCT TGATCCATTG CGACCTGACA 1380
TCCGTTTATG GCACCGTGGT AATGAACAGG ACTGTTTAT TCTTGGGGAC TGGAGATGGC 1440
CAGTTACTTA AGTTATTCTT TGGTGAGAAT TTGACTTCAA ATTGTCCAGA GGTATCTAT 1500
GAAATTAAAG AAGAGACACC TGTTTTCTAC AAACCTCGTT CTGATCTCTG GAAGAATATC 1560
TACATTTATC TAACAGCTGG GAAAGAGGTG AGGAGAATTC GTGTTGCAAA CTGCAATAAA 1620
CATAAATCCT GTTCGAGTG TTTAACAGCC ACAGACCCCT ACTGCGGTTG GTGCCATTG 1680
CTACAAAGGT GCACTTTTCA AGGAGATTGT GTACATTGAG AGAACTTAGA AAACCTGGCT 1740
GATATTTCTG CTGGAGCAAA AAAGTGCCCT AAAATTCAGA TAATTGGAAG CAGTAAAGAA 1800

```



AAGACTACAG TGAATATGTT GGGAAAGCTTC TCTCCAAGAC ACTCAAAGTG CATGGTGAAG 1860  
 AATGTGGACT CTAGCAGGGA GCTCTGCCAG AATAAAAGTC AGCCCAACCG GACCTGCACC 1920  
 TGTAGCATCC CAACCAAGAGC AACCTACAAA GATGTTTCAG TTGTCAACGT GATGTTCTCC 1980  
 TTCCGTTCTT GSAATTTATC AGACAGATTC AACTTTACCA ACTGCTCATC ATTTAAAGAA 2040  
 5 TGCCAGCAT GCGTAGAAAC TGGCTGCGCG TGGTGTAAAA GTGCAAGAAG GTGTATCCAC 2100  
 CCCTTCACAG CTTCGCAACC TTCTGATTAT GAGAGAAACC AGGAACAGTG TCCAGTGGCT 2160  
 GTGAGAAAGA CATCAGGAGG AGGAAGACCC AAGGAGAAAC AGGGGAACAG AACCAACCAG 2220  
 GCTTTACAGG TCTTCTACAT TAAGTCCATT GAGCCACAGA AAGTATCGAC ATTAGGGAAA 2280  
 10 AGCAACGTGA TAGTAACGGG AGCAAACTTT ACCCGGGCAT CGAACATCAC AATGATCCTG 2340  
 AAAGGAACCA GTACCTGTGA TAAGGATGTG ATACAGGTTA GCCATGTGCT AAATGACACC 2400  
 CACATGAATC TCTCTCTTCC ATCAAGCCGG AAAGAAATGA AGGATGTGTG TATCCAGTTT 2460  
 GATGGTGGGA ACTGCTCTTC TGTGGGATCC TTATCCTACA TTGCTCTGCC ACATTGTTC 2520  
 CTTATATTTT CTGCTACCACT CTGGATCAGT GGTGGTCAAA ATATAACCAT GATGGGCAGA 2580  
 15 AATTTTGTAT TAATTGACAA CTTAATCATT TCACATGAAT TAAAAGGAAA CATAAATGTC 2640  
 TCTGAATATT GTGTGGGAC TTACTGCGGG TTTTTCAGCC CCAGTTTAAA GAGTTCAAAA 2700  
 GTGCGCAAGT ATGCTCACTG GAAGCTGAGA GTACAAGACA CCTACTTGA TGTGGAAACC 2760  
 CTGCAGTATC GGGAGGACCC CAGATTACAG GGGTATCGGG TGGAAATCGA GGTGACACA 2820  
 GAACCTGAAG TGAATAATCA AAAAGAAAT GACAACCTCA ATATTTCCAA AAAAGACATT 2880  
 20 GAAATTAATC TCTTCCATGG GGAATATGG CAATTAATTT GCAGTTTGA AATATTACT 2940  
 AGAATCAAG ATCTTACCAC CATCTTTGC AAAATTAAG GCATCAAGAC TGCAAGCACC 3000  
 ATTGCCAAT CTCTCAAGAA AGTTCCGGTC AAGCTGGGAA ACCTGGAGCT CTACGTCGAG 3060  
 CAGGAGTCAG TTCCTTCCAC ATGGTATTTT CTGATTGTGC TCCTGTCTT GCTAGTGATT 3120  
 GTCAATTTT CTGCGTGGG GGTGACCAGG CACAAATCGA AGGAGCTGAG TCGCAACAG 3180  
 25 AGTCAACAC TAGAATTGCT GGAAGCCGAG CTCGGAAGG AGATACGTGA CGGCTTTGCT 3240  
 GAGCTGCAGA TGGATAAATT GGATGTGGTT GATAGTTTGG GAACTGTTC CTTCCTTGAC 3300  
 TACAAACATT TTGCTCTGAG AACCTTCTTC CCTGAGTCAG GTGGCTTAC CCACATCTTC 3360  
 ACTGAAGATA TGCATAACAG AGACGCCAAC GACAAGAATG AAAGTCTCAC AGCTTTGGAT 3420  
 GCGCTAATCT GTAATAAAGG CTTTCTTGT ACTGTCTCC ACACCTTGA AAAGCAGAAG 3480  
 30 AACCTTTCTG TGAAGGACAG GTGTCTGTT GCCTCTCTCC TAACCATGTC ACTGCAAAAC 3540  
 AAGCTGGTCT ACCTGACCAG CATCTAGAG GTGCTGACCA GGGACTTGAT GGAACAGTGT 3600  
 AGTAACATGC AGCCGAAACT CATGCTGAGA CGCAGGAGT CGCTCGTGA AAAACTCTCTC 3660  
 ACAAACTGGA GTGCGTCTG CCTTCTGGA TTCTCTCGGG AGACTGTGCG AGAGCCCTTC 3720  
 TATTTGTCTG TGACGACTCT GAACAGAAAT ATTAACAAGG GTCCCGTGA TGTAACTACT 3780  
 35 TGCAAGCCCC TGTACACACT TAATGAAGAC TGGCTGTGT GGCAGGTTCC GSAATTCAGT 3840  
 ACTGTGGCAT TAAAGCTGCT CTTTGAAAA ATCCCGGAAA ACAGAGGTGC AGATGTCTGT 3900  
 CGGAATATT CGATCAATGT TCTCGACTGT GACACCATTC GCCAAGCCAA AGAAAAGATT 3960  
 TTCCAAGCAT TCTTAAGCAA AATGGCTCT CCTTATGGAC TTCAGCTTAA TGAATTTGGT 4020  
 CTTGAGCTTC AATGGGCAAC AGCAGAGAAA GAACTTCTG ACATCGACAG TTCTCCGTG 4080  
 40 ATTCTTGAAG ATGSAATCAC CAAGCTAAAC ACCATTGGCC ACTATGAGAT ATCAATGGGA 4140  
 TCCACTATAA AAGTCTTTAA GAAGATAGCA AATTTTACTT CAGATGTGGA GTACTCGGAT 4200  
 GACCACTGCC ATGCTGATTT ACCAGATTCC GAAGCATTCC AAGATGTGCA AGGAAGAGA 4260  
 CATCGAGGGA AGCAACAAGT CAAAGTAAAA GAAATGTATC TGACAAAGCT GCTGTGAGCC 4320  
 AAGGTGGCAA TTCTTCTGCT GCTTGAAAA CTTTTAGAA GCATTGTGAG TTTACCAAC 4380  
 45 AGCAGAGCTC CATTGCTAT AAAATACTTT TTTGACTTTT TGGACGCCA GGCTGAAAA 4440  
 AAAAAATCA CAGATCTGTA CGTGTACAT ATTTGAAAA CAAACAGCCT TCCCTTCTG 4500  
 TTTGGGTAA ACATCTGAA GAACCTCAG TTTGCTTTG ACATTAAGAA GACACCACT 4560  
 ATAGACGCT GTTGTCTAGT GATTGCCAG GCATTCATGG ATGCATTTTC TCTCAGAG 4620  
 50 CAGCACTAG GGAAGGAAGC ACCAACTAAT AAGCTTCTCT ATGCCAAGGA TATCCCAAC 4680  
 TACAAAGAAG AAGTAAATC TTATTACAA GCAATCAGGG ATTTGCCTCC ATTGTCAATC 4740  
 TCAGAAATGG AAGATTTTTT AACTCAGGAA TCTAAGAAAC ATGAAATGA ATTTAATGAA 4800  
 GAAGTGGCTC TGACAGAAAT TTACAAATAC ATCGTAAAA ATTTTGATGA GATTCTAAT 4860  
 AAATAGAAAG GAGACAGAGG GCTGGAAGAA GCTCAGAAAC AACTCTTGCA TGTAAAGTC 4920  
 TATTGTGATG AAAGAGAAGAA ATGCAAGTGG ATGTAAGCAC TCTGGGGCTT GCTTAATCT 4980  
 55 GGCAAAGTTC TTCAGACGAC TTCCGAGCAA AATGGCTGCT TGAGCTACTC TGTGTCTGTA 5040  
 ATTTGTGTGT TGCACATAGG TTCCACTTTG GGCAGTGTCT TTTTAAGAGA CCAAGGCACA 5100  
 TGCACAGCTT TTAGAAGCA A 5121

Seq ID NO: C128 DNA Sequence  
 Nucleic Acid Accession #: NM\_002185.1  
 Coding sequence: 23..1402

1 11 21 31 41 51  
 65 CTCTCTCTCT ATCTCTCTCA GAATGACAA TCTAGGTACA ACTTTTGGCA TGGTTTTTTC 60  
 TTTACTTCAA GTCGTTTCTG GAGAAAGTGG CTATGCTCAA AATGGAGACT TGAAGATGC 120  
 AGAACTGGAT GACTACTCAT TCTCATGCTA TAGCCAGTTG GAAGTGAATG GATCGCAGCA 180  
 TTCACTGACC TGTGCTTTTG AGGACCCAGA TGTCAACACC ACCAATCTGG AATTGAAAT 240  
 ATGTGGGGCC CTGTGGAGG TAAAGTGCTT GAAITTCAGG AAACCTACAAG AGATATATT 300  
 70 CATCGAGACA AAGAAATTCT TACTGATTGG AAAGAGCAAT ATATGTGTGA AGGTGGAGA 360  
 AAAGAGTCTA ACCTGCAAAA AAATAGACCT AACCACTATA GTTAAACCTG AGGCTCCTTT 420  
 TGACCTGAGT GTCATCTATC GGAAGGAGC CAATGACTTT GTGGTGACAT TTAATACATC 480  
 ACATCTGCA AAGAAGTATG TAAAGTTTT AATGCATGAT GTAGCTTACC GCCAGGAAAA 540  
 GGAATGAAAC AATGGACGC ATGTGAATTT ATCCAGCACA AAGCTGACAC TCCTGCAGAG 600  
 75 AAAGCTCCAA CCGCAGCAA TGTATGAGAT TAAAGTGA TCCATCCCTG ATCACTATT 660  
 TAAAGGCTTC TGGAGTGAAT GGAATCCAG TTATTACTTC AGAATCCAG AGATCAATA 720  
 TAGCTCAGGG GAGATGGATC CTATCTTACT AACCATCAGC ATTTTGAGTT TTTTCTCTGT 780  
 CGCTCTGTTG GTCATCTTGG CCTGTGTGTT ATGGAAGAAA AGGATTAAGC CTATCGTATG 840  
 80 GCCAGTCTC CCGCATATA AGAAGACTCT GGAACATCTT TGTAAAGAAC CAAGAAAAAA 900  
 TTTAATGTG AGTTTCAATC CTGAAAGTTT CTGCACTGC CAGATTCTA GGTGGATGA 960  
 CATTCAGCT AGAGATGAAG TGAAGGTTT TCTGCAAGAT ACGTTTCTTC AGCAACTAGA 1020  
 AGAATCTGAG AAGCAGAGGC TTGAGGGGGA TGTGCAGAGC CCAACTGCT CATCTGAGGA 1080  
 TGTAGTGTCT ACTCCAGAAA GCTTTGGAAG AGATTCTATC CTCACATGCC TGGCTGGGAA 1140  
 TGTCACTGCA TGTGACGCC CTATTCTCTC CTCTCCAGG TCCTAGACT GCAGGAGAG 1200  
 TGGCAAGAA GGCCTCATG TGTACCAGGA CCTCTGCTT AGCCTGGGA CTACAAACAG 1260



CACGCTGCCC CCTCCATTTT CTCTCCAATC TGGAATCCTG ACATTGAACC CAGTTGCTCA 1320  
 GGGTCAGCCC ATTCTTACTT CCCTGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC 1380  
 CAGCTTCTAC CAAAACCACT GAAGTGTAAAG AAACCCAGAC TGAACCTTACC GTGAGCGACA 1440  
 AAGATGATT AAAGGGAAG TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAGACAA 1500  
 AATTAGCAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCACTCTT 1560  
 CCTGAGTTCA GTGGCACTCA ACATGAGTCA AGAGCATCCT GCTTCTACCA TGTGGATTG 1620  
 GTCAAGGT TTAAGGTGAC CCAATGATT AGCTATTT 1658

Seq ID NO: C129 DNA Sequence  
 Nucleic Acid Accession #: NM\_002722.1  
 Coding sequence: 15..302

1 11 21 31 41 51  
 15 ACTCTGGACT CCGGATGGCT GCGGCAGGCC TCTGCCTCTC CCTGCTGCTC CTGTCCACCT 60  
 GCGTGGCTCT GTTACTACAG CCACTGCTGG GTGCCAGGG AGCCCCACTG GAGCCAGTGT 120  
 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCAGTA TGCAGCTGAT CTCCTAGAT 180  
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAAGACA CAAAGAGGAC ACGCTGGCCT 240  
 TCTGGAGTG GGGTCCCGG CATGCTGCTG TCCCAGGGA GTCAGCCCG CTGGACTTAT 300  
 20 AATGCCACT TCTGCTCTCT ACGACTCCAT GAGCAGCGCC AGCCCAGCTC TCCCCTCTGC 360  
 ACCCTGGCT CTGCCAAAG CTGCTCCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420  
 AAGCC 425

Seq ID NO: C130 DNA Sequence  
 Nucleic Acid Accession #: NM\_032545.1  
 Coding sequence: 47..718

1 11 21 31 41 51  
 30 AAACGTATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA 60  
 CCATGTCAGG CTCTCTGTTA CCGTCAGTTT GGCATTACAG ATCATCAATT TGGGAAACAG 120  
 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTG CCACTCAGAA 180  
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240  
 CGAGGGCTGG GGGCCGAGG AGCGCTCCC CTACTCCCGG GCTTTCGAG AGGGTGGCTC 300  
 35 CGCGGGGCGG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCGAGT TCTGCGTGTG 360  
 CCGGCGCCAC TTCACCGGCG GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420  
 CCTGGAGCAC GGAGCCTGGA CCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGCG 480  
 CTGCACTGC CTCCCTCTCC AGACGCCCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540  
 40 CCACGCTCAG GGGCCGAGCG CCGGGGGCGC GCCACGCTG CTACTCTTGC TCCCTGCGC 600  
 ACTCTGACAC CGCTCTGTC GCCCGGATGC GCCCGGCGAC CCTCGGTCCC TGGTCCCTTC 660  
 CGTCTCCAG CGGAGCGCGC GCCCTGCGG AAGGCGGGA CTGCGGCATC GCCTTTAATT 720  
 TTCTATGTTG TAAATAATAG ATGTGTTAG TTACCGTAA GCTGAAGCAC TGGGTGAATA 780  
 TTTTATGTG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAATA AAAAAAATA 840  
 AAAAAA 846

Seq ID NO: C131 DNA Sequence  
 Nucleic Acid Accession #: NM\_006533.1  
 Coding sequence: 72..467

1 11 21 31 41 51  
 50 AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCTTGCTCA CTCTCTTGCT 60  
 CACAGTCCAC GATGGCCCGG TCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120  
 TCTCCGACAC TGGTGTACAG GGTGGTCTTA TGGCCAAAGT GGTGACCGG AAGCTGTGTG 180  
 55 CGGACACAGA GTGACGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240  
 CCGACTGCGG ATTCTGTGAC ATTACCGGG GCCAAGTGTG GTATGTCTTC TCCAAGCTGA 300  
 AGGGCGGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360  
 CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG 420  
 60 GCAAGTCTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480  
 CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAAAATC AATCAGCCCA GTGCAAAAC 538

Seq ID NO: C132 DNA Sequence  
 Nucleic Acid Accession #: AB064272  
 Coding sequence: 1..708

1 11 21 31 41 51  
 65 ATGACACAAG TCACAGAAAA GTCCACAGAA CACCCAGAAA AGACCACGTC AACCCAGAG 60  
 AAAACCAACA GAACCCAGGA AAAGCCTACG CTACTACTAG AGAAGACCAT ATGCACCAAA 120  
 70 GGGAAAAACA CACCACTCCC AGAAAAGCCT ACAGAAAACC TGGGGAACAC CACACTGACC 180  
 ACTGAGACCA TAAAGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240  
 ACAAGACTTA TAAACCTTC AGTCAAGTTC ACAGAGACA AATCTCTCAC TACTACCTCT 300  
 TCTCATCTAA ATAAAACTGA AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCCTCAT 360  
 75 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAGCCA CAGGAAACGA GAGCCATCCA 420  
 TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCACGCTG GACAGATGGG AGAGATGAT 480  
 TCATTCCCTG CATGGGCCAT AGTTATTGTG GTCCCTGGTG CTGTGATTCT CCTCTGGTG 540  
 TTCCTGGCC TGATCTCTT GGTCTCCTAT ATGATGCGGA CACGCGGCAC ACTAACCCAG 600  
 AACACCCAGT ACAATGATGC AGAGGATGAG GGTGCCCCCA ATTCTACCC GGTCTACCTG 660  
 80 ATGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA 708

Seq ID NO: C133 DNA Sequence  
 Nucleic Acid Accession #: NM\_080870.1  
 Coding sequence: 3..710

	1	11	21	31	41	51	
5	AGATGACACA	AGTCACAGAA	AAGTCCACAG	AACACCCAGA	AAAGACCACG	TCAACCCACG	60
	AGAAAAACCA	AAGAACCCCA	GAAGAGCCTA	CGCTATACTC	AGAGAAGACC	ATATGCACCA	120
	AAGGGAAAAA	CACACCAGTC	CCAGAAAAGC	CTACAGAAAA	CCTGGGGAAC	ACCACACTGA	180
	CCACTGAGAC	CATAAAAGCC	CCAGTAAAGT	CCACAGAAAA	CCCAGAAAAA	ACAGCAGCAG	240
	TCACAAAGAC	TATAAAACCT	TCAGTCAAGG	TCACAGGAGA	CAAACTCTCT	ACTACTACCT	300
10	CTTCTCATCT	AAATAAAACT	GAAGTTACTC	ATCAGGTGCC	CACTGGTTCT	TTCAACCTCA	360
	TTACATCTAG	AAAGAGCTTG	AGTTCTATCA	CATCAGAAGC	CACAGGAAAC	GAGAGCCATC	420
	CATACCTCAA	TAAAGATGGC	TCACAGAAAG	GTATCCACGC	TGGACAGATG	GGAGAGAATG	480
	ATTCAATCCC	TGCATGGGCC	ATAGTTATTG	TGGTCTCGGT	GGCTGTGATT	CTCCTCCTGG	540
	TGTTCTCTGG	CCTGATCTTC	TTGGTCTCCT	ATATGATGCG	GACACGCCGC	ACACTAACCC	600
15	AGAACACCCA	GTACAATGAT	GCAGAGGATG	AGGGTGGCCC	CAATTCTTAC	CCGGTCTACC	660
	TGATGGAGCA	GCAGAACTTT	GGCATGGGCC	AGATCCCTTC	CCCAOGGTGA	TCTTGGAGTA	720
	GGCGGCCAGC	CCTGCTCTTT	CCATGCTCTG	CCCCCTTCTT	GGATGAGGAA	CCGGACTCAC	780
	AATTTCTATT	TCGGGGACTA	CAGGAAGGGC	AGAGAATACT	GACGGTTACC	AGTATTAAAC	840
	CTTCATCTGT	TCTTGAACCT	GGTTGGGGAA	TGAGGTGATA	AGCAAGGAGG	GTGTAAGTTT	900
20	AGGGGACAAA	GAAGAAAGAA	TGAATAATAC	GAGCAGACAT	TCTCTGTAGA	AGGTAATGGT	960
	CTGAGAATGA	AAAGGTGTTT	GATGGACATG	TTGTGGGGCC	ACCAATGCAG	AACACTGCAC	1020
	TGAGTCTTAA	AGGAAGGACA	GGAGCCTTAT	AGGCAATGCC	CCAGACTGAC	TTGTGAGTGG	1080
	GGTTTATGGG	GAAGGGGAGG	GACTGAGGGC	AGAGTCTCTG	GGTTTCAGGA	CAGCATTATG	1140
	TTAATTTCCG	TCACTATTAC	TTAAGAGTTT	GTGTGTAAC	AGGCTCATCT	CTGAGTTCTC	1200
25	AGGACCCCTG	CCCCCACC	CATTTTTTTA	ATGAAAAAAA	AAAACAAAAA	AAACGGATCC	1260
	AAGAAGAAAA	GAGAATTTAT	TTCTTTCTCC	ACTCTCTCCA	TGCCCTGGAG	AAAAAAAAGT	1320
	CCAGAAGAAA	TCATAAATAT	CTCTCATCTA	CATGGTTGCT	TCTCTTCTCT	CCCAAAATCCC	1380
	TTAGTTTTCC	TAAATGTCTA	CAGTGGACGC	CCTGTTGGTT	TGGCTTGCTG	GGTTGTGGGT	1440
	GGACACGCAA	GGAGGGGATT	TTTATTTGGC	CAGCAGTCTC	ACCCACTGAT	CTCCACCCCA	1500
30	GACCTTCCTT	GATGGGTGTC	TCAGCATTTA	TTTTCTCTGC	TCTTCCACCA	AAAGCCAGCT	1560
	GTAGCTTTAT	CTCGTAAAG	TTACCATCT	TCTCTACTGT	CCCATTCCTC	TCTCTCCCA	1620
	CCTTCACCCC	AGATTCAAGT	TTTCTCTCTT	GTAGGCATTT	CATCTGTGTG	TGTTTTCTGG	1680
	ATTTCTCTCT	TCTCTTCTTA	TGGCCATTTC	ACCTTATTAC	TGATTGGGTA	GAGGGGGAAA	1740
35	AGGAGAATGA	TGATGATAGT	TTCTTCTGT	CTATTGACCT	TTTTTATAAT	AAAGTATAAC	1800
	ATGTT						1805

Seq ID NO: C134 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..10674

40	1	11	21	31	41	51	
	ATGTGGCCTC	GCCTGGCCTT	TTGTTGCTGG	GGTCTGGCGC	TCGTTTCGGG	CTGGGCGACC	60
45	TTTCAGCAGA	TGTCCCCTGC	GCGCAATTTT	AGCTTCCGCC	TCTTCCCCGA	GACCGCGCCC	120
	GGGGCCCCCG	GGAGTATCCC	CGCGCGCCCC	GCTCCTGGCG	ACGAAGCGGC	GGGAGCAGA	180
	GTGGAGCGGC	TGGGCCAGGC	GTTCGGGCGA	CGCGTCCGCG	TGCTGCGGGA	GCTCAGCGAG	240
	CGCTCGGAGC	TGTTCTTCTT	GGTGGATGAT	TCGTCCAGCG	TGGGCGAAGT	CAACTTCCGC	300
	AGCGACGCAA	TTTCTCTCG	CAAGCTGCTG	TCCGACTTCC	CGGTGGTGCC	CACGGCCACG	360
50	CGCGTGGCCA	TCGTGACCTT	CTGTCCCAAG	AACTACGTGG	TGCCCGCGGT	CGATTACATC	420
	TCACCCCGCC	GCGCGCGCCA	GCACAAGTGC	GCGCTGCTCC	TCCAAGAGAT	CCCTGCCATC	480
	TCCTACCGAG	GTGGCGGCAC	CTACACCAAG	GGCGCCTTCC	AGCAGCGCGC	GCAAAATCTT	540
	CTTCATGCTA	GAGAAAACCT	AACAAAAGTT	GTATTTCTCA	TCATCTGATG	ATATTCCAAT	600
	GGGGGAGAGC	CTAGACCAAT	TGCAGCGTCA	CTGCGAGATT	CAGGAGTGGA	GATCTTCACT	660
55	TTTGGCATAT	GGCAAGGGAA	CATTCAGAG	CTGAATGACA	TGGCTTCCAC	CCCAAGGAG	720
	GAGCATCTGT	ACCTGTCTCA	CAGTTTGA	GAATTTGAGG	CTTTAGCTCG	CCGGGCATTG	780
	CATGAAGATC	TACCTTCTGG	GAGTTTATT	CAAGATGATA	TGGTCCACTG	CTCATATCTT	840
	TGTGATGAAG	GCAAGGACTG	CTGTGACCGA	ATGGGAAGCT	GCAATGTGG	GACACACACA	900
	GGCCATTTTG	AGTGCATCTG	TGAAAAGGGG	TATTAACGGG	AAGGTCTGCA	GTATGAATGC	960
60	ACAGCTTGCC	CATCGGGGAC	ATACAAACCT	GAAGGCTCAC	CAGGAGGAAT	CAGCAGTTGC	1020
	ATTCATGTCT	CTGATGAAAA	TCACACCTCT	CCACCTGGAA	GCACATCCCC	TGAAGACTGT	1080
	GTCTGCAGAG	AGGATACAG	GGCATCTGGC	CAGACCTGTG	AACTTGTCCA	CTGCCCTGCC	1140
	CTGAAGCCTC	CGAAAAATGG	TTACTTTATC	CAAAACACTT	GCAACAACCA	CTTCAATGCA	1200
	GCCTGTGGGG	TCCGATGTCA	CCCTGGATT	GATCTTGTGG	GAAGCAGCAT	CATCTTATGT	1260
65	CTACCCCAATG	GTTTGTGGTC	CGGTTCAAG	AGCTACTGCA	GAGTAAGAAC	ATGTCTCAT	1320
	CTCCGCCAGC	CGAAACATGG	CCACATCAGC	TGTTCTACAA	GGGAAATGTT	ATATAAGACA	1380
	ACATGTTTGG	TGSCCTGTGA	TGAAGGGTAC	AGACTAGAAG	GCAGTGATA	GCTTACTTGT	1440
	CAAGGAAACA	GCCAGTGGGA	TGGGCCAGAA	CCCCGGTGTG	TGGAGCGCCA	CTGTTCCACC	1500
	TTTCAGATGC	CCAAAGATGT	CATCATATCC	CCCCACAAC	GTGGCAAGCA	GCCAGCCAAA	1560
70	TTTGGGACGA	TCTGCTATGT	AAGTTGCCCG	CAAGGGTTCA	TTTTATCTGG	AGTCAAAGAA	1620
	ATGCTGAGAT	GTACCACTTC	TGAAAATGG	AATGTGGGAG	TTAGGGCAGC	TGTGTGTA	1680
	GACGTGGAGG	CTCCTCAAT	CRACTGTCTT	AAGGACATAG	AGGCTAAGAC	TCTGGAACAG	1740
	CAAGATTCTG	CCAATGTTAC	CTGGCAGATT	CCAACAGCTA	AAGACAACCT	TGGTGAAGAA	1800
	GTGTCACTGC	ACGTTTCACT	AGCTTTCACT	CCACCTTACC	TTTTCCCAAT	TGGAGATGTT	1860
75	GCTATCTGAT	ACACGGCAAC	TGACCTATCC	GGCAACCAAG	CCAGCTGCAT	TTTCCATATC	1920
	AAGGTATTGT	ATGCAGAAC	ACCTGTCTCA	GACTGGTGCA	GATCTCCACC	TCCCGTCCAG	1980
	GTCTCGGAGA	AGGTACATGC	CGCAAGCTGG	GATGAGCCTC	AGTTCTCAGA	CAACTCAGGG	2040
	GCTGAATTTG	TCATTACCAG	AAGTCATACA	CAAGGAGACC	TTTTCCCTCA	AGGGGAGACT	2100
	ATAGTACAGT	ATACAGCCAC	TGACCCCTCA	GGCAATAACA	GGACATGTGA	TATCCATATT	2160
80	GTACATAAAG	GTTCTCCCTG	TGAAATTTCCA	TTCAACCTG	TAAATGGGGA	TTTTATATGC	2220
	ACTCCAGATA	ATACTGGAGT	CAACTGTACA	TTAACTTGCT	TGGAGGGCTA	TGATTTTACA	2280
	GAAGGGTCTA	CTGACAGATA	TTATTGTGCT	TATGAAGATG	CGGTCTGGAA	ACCAACATAT	2340
	ACCCTGAAT	GGCCAGACTG	TGCCAAAAAA	CGTTTTGCAA	ACCAGGGGTT	CAAGTCTCTT	2400
	GAGATGTTCT	ACAAAGCAGC	TCGTTGTGAT	GACACAGATC	TGATGAAGAA	TTTTTCTGAA	2460
	GCATTGTAGA	CGACCTTGGG	AAAAATGGTC	CCATCATTTT	GTAGTGATGC	AGAGGACATT	2520

5 GACTGCAGAC TGGAGGAGAA CCTGACCAAA AAATATTGCC TAGAATATAA TTATGACTAT 2580  
 GAAAATGGCT TTGCAATTGG ACCAGGTGGC TGGGGTGACG CTAATAGGCT GGATTACTCT 2640  
 TACGATGACT TCGTGGACAC TGTGCAAGAA ACAGCCACAA GCATCGGCAA TGCCAAGTCC 2700  
 TCACGGACTA AAAGAAGTGC CCCATTATCT GACTATAAAA TTAAGTTAAT TTTAATCATC 2760  
 10 ACAGCTAGTG TGCCATTACC CGATGAAAGA AATGATACCC TTGAATGGGA AAATCAGCAA 2820  
 CGACTCCCTC AGACATTGGA AACTATCACA AATAAAGTGA AAAGGACTCT CAACAAGAC 2880  
 CCCATGTATT CCTTTAGCT TGCAATCAGAA ATACTTATAG CCGACAGCAA TTCATTAGAA 2940  
 ACAAATAAGG CTTCCTCCCTT CTGCAGACCA GGCTCAGTGC TGAGAGGGCG TATGTGTGTC 3000  
 AATTGCCCTT TGGGAACCTA TTATAATCTG GAACATTTC CCGTGTGAAG CTGCCGGATC 3060  
 15 GGATCCTATC AAGATGAAGA AGGCAACTT GAGTGCAAGC TTTGCCCTC TGGGATGTAC 3120  
 ACGGAATATA TCCATTCAAG AAACATCTCT GATTGTAAAG CTCAGTGTAA ACAAGGCC 3180  
 TACTCATACA GTGGACTTGA GACTTGTGAA TCGTGTCCAC TGGGCACCTA TCAGCCAAAA 3240  
 TTTGGTTCCC GGAGCTGCCT CTGCTGTCCA GAAAAACCTT CAATCTGTAA AAGAGGAGCC 3300  
 GTGAACATTT CTGCATGTGG AGTCTCTTGT CCAGAAGGAA AATTCTCGCG TTCTGGGTTA 3360  
 20 ATGCCCTGTC ACCCATGTCC TCGTGAATAT TACCAACCTA ATGCAGGAA GGCTTCTGC 3420  
 CTGGCTGTC CCTTTATGG AACTACCCCA TTGCTGTTT CCAGATCCAT CACAGAATGT 3480  
 TCAACTTCAG TTCTGAATAT TACTATTTTC GGTGGATTG GGCATCTGGA GTTGTAAAT 3540  
 TGTCTTCTG AGGTTTTCCTA TGAATGCTTC TTTAACCTT GCCACAATAG TGGAACTGTC 3600  
 CAGCAACTTG GCGTGGTTA TGTGTCTCT TGTCCACTG GATATACAGG CTAAAGTGT 3660  
 25 GAAACAGACA TCGATGAGTG CAGCCCATG CCTTGCTCA ACAATGGAGT TTGTAAGAC 3720  
 CTAGTTGGGG AATTCAATTG TGAGTGCCCA TCAGGTTACA CAGGTGAGCG GTGTGAAGAA 3780  
 AATATAAATG AGTGTAGCTC CAGTCTCTGT TTAATAAAG GAATCTGTGT TGATGTTGTG 3840  
 GCTGGCTATC GTTGCAATGG TGTGAAGGAA TTTGTAGGCC TGCAATGTGA AACAGAATGC 3900  
 AATGAATGCC AGTCAAAACC ATGCTTAAAT AATGCACTCT GTGAAGACCA GGTGGGGGA 3960  
 30 TTCTTGTCGA AATGCCACC TGGATTTTGT GGTACCGAT GTGGAAGAA CGTGTATGAG 4020  
 TGTCTCAGTC AGCCATGCAA AATGGAGCT ACCTGTAAAG ACGGTGCCAA TAGCTTCAGA 4080  
 TGCTGTGTG CAGCTGGCTT CACAGGATCA CACTGTGAAT TGAACATCAA TGAATGTGAG 4140  
 TCTAATCCAT ATGTGAATGG GGCACCTGT GTGGATGAAT TAAATTCATA CAGTTGTAAA 4200  
 TGTACGCCAG GATTTTCAGG CAAAAGGTGT GAAACAGAAC AGTCTACAGG CTTTAACTGT 4260  
 35 GATTTTGAAG TTTCTGCTAT CTATGATAT GTCATGCTAG ATGGCATGCT CCCATCTCTC 4320  
 CATGCTCTAA CCTGTACCTT CTGGATGAAA TCTCTGAGC ACATGAACCTA TGGAAACCA 4380  
 ATCTCTATG CAGTTGATAA CGGCAGCGAC AATACCTTGC TCCTGACTGA TTATAACGGC 4440  
 TGGGTCTTAT ATGTGAATGG CAGGGAAGAA ATAACAACT GTCCCTCGT GAATGATGGC 4500  
 AGATGGCATC ATATTGAAT CACTTGGACA AGTGCCCAAT GCATCTGGAA AGTCTATATC 4560  
 40 GATGGGAAAT TATCTGACCG TGGTCTGGC CTCTCTGTTG GTTGGCCAT ACCTGGTGGT 4620  
 GGTGCGTTAG TCTGCGGCA AGAGCAAGAC AAAAAAGGAG AGGGATTGAG CCCAGCTGAG 4680  
 TCTTTTGTGG GCTCCATAAG CCAGCTCAAC CTCTGGGACT ATGCTCTGTC TCCACAGCAG 4740  
 GTGAAGTCA TGGCTACCTC CTGCCAGAG GAACCTCAGT AAGGAACCGT GTTAGCATGG 4800  
 CCTGATTTCT TGTGAGAAAT TGTGGGAAA GTGAAGATCG ATCTTAAGAG CATATTTTGT 4860  
 45 TCTGATTGCC CACGCTTAGG AGGTCAGTG CCTCATCTGA GAACCTGATC TGAAGATTGA 4920  
 AAGCCAGGTT CCAAAGTCAA TCTGTTCTGT GATCCAGGCT TCCAGCTGGT CCGGAACCTT 4980  
 GTGCAGTACT GTCTGAATCA AGGACAGTGG ACACAACCCAT TTCTCTACTG TGAAGCATT 5040  
 AGCTGTGGGG TCCCACTCC TTTGGGAAT GGCTTCCATT CAGCCGATGA CTTCTATGCT 5100  
 50 GGACAGCAG TAACTACCA GTGCAACAT GGCTACTATC TATTGGGTGA CTCAAGGATG 5160  
 TTCTGTACAG ATAATGGGAG CTGGAACGGC GTTTCACCAT CCTGCTTGA TGTGTATGAG 5220  
 TGTGCAATTG GATCAGATTG TAGTGAGCAT GCTTCTTGCC TGAACGTAGA TGGATCTTAC 5280  
 ATATGTTTAT GTGTCACACC GTACACAGGA GATGGGAAA ACTGTGAGA ACCTATAAAA 5340  
 TGTAAAGCTC CAGGAATCC GGAATAATGG CACTCCTCAG GTGAGATTGA TACAGTAGGC 5400  
 GCGGAGTCA CATTTCTGTG TCAGGAAGGA TACCAGTTGA TGGAGTAAAC CAAATACACA 5460  
 55 TGTTTGAGT TCTGAGAAAT GAATCATCTA ATACCATATT GTAAAGCTGT TTCTGTGGT 5520  
 AAACCGGCTA TCCAGAAAA TGGTTGCTAT GAGGAGTTAG CATTACTTTT TGGCAGCAA 5580  
 GTGACATATA GGTGTATATA AGGATATACT CTGGCCGGTG ATAAAGATC ATCTGTCTT 5640  
 GCTAACAGTT CTGGAGTCA TTCCCTCTCT GTGTGTGAAC CAGTGAAGTG TTCTAGTCCG 5700  
 GAAATATATA ATATGGAAGA ATATATTTTG AGTGGGCTTA CCTACCTTTC TACTGCATCA 5760  
 60 TATTATGCG ATACAGATA CAGCTTACAG GGCCCTTCCA TTATTGAATG CAGGCTTCT 5820  
 GGATCTGGG ACAGAGGCC ACCCTGCTGT CACCTCGTCT TCTGTGAGA ACCACTGCC 5880  
 ATCAAGATG CTGTCTATAC GGGGAATAAC TTCCTTTCA GGAACACCGT CACTTACACT 5940  
 TGCAAGAAG GCTATACTCT TGTGTCTCT GACACCATG AATGCTGGC CGACGGCAG 6000  
 TGGATGAGAA GTGACAGCA GTGCTGGCT GTCTCTGTG ATGAGCCACC CATTGTGAGC 6060  
 65 CAOGCTCTC CAGAGACTGC CATGSGCTC TTTGGAGACA TTGATTCTA CTACTGCTCT 6120  
 GATGTTTACA GCCTAGCAGA CAATCCAG CTCTCTGCA ATGCCAGGG CAAGTGGTA 6180  
 CCCCCAGAG GTCAAGACAT GCCCGTTGT ATAGCTCAT TCTGTGAAA ACCTCCATCG 6240  
 GTTCTTATA GCATCTTGA ATCTGTGAGC AAAGCAAAAT TTGCAGCTG CTCAATTGTG 6300  
 AGCTTTAAT GCATGGAAG CTTTGTACTG AACACCTCAG CAAAGATTGA ATGATGAGA 6360  
 70 GGTGGGCTG GGAACCTTC CCCCATGTC ATCCAGTGA TCCCTGTGCG GTGTGGAGAG 6420  
 CCACCAAGCA TCAATGAATG CTATGCAAGT GATCAAACT ACAGTTTGG AGCCATGGTG 6480  
 GCTTACAGCT GCAACAAGGG GTTCTATAC AAAGGGGAAA AGAAGAGCAC CTGCGAAGCC 6540  
 ACAGGGCAGT GGAGTAGTCC TATACCGAG TGCCACCCGG TATCTTGTGG TGAACCACT 6600  
 AAGGTTGAGA ATGGCTTCT GGAGCATACA ACTGGCAGGA TCTTTGAGAG TGAAGTGAGG 6660  
 75 TATCAGTGA ACCCGGCTA TAAGTCAGTC GGAAGTCTCT TAITGTCTG CCAAGCCAAT 6720  
 CGCCACTGGC ACAGTGAATC CCCTCTGATG TGTGTTCTCT TCGACTGTGG AAAACCTCCC 6780  
 CCGATCCAGA ATGGCTTCAT GAAAGAGGAA AACTTTGAAG TAGGGTCCAA GGTTCAGTTT 6840  
 TTTCTGAATG AGGTTATGA GCTTGTGGT GACAGTTCTT GGACATGTCA GAAATCTGGC 6900  
 AATGGAATA AGAAGTCAA TCCAAGTGC ATGCTGCCA AGTGGCCAGA GCGGCCCTC 6960  
 80 TTGGAACAC AGCTAGTATT AAAGGAGTTG ACCACGAGG TAGGAGTTGT GACATTTTCC 7020  
 TGTAAAGAG GGCATGCTCT GCAAGGCCCC TCTGTCTGTA AATGCTTGC ATCCAGCAA 7080  
 TGGATGACT CTTTCCCTGT TTGTAAGATT GTTCTTTGTA CCCCACCTCC CCTAATTTCC 7140  
 TTTGGTGTCC CAGTCTCTT TCTGCTCTT CATTTGGAA GTACTGTCAA GTATTCTGT 7200  
 GTAGTGGGT TTTTCTAAG AGGAAATCT ACCACCTCT GCCAACCTGA TGGCACTGG 7260  
 AGCTCTCCAC TGCCGAAATG TGTTCAGTA GAATGTCCC AACCTGAGGA AATCCCAAT 7320  
 GGAATCATG ATGTGCAAG CCTTGCCTAT CTCAGCACAG CTCTCTATAC CTGCAAGCCA 7380  
 GGCTTTGAAT TGGTGGGAAA TACTACCACC CTTTGTGGAG AAAATGGTCA CTGGCTTGA 7440  
 GGAACCAAC CATGTAAGC CATTGAGTGC CTGAAACCA AGGAGATTIT GAATGGCAA 7500  
 TTCTCTTACA CGGACCTACA CTATGGACAG ACCGTACCT ACTCTGCA CCGAGGCTTT 7560

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

```

CGGCTCGAAG GTCCAGTGC CTTGACCTGT TTAGAGACAG GTGATTGGGA TGTAGATGCC 7620
CCATCTTGCA ATGCCATCCA CTGTGATTCC CCACAACCCA TTGAAATG TTTTGTAGAA 7680
GGTGACAGATT ACAGCTATGG TGCCATAATC ATCTACAGTT GCTTCCCTGG GTTTCAGGTG 7740
GCTGGTCATG CCATGCAGAC CTGTGAAGAG TCAGGATGGT CAGTTCCAT CCCACATGT 7800
ATGCCAATAG ACTGTGGCCT CCCCTCTCAT ATAGATTTTG GAGACTGTAC TAAACTCAAA 7860
GATGACCAGG GATATTTTGA GCAAGAAGAC GACATGATGG AAGTTCCATA TGTGACTCCT 7920
CACCCCTCTT ATCATTGGG AGCAGTGGCT AAAACCTGGG AAAATACAAA GGAGTCTCCT 7980
GCTACACATT CATCAAACTT TCTGTATGGT ACCATGGTTT CATACACCTG TAATCCAGGA 8040
TATGAACCTT TGGGGAACCC TGTGCTGATC TGCCAGGAAG ATGGAACCTG GAATGGCAGT 8100
GCACCATCTT GCATTTCAAT TGAATGTGAC TTGCCTACTG CTCTGAAAA TGGCTTTTTG 8160
CGTTTACAG AGCTAGCAT GGAAGTGGT GTGCAGTATA GCTGTAAACC TGGACACATT 8220
CTAGCAGGCT CTGACTTAAG GCTTTGTCTA GAGAATAGAA AGTGGAGTGG TGCCCTCCCA 8280
CGCTGTGAAG CCATTTTCATG CAAAAAGCCA AATCCAGTCA TGAATGGATC CATCAAAGGA 8340
AGCAACTACA CATACCTGAG CACGTTGTAC TATGAGTGTG ACCCCGGATA TGTGCTGAAT 8400
GGCACTGAGA GGAGAACATG CCAGGATGAC AAAAAGTGGG ATGAGGATGA GCCCATTTGC 8460
ATTCTGTGAG AGCTCAGATG GGGAGTGGT TCAGCCAAATG GCCAGGTGAG AGGAGACGAG 8520
TACACATTCG AAAAAGAGAT TGAATACACT TGCAATGAAG GGTTCTTGCT TGAGGGAGCC 8580
AGGAGTCCGG TTTGTCTTGC CAATGGAAGT TGGAGTGGAG CCACTCCCGA CTGTGTGCCT 8640
GTCAGATGTG CCACCCCGCC ACAACTGGCC AATGGGGTGA CGGAAGGCCT GGAATATGGC 8700
TTCATGAAGG AAGTAACATT CCACCTGTAC GAGGGCTACA TCTTGACCGG TGCTCCAAAA 8760
CTACCTGTG CTACCTGATG CAACTGGGAT GCAGAGATTG CTCTCTGTAA ACCAGTCAAC 8820
TGTGGACCTC CTGAAGATCT TGCCCATGGT TTCCCTAATG GTTTTCTCTT TATTTCATGGG 8880
GGCCATCGAG TTTGTCTTGC CAATGGAAGT TGGAGTGGAG CCACTCCCGA CTGTGTGCCT 8940
TGCCCTCTCA ATGGCTCTG GAGTGGCAGC TCACCTTCTT GCCTGCCTTG CAGATGTCTC 9000
ACACCACTAA TTGAATATGG AACTGTCAAT GGGACAGATT TTGACTGTGG AAAGGCAGCC 9060
CGGATTCAGT GCTTCAAGAG CTTCAGCTC CTAGGACTTT CTGAATCAC CTGTGAAGCC 9120
GATGGCCAGT GGAGCTCTGG GTTCCCCAC TGTAACACA CTCTCTGTGG TTCTCTTCCA 9180
ATGATACCAA ATGCGTTTCA CTGTGAGACC AGCTCTTGGG AGGAAAATGT GATAACTTAC 9240
AGCTGCAGGT CTGATATGT CATACAAGGC AGTTCAGATC TGATTGTATC AGAGAAAGGG 9300
GTATGGAGCC AGCCTTATCC AGTCTGTGAG CCCTTGTCCT GTGGGTCCCG ACCGTCTGTC 9360
GCCAATGCAG TGGCAACTGG AGAGGCACAC ACCTATGAAA GTGAAGTGAA ACTCAGATGT 9420
CTGGAAGGTT ATACGATGGA TACAGATACA GATACATTCA CCTGTGAGAA AGATGGTCGC 9480
TGGTTCCCTG AGGAATCTC CTGCAGTCTT AAAAATGTGC CTCTCCCGGA AAACATAACA 9540
CATATACTTG TACATGGGGA CGATTTTCA GTGAATAGGC AAGTTTCTGT GTCATGTGCA 9600
GAAGGGTATA CCTTTGAGGG AGTTAACATA TCAGTATGTC AGCTTGATGG AACCTGGGAG 9660
CCACCATCTT CCGATGAATC TTGCAGTCCA GTTCTTGTG GGAACCTGA AAGTCCAGAA 9720
CATGGATTGG TGGTTGGCAG TAAATACACC TTGAAAGCA CAATTATTTA TCAGTGTGAG 9780
CTGCTCTGAA AGGAGTATG GAACAGGGAA CGTGTCTGCC AGGAGAACAG ACAGTGGAGT 9840
GGAGGGGTGG CAATATGCAA AGAGACCAGG TGTGAACTC CACTTGAAAT TCTCAATGGG 9900
AAAGCTGACA TTGAAAACAG GACGACTGGA CCCAAGCTGG TATATTCTCG CAACAGAGGC 9960
TACAGTCTTG AAGGGCCATC TGAGGCACAC TGACAGAAA ATGGAACCTG GAGCCACCCA 10020
GTCCCTCTCT GCAAAACAAA TCCATGCCCT GTTCTTTTGG TGAATCCCGA GAATGTCTCTG 10080
CTGTCTGAAA AGGAGTATTTA TGTGATCAG AATGTGTCCA TCAAATGTAG GGAAGGTTTT 10140
CTGCTGCAGG GCCACGGCAT CATTACCTGC AACCCCGACG AGACGTGGAC ACAGACAAGC 10200
GCCAATGTG AAAAATCTC ATGTGGTCCA CCAGCTCAGG TAGAAAATGC AATTGCTCGA 10260
GGCGTACATT ATCAATATGG AGACATGATC ACCTACTCAT GTTACAGTGG ATACATGTTG 10320
GAGGGTTTCC TGAGAGTGTG TTGTTTAGAA AATGGAACAT GGACATCACC TCCTATTTCG 10380
AGAGCTGTAT ACATATGACG CATCGTGTCC CTGAGCGAGA CCGCCCAATG TGGTCCCCCC 10440
TCCGTCCAG AGGGCTGGAT GGGCGGCTC TGTGAAGAAC CAATCTGCAT TCTTCCCTGT 10500
CTGAACGGAG GTGCGTGTGT GGGCCCTTAC CAGTGTGACT GCCCGCTTGG CTGGACGGGG 10560
TCTCGCTGTC ATACAGCTGT TTGCCAGTCT CCTGCTTAA ATGGTGGAAA ATGTGTAAGA 10620
CCAAACCGAT GTCACTGTCT TTCTTCTTGG ACGGGACATA ACTGTTCCAG GTAA 10674

```

Seq ID NO: C135 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..390

60  
65

```

1 11 21 31 41 51
| | | | |
ATGAGGTTCA GTGTCTCAGG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT 60
TATGTGTGAG TCTGTCTCCT CCTCTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGGTCA 120
GAACCATGCG TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTGGAG 180
CAGTGTCTGT ACATATGACG CATCGTGTCC CTGAGCGAGA CCGCCCAATG TGGTCCCCCC 240
TGCACTTCTT GGCCTGTCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAAGCAT 300
TTTGTGTGTA AGCTGAAGGT TCAGGGTGTG AATTCCAGT GCCACTATC TCCATCTCC 360
AGTAAATGTG AAAGAGGCCG GATATGTTAG

```

Seq ID NO: C136 DNA Sequence  
Nucleic Acid Accession #: BC035671.1  
Coding sequence: 126..1745

75  
80

```

1 11 21 31 41 51
| | | | |
GGCAGCGACT GCGCCCCGTC CCGGCGCGCG GCTCGTCTCG AGAGGAGGCG GCCCGGCCG 60
GGCAGCTGCG GCTCGGATC CGTCGAGGGG AGGCGGAGCT TGCCAGCTG GCGCCGACG 120
GGGTCTATGT GCCCGGCGCC CGCGCGCGCG GCGCACTGGC GCGGGCTGCC GGGCGGGGCC 180
TCTGGCTTGT GCTGCTCGCG GTCTCCGCCC CGCTCCGCGT GCAGGCGGAG GAGCTGGGTG 240
ATGGCTGTGG ACACCTAGTG ACTTATCAGG ATAGTGGCAC AATGACATCT AAGAATTATC 300
CCGGGACCTA CCCCAATCAC ACTGTTTGGG AAAAGACAAT TACAGTACCA AAGGGGAAAA 360
GACTGATTCT GAGGTGGGA GATTGGGATA TGAATCCCA GACCTGTGCT TCTGACTATC 420
TTCTCTTTC CAGCTCTTCA GATCAATATG GTCCATCTG TGAAGTATG ACTGTTCCCA 480
AAGAACTCTE GTTGAACACA AGTGAAGTAA CCGTCCGCTT TGAGAGTGA TCCACATTT 540
CTGGCCGGGG TTTTGTGCTG ACCTATGCGA GCAGCGACCA TCCAGATTTA ATAACATGTT 600

```

5  
10  
15  
20  
25

```

TGGAACGAGC TAGCCATTAT TTGAAGACAG AATACAGCAA ATTCGCCCCA GCTGGTTGTA 660
GAGACGTAGC AGGAGACATT TCTGGGAATA TGGTAGATGG ATATAGAGAT ACCTCTTTAT 720
TGTGCAAGC TGCCATCCAT GCAGGAATAA TTGCTGATGA ACTAGTGGC CAGATCAGTG 780
TGCTTCAGCG CAAAGGGATC AGTCGATATG AAGGGATTCT GGCATAGGT GTTCTTTCGA 840
GGGATGGTTC CCTGTCAGAC AAGCGATTTC TGTTTACCTC CAATGGTTGC AGCAGATCCT 900
TGAGTTTGA ACCTGACGGG CAAATCAGAG CTTCCTCTC ATGGCAGTCG GTCAATGAGA 960
GTGGAGACCA AGTTCACCTG TCTCCTGGCC AAGCCCGACT TCAGGACCAA GGCCCATCAT 1020
GGGCTTGGG CGACAGTAGC AACAAACACA AACCAAGAGA GTGGCTGGAG ATCGATTGGS 1080
GGGAGAAAAA GAAATAACA GGAATTAGGA CCACAGGATC TACACAGTCG AACTTCAACT 1140
TTTATGTTAA GAGTTTTGTG ATGAACCTCA AAAACAATAA TTCTAAGTGG AAGACCTATA 1200
AAGGAATTGT GAATAATGAA GAAAGGTGTG TTCAGGGTAA CTCTAACITT CGGGACCCAG 1260
TGCAAAACAA TTTTCATCCT CCATCGTGG CCAGATATGT GCGGGTTGTC CCCAGACAT 1320
GGCACCAGAG GATAGCCTTG AAGGTGGAGC TCATTGGTTG CCAGATTACA CAAGGTAATG 1380
ATTCAATGGT GTGGCGCAAG ACAAGTCAAA GCACCAAGTG TTCAACTAAG AAGAAGATG 1440
AGACAATCAC AAGGCCCATC CCCTCGAAG AACATCCAC AGGAATAAAC ATTACAACGG 1500
TGGCTATTTC ATTTGTTGCTC CTGTTGTGCC TGGTGTGTC TGGAAATGGG ATCTTTGCAG 1560
CCTTTAGAAA GAAGAGAGAG AAAGGAAGTC CGTATGGATC AGCAGAGGCT CAGAAAACAG 1620
ACTGTGAGAA CGAGATTAAA TATCCCTTTG CCAGACATCA CTCAGCTGAG TTTACCATCA 1680
GCTATGATAA TGAGAGAGAG ATGACACAAA AGTTAGATCT CATCACAAGT GATATGSCAG 1740
GTAACTCCG TTGACTGCCA AAATAGCATC CCCAACGTGC AGCCCTCCGC ATCTATCAGC 1800
AGGTTGCCCC GGATGATGATC CAGAGATGAG GATCGGAACA CCAATGTTCT TCCCACCCTA 1860
ACAACAACAA AGGGCAGTAA ATTAAAGTAC TCCTTGTAAG GTACAGTTAC CGATTAATCT 1920
AGAGATAAAA TATTTTCTTA AAAATATATT TCATTAAACA CCTATGCTGT CTCTATAAAA 1980
AAAAAATAAA AAAAAATAAA AAAAAATAAA 2040

```

Seq ID NO: C137 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1761

30  
35  
40  
45  
50  
55  
60

```

1 11 21 31 41 51
| | | | |
ATGGGATTGG GTGCGGGGCA GCGACTGCGC CCGGTCCCGG GCGCGGCTC GTCCGCAGAG 60
GAGGCGGCCC GGCCCGGGCA GCTGCGGCTC GGGATCCGTC GAGGGGAGGC CGAGCTTGCC 120
AAGCTGGGCG CCAGCGGGGT CATGGTGCCC GCGCGCCGCG GCGCGGCGCG ACTGGCGCGG 180
GCTGCGGGGC GGGGCTCCTC GGCCTTGCTG CTCGCGGTCT CCGCCCGGCT CCGGCTGCAG 240
GCGAGGAGAG TGGGTGATGG CTGTGGACAC CTAGTGACTT ATCAGGATAG TGGCACAAATG 300
ACATCTAAGA ATTATCCCGG GACCTACCCC AATCACAATG TTTGCGAAAA GACAATTACA 360
GTACCAAGGG GGAAGAAGAG GATTCTGAGG TTGGGAGATT TGGATATCGA ATCCAGAGCC 420
TGTGCTTCTG ACTATCTTCT CTTCACCAGC TCTTCAGATC AATATGGTCC ATACTGTGAG 480
AGTATGACTG TTCCCAAGA ACTCTTGTG AACACAAGTG AAGTAACCGT CCGCTTTGAG 540
AGTGGATCCC ACATTTCTGG CCGGGGTTTT TTGCTGACCT ATGCGAGCAG CGACCATCCA 600
GATTTAATAA CATGTTTGA ACGAGCTAGC CATTATTTGA AGACAGAATA CAGCAAAATC 660
TGCCCAAGGG GTGTAGAGA CGTAGCAGGA GACATTTCTG GGAATATGGT AGATGGATAT 720
AGAGATAACT CTTTATTGTC CAAAGCTGCC ATCCATGCAG GAATAATTGC TGATGAACCTA 780
GATGGCCAGA TCAGTGTGCT TCAGCGCAAA GGGATCAGTC GATATGAAGG GATTCTGGCC 840
AATGGTGTTC TTTCGAGGGA TGGTTCCTGT TCAGACAAGC GATTCTGTGT TACCTCCAAT 900
GGTTGCGACA GATCCTTGAG TTTTGAACCT GACGGGCAAA TCAGAGCTTC TTCTCATAGG 960
CAGTCGGTCA ATGAGAGTGG AGACCAAGTT CACTGGTCTC CTGGCCAAAG CCGACTTCAG 1020
GACCAAGGCC CATCATGGGC TTCGGGCGAC AGTAGCAACA ACCACAAACC ACGAGAGTGG 1080
CTGGAGATCG ATTTGGGGGA GAAAAAGAAA ATAACAGGAA TTAGSACCAC AGGATCTACA 1140
CAGTCGAAGT TCACTTTTGA TGTTAAGAGT TTTGTGATGA ACTTCAAAAA CAATAATTCT 1200
AAGTGAAGA CCTATAAAGG AATTGTGAAT AATGAAGAAA AGGTGTTTCA GGGTAACCTC 1260
AAGTTTCGGG ACCCAGTGCA AAACAATTTC ATCCCTCCCA TCGTGCCGAC ATATGTGCGG 1320
GTTGTCCCCC AGACATGGCA CCAGAGGATA GCCTTGAAGG TGGAGCTCAT TGGTTGCCAG 1380
ATTACCAAG GTAATGATT ATTGGTGTGG CGCAAGACAA GTCAAGCAGC CAGTGTTCAT 1440
ACTAAGAAAG AAGATGAGAC AATCACAAGG CCCATCCCTC CGAAGAAAC ATCCACAGGA 1500
ATAAACATTA CAACGGTGGC TATTCATATG GTGCTCCTTG TTGCTCTGGT GTTTGCTGGA 1560
ATGGGAGTGG ACATTCCTGT TAGAAAGAAG AAGAAGAAAG GAAGTCCGTA TGGATCAGCA 1620
GAGGCTCAGA AAACAGACTG TTGGAAGCAG ATTAAATATC CCTTTGCCAG ACATCAGTCA 1680
GCTGAGTTTA CCATCAGCTA TGATAATGAG AAGGAGATGA CACAAAAGTT AGATCTCATC 1740
ACAAGTGATA TGGCAGGTTA A 1761

```

Seq ID NO: C138 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2310

65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ATGTTCCAGC GGCAGGAAAG ATTTCTTGAC TTATCTTCAG CTGAAGCAGT GGCAGCTTGG 60
ATATTACATC AACATCCTGA CATTATTAAC AAAGGTGATG GCTGTGGACA CCTAGTGACT 120
TATCAGGATA GTGGCACAAT GACATCTAAG AATTATCCCG GGACCTACCC CAATCAGACT 180
GTTTGCAGAA AGACAATTAC AGTACCAAGG GGGAAAAGAC TGATTCTGAG GTTGGGAGAT 240
TTGGATATCG AATCCAGAC CTGTGCTTCT GACTATCTTC TCTTCACCAG CTCTTCAGAT 300
CAATATGGAA TGCAGAGGGA GGAGGAGACA GAAGTGCTTT GTCTTTTCACT GGCCTGGGCT 360
CAGAGAGTGG ACATTCCTGT GCAGCTGTGG CCCAGCTTCC TGGAAAGGTTG GAAGGTCAT 420
GCTGATGCAA GAGGTCCATA CTGTGGAGT ATGACTGTTC CCAAGAACT CTGTGTGAAC 480
ACAAGTGAAG TAACCGTCCG CTTTGAGAGT GGATCCACCA TTTCTGGCCG GGGTTTTTTG 540
CTGACCTATG CGAGCAGOGA CCATCCAGAT TTAATAACAT GTTTGGAACG AGCTAGCCAT 600
TATTTGAAGA CAGAATACAG CAAATTCTGC CCAGCTGGTT GTAGAGACGT AGCAGGAGAC 660
ATTTCTGGGA ACATTTGTGA TGGATATAGA GATACCTCTT TATTTGTCAA AGCTGCCATC 720
CATGCAGGAA TAATGTCTGA TGAACTAGGT GGCCAGATCA GTGTGCTTCA GCGCAAGAGG 780
ATCAGTCCAT ATGAAGGGAT TCTGGCCAAT GGTGTCTTTT CGAGGGATGG TTCCCTGTCA 840
GACAAAGCAT TTCTGTTTAC CTCCAATGGT TGCAGCAGAT CCTTGAGTTT TGAACCTGAC 900
GGGCAAAATCA GAGCTTCTTC CTCATGGCAG TCGGTCAATG AGAGTGGAGA CCAAGTTTCA 960

```

5  
10  
15  
20  
25

TGGTCTCCTG GCCAAGCCCG ACTTCAGGAC CAAGGCCCAT CATGGGCTTC GGGCGACAGT 1020  
AGCAACCAACC ACAAAACACG AGAGTGGCTG GAGATCGATT TGGGGGAGAA AAAGAAAATA 1080  
ACAGGAATTA GGACCAACAG ATCTACACAG TCGAACTTCA ACTTTTATGT TAAGAGTTTT 1140  
GTGATGAATC TCAAAAACAA TAATTCTAAG TGGAAAGACCT ATAAAGGAAT TGTGAATAAT 1200  
GAAGAAAAGG TGTTTCAGGG TAACTCTAAC TTTGGGGACC CAGTGC AAAA CAATTTTCATC 1260  
CCTCCCATCG TGGCCAGATA TGTGCGGGTT GTCCCCCAGA CATGGCACCA GAGGATAGCC 1320  
TTGAAGGTGG AGCTCATTTG TTGCCAGATT ACACAAGGTA ATGATTTCATT GGTGTGGGCG 1380  
AAGACAAGTC AAGCACCCAG TGTTC AACT AAGAAAGAAG ATGAGACAAT CACAAGGCC 1440  
ATCCCCTCGG AAGAAACATC CACAGATGCC ATGCCAGTGC AGATTGTCCG AGACCATACC 1500  
CAGATGATCT CACAAAGGGA GAATCTGGGA CCTGATGAGG GCMAAATACC TTTTAAAGGC 1560  
ACAGCGGAAA GCATGGTTAG AGTAGTGT TT GCTGTGTGG TTAATGACCT TGGCATGCTG 1620  
TTCTTAGCAC ACACACCTGA GGAGGACATT GATCACTACT GTTGGAAACA GATTAAATAT 1680  
CCCTTTGCCA GACATCAGTC AGCTGAGTTT ACCATCAGCT ATGATAATGA GAAGGAGATG 1740  
ACACAAAAGT TAGATCTCAT CACAAGTGAT ATGCCAGATT ACCAGCAGCC CCTCATGATT 1800  
GGCACCCGGA CAGTCACGAG GAAGGGCTCC ACCTTCGGC CCATGGACAC GGATGCCGAG 1860  
GAGGCAGGGG TGAGCACCGA TGCGGGGGC CACTATGACT GCCCGCAGGG GCCCGGCCGC 1920  
CAGGAGTAGC CGCTGCCCTT GGCGCCCCCG GAGCCGAGT ACGCCACGCC CATCGTGGAG 1980  
CGGCAGGTGC TGCGCGCCCA CACGTTCTCT GCGCAGAGCG GCTACCGCGT CCCAGGGCCC 2040  
CAGCCCGGCC ACAAACTCT CCTCTCTCTG GGCGCTTCT CCCCCTAGC GGGTGTGGGC 2100  
GCCCAGGACG GAGACTATCA AAGGCCACAC AGCGCACAGC CTGCGGACAG GGGCTACGAC 2160  
CGGCCCAAAG CTGTCAAGCG CCTCGCCACC GAAAGCGGGC ACCCTGACTC TCAGAAGCCC 2220  
CCAAACGATC CCGGACGAG TGACAGTAT TCTGCCCCCA GAGACTGCCT CACACCCCTC 2280  
AACCAGACGG CCATGACTGC CCTTTGTGA 2310

Seq ID NO: C139 DNA Sequence  
Nucleic Acid Accession #: NM\_004616.2  
Coding sequence: 180..893

30  
35  
40  
45  
50

1 11 21 31 41 51  
AGTGCCCCAG GAGCTATGAC AAGCAAAGGA ACATACTTGC CTGGAGATAG CCTTTGCGAT 60  
ATTTAAATGT CCGTGGATAC AGAAATCTCT GCAGGCAAGT TGCTCCAGAG CATATTGCAG 120  
GACAAAGCTG TAACGAATAG TTAATTCAC GGCACTCTGA TTCTTAATCC TTTTCCGAAA 180  
TGGCAGGTGT GAGTGCCCTG ATAAATATT CTATGTTTAC CTCAACTTC TTGTTCTGGC 240  
TATGTGGTAT CTGATCTCTA GCATTAGCAA TATGGGTACG AGTAAGCAAT GACTCTCAAG 300  
CAATTTTGG TCTGAAGAT GTAGGCTCTA GCTCTACGT TGCTGTGGAC ATATTGATTG 360  
CTGTAGGTGC CATCATCATG ATTCTGGGCT TCTCTGGATG CTGCGTGCT ATAAAAGAAA 420  
GTGCTGTCAT GCTTCTGTGT TTTTTCATAG GCTTCTTCT GATCCTGCTC CTGCAAGTGG 480  
CGACAGGTAT CCTAGGAGCT GTTTTCAAAT CTAAGTCTGA TCGATTGTG AATGAACTC 540  
TCTATGAAAA CACAAGCTT TTGAGCGCCA CAGGGGAAAG TGAAAAACAA TTCCAGGAAG 600  
CCATAATTGT GTTTCAGAAA GAGTTTAAAT GCTCGGTTT GGTCAATGGA GCTGCTGATT 660  
GGGGAATATA TTTTCAACAC TATCCTGAAT TATGTGCCCT TCTAGATAAG CAGAGACCAT 720  
GCCAAGCTA TAATGGAAAA CAAAGTTTACA AAGAGACCTG TATTTCTTTC ATAAAAGACT 780  
TCTTGGCAAA AAATTTGATT ATAGTTATTG GAATATCAT TGGACTGGCA GTTATTGAGA 840  
TACTGGGTTT GGTGTTTCT ATGTCCTGT ATTGCCAGAT CGGGAACAAA TGAATCTGTG 900  
GATGATCAAA CCTATCGTCA GTCAAAACCC TTTAAATGT TGCTTTGGCT TTGTAAATTT 960  
AAATATGTAA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TAAATATGTC TCGGCTAGCT 1020  
AGACCACAGA TATCTTCTAG ACATATTGAA CACATTTAAG ATTTGAGGGA TATAAGGGA 1080  
AATGATATGA ATGTGTATTT TTAATCAAAA TAAAGTAAC TGTTTACGTT AAAAAAATA 1140  
AAAAAATAA 1159

Seq ID NO: C140 DNA Sequence  
Nucleic Acid Accession #: NM\_004617.2  
Coding sequence: 232..840

55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
CTTCAGGTCA GGGAGAATGT ATAAATGTCC ATTGCCATCG AGGTTCTGCT ATTTTGTAGA 60  
AGCTGAAGCA ACTCCAAGGA CACAGTTCAC AGAAATTTGG TTCTCAGCCC CAAATACTG 120  
ATTGAATTGG AGACAATTAC AAGGACTCTC TGGCCAAAAA CCTTGAAGA GGCCCGTGA 180  
AGGAGGCAGT GAGGAGCTTT TGATTGCTGA CCTGTGTCGT ACCACCCAG AATGTGCACT 240  
GGGGGCTGTG CCAGATGCCCT GGGGGGGACC CTCATTCCCC TTGCTTTTIT TGGCTTCTG 300  
GCTAACATCC TGTTATTTT TCTGGAGGA AAAGTGATAG ATGACAACGA CCACCTTTCC 360  
CAAGAGATCT GGTTTTTCGG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTCCCTGCG 420  
CTGGTGTCT TGCGCCTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCAA CGAGGGCTGT 480  
GGGAAGCGAT TTGCGATGTT CACCTCCAGC ATATTGCTG TGTTGGATT CTGGGAGCT 540  
GGATACTCGT TTATCATCTC AGCCATTTC AACAACAAGG GTCTTAAATG CCTCATGGCC 600  
AATAGTACAT GGGGCTACCC CTTCACGAC GGGGATTATC TCAATGATGA GGCCTTATGG 660  
AACAAAGTGC GAGAGCCTCT CAATGTGGTT CCTTGGAAATC TGACCTCTT CTCCATCCTG 720  
CTGGTGTAG GAGGAATCCA GATGGTTCTC TGCGCCATCC AGGTGGTCAA TGGCCTCCTG 780  
GGGACCTCT GTGGGACTG CCAAGTGTGT GGCTGCTGTG GGGAGATGG ACCCGTTTAA 840  
ACCTCCGAGA TGAGTGCTC AGACTCTACA GCATGACGAC TACATTTCT TTTCAATAAA 900  
CTTCTCTCT TCTTGAATTT ATTAATTCCT ATCTGCTTCC TAGCTGATAA AGCTTAGAAA 960  
AGGCAGTTAT TCTTCTTTC CAACAGCCTT TGCTCGAGTT AGAATTTGT TATTTTCAA 1020  
TAAAAATAG TTTGGCCACT TAACAAATTT GATTATATAA TCTTCAAAT TAGTTCCTTT 1080  
TTAGAAATTA CCAACAGGT CAAAGCATAC TTTTCATGAT TTTTATTA CAAATGTAAA 1140  
ATGTATAAAG TCACATGATC TGCCATACTA CTCTTTGTA TATAAGATG TTTATATCTT 1200  
TGGAAAGTTT ACATAAATCA AAGGAAGAAA GCACATTAA AATGAGAAAC TAAGACCAAT 1260  
TTCTGTTTTT AAGAGGAAAA AGAATGATTG ATGTATCCTA AGTATTGTTA TTTGTTGTCT 1320  
TTTTTGTCTG CTTGTCTTGA GTTGCTTGTG ACTGATCTT TGAGGCTGTC ATCATGGCTA 1380  
GGGTCTTTTT ATGTATGTTA AATTAATAAC TGAATTCAGA GGTAACTG 1428

Seq ID NO: C141 DNA Sequence  
Nucleic Acid Accession #: NM\_002381.2

Coding sequence: 64..1524

```
1      11      21      31      41      51
5  AAATCCGAGC CTGCGGTGGG CTCCTGGCCC CCGAOGGACA CCACCAGGCC CACGGAGCCC 60
  ACCATGCGCG GCCCGGCCCG CGCGCGCGCG CTCCTGGGAC TCCTCTGCTG GCTCTGGCCG 120
  CTGCTGCTGC TGCCCTCCGC CGCCCCCGAC CCGTGGGCCG GCGCGGCTT CCGGAGGCTG 180
  GAGACCGGAG GTCCCGGGGG CAGCCCTGGA CGCGCCCGCT CTCCTGCGGC TCCCGACGGC 240
  GCGCCGCTT CGGGACACG CGAGCCTGGC CGCGCCCGCG GTGCAGGTGT TTGCAAGAGC 300
10 AGACCCCTGG ACCTGGTGT TATCATTGAT AGTTCTCGTA GCGTACGGCC CTTGGAATTC 360
  ACCAAGTGA AAACCTTTGT CTCCTGGATA ATCGACACTC TGGACATTGG GCCAGCCGAC 420
  ACGCGGGTGG CAGTGGTGAA CTATGCTAGC ACTGTGAAGA TCGAGTTCCA ACTCCAGGCC 480
  TACACAGATA AGCAGTCCCT GAAGCAGGCT GTGGGTGAA TCACACCCCT GTCAACAGGC 540
  ACCATGTGAG GCTAGCCAT CCAGACGACA ATGGACGAG CCTTCACAGT GGAGGCGAGG 600
15 GCTCGAGAGC CCTCTTCTAA CATCCCTAAG GTGCCATCA TTGTTACAGA TGGGAGGCC 660
  CAGGACCAAG TGAATGAAGT GCGGCTCGG GCCCAAGCAT CTGGTATTGA GCTCTATGCT 720
  GTGGGCGTGG ACCGGGCGAG CATGGCGTCC CTCAGATGA TGGCCAGTGA GCCCTTAGAG 780
  GAGCATGTTT TCTACGTGGA GACCTATGGG GTCAATTGAG AACTTTCCTC TAGATTCCAG 840
  GAAACCTTCT GTGCGCTGGA CCCCTGTGTG CTTGGAACAC ACCAGTGCCA GCACGTCTGC 900
20 ATCAGTGATG GGAAGGCGAA GCACCACTGT GAGTGTAGCC AAGGATACAC CTTGAATGCC 960
  GACAAGAAAA CGTGTTCAGC TCTTGATAGG TGTGCTCTTA ACACCCACGG ATGTGAGCAC 1020
  ATCTGTGTA ATGACAGAGG TGGCTCTTAT CATTTGTAGT GCTATGAAGG TTATACCTTG 1080
  AATGAAGACA AGCAAACTTG TTCAGCTCAA GATAAATGTG CTTTGGGTAC CCATGGGTGT 1140
  CAGCACATTT GTGTGAATGA CAGAACAGGG TCCCATCAT GTGAATGCTA TGAGGGCTAC 1200
25 ACTCTGAATG CAGATAAAAA AACATGTTCA GTCCGTGACA AGTGTGCCCT AGGCTCTCAT 1260
  GGTGCGCAGC ACATTTGTGT GAGTGTAGGG GCGCATCCT ACCACTGTGA TTGCTATCCT 1320
  GGTACACCTT TAAATGAGGA CAAGAAAAACA TGTTCAGCCA CTGAGGAAGC ACGAAGACTT 1380
  GTTTCACCTG AAGATGCTTG TGGATGTGAA GCTACACTGG CATTCCAGGA CAAGGTGAGC 1440
  TCGTATCTTC AAGACTGAA CACTAACTT GATGACATT TGGAGAAGT GAAATATAAT 1500
30 GAATATGGAC AAATACATCG TTAATTTGCT CCAATTTCTC ACCTGAAAT GTGGACAGCT 1560
  TGGTGTACTT AATACTCATG CATCTTTTG CACACCTGTT ATTGCCAATG TTCCTGCTAA 1620
  TAATTTGCCA TTATCTGTAT TAATGCTTGA ATATTACTGG ATAAATTTGA TGAAGATCTT 1680
  CTGCAAGATC AGCAAACTTG TTCCAAGGAA ATACATATGC AGATACTTAT TAAGAGCAAA 1740
  CTTTAGTGTC TCTAAGTTAT GACTGTGAAA TGATTGGTAG GAAATAGAAT GAAAGTTTA 1800
35 GTGTTCTTT ATCTACTAAT TGAGCCATTI AATTTTAA TGTTTATATT AGATAACCAT 1860
  ATTCACAATG GAAACTTTAG GCTAGTTTC TTTTGATAGT ATTTATAATA TAAATCAATC 1920
  TTATCTGTA GAGTGCAAAAT TGTACAAGGT ATTTACACAT ACNACTTCAT ATAAGTGA 1980
  TGAATGTAAT TTTGAACCTG TTAACACTTT TGTTTTTTGT CTTATTTTGT TGGAGTATTA 2040
  TTGAAGATGT GATCAATAGA TTGAATACA CATATCTAAA AATAGTTAAC ACAGATCAAG 2100
40 TGAACATTAC ATTGCCATTI TTAATTCATT CTGGTCTTTG AAGAAATGT ACTACTAAG 2160
  AGCACTAGTT GTGAATTTAG GGTGTTAAAC TTTTACCACA GTACAAAAT CCCAAATTCA 2220
  CTTATATTAT TTGCTTCAGG ATCCAAGTGA CAAAGTTATA TATTTATAAA ATTGCTATAA 2280
  ATCGACAAA TCTAATGTTG TCTTTTAAAT GTTAGTGATC CACCTGCCTC AGCCTCCCAA 2340
  AGTGCTGGGA TTACAGGCTT GAAAGTCAA CTTTTTTTA CTTATATATT TGATACATAT 2400
45 AATTCCTTTG GCTTTGAAAC TTGCAACTT GAGAACAAA CAGTCTTTTA AATTTTGAC 2460
  TGCTCAATTC TGTTTTCGT TTGATTGTC TTTAATATAA TAAAGTTAT TACCTTTACA 2520
  TATTATCATG TCTATTTTG ATGACTCATC AATTTTGCT ATTAAGATA TTTCTTTAAA 2580
  TTAACAAAAA AAAAAAAA 2599
```

Seq ID NO: C142 DNA Sequence  
Nucleic Acid Accession #: NM\_016639.1  
Coding sequence: 40..429

```
1      11      21      31      41      51
55 GCGGCGGCG CAGACAGCG CGGGCGCAGG ACGTGCACTA TGGCTGGGG CTGCTGCGC 60
  CGGTTGCTGC GGCTCTCTGT GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCGCGG 120
  GAGCAAGCGC CAGGCAACGC CCCCTGCTCC CGCGCGAGCT CTTGGAGCGC GGACCTGGAC 180
  AAGTGCAATG ACTGCGCGT TTGCAAGGCG CGACCGCACA GCGACTTCTG CTTGGGCTGC 240
  GCTGCAGCAC CTCCTGCCCC CTTCCGGCTG CTTTGGCCCA TCCTTGGGG CGCTCTGAGC 300
  CTGACCTTCG TGCTGGGGCT GCTTCTGCGC TTTTGGTCT GGAGACGATG CGCGAGGAGA 360
  GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGCGAGAGG GCTGCCAGC TGTGGCGCTG 420
  ATCAGTGAC AATGTGCCCC CTGCCAGCG GGGCTGCGCC ACTCATCAT CATTTCATCA 480
65 TTCTAGAGCC AATGCTGCGC TCCAGAGCG GCGGGGAGCC AAGTCTCTCC AACCACAAG 540
  GGGGTGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
  AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
  ACACAAACAG TGACACTGAC TAAGGAACTG CAGCATTGCG ACAGGGGAGG GGGGTGCCCT 720
  CCTTCTTAG GACCTGGGG CAGGCTGAC TTGGGGGCA GACTTGACAC TAGGCCCCAC 780
70 TCACTCAGAT GTCTGAAAT TCCACCAOG GGTTCACCT GGGGGTTAG GGACCTATT 840
  TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCAACTC 900
  CCCAAGCGG GAGGAGATA TTTATTTGG GAGAGTTTG GAGGGGAGG AGAATTTATT 960
  AATAAAGAAA TCTTTAATTT TAAAAAAA AAAAAAAA 998
```

Seq ID NO: C143 DNA Sequence  
Nucleic Acid Accession #: NM\_001819  
Coding sequence: 113..2146

```
1      11      21      31      41      51
80 CCAGGAGGCA CGCTGGTTTT CCGGGGCGCG TCCATCGCGC CTTCTCTCTG CGCTGCTT 60
  CTCGGTCCA GCGCCATCT TCCTTTCCGC ACAGGGGCGG CCGAGCGGG CCATGCAGCC 120
  AACGCTGCTT CTAGCCTCC TGGAGCGGT GGGGCTGGCG GCTGTCAATT CCATGCCAGT 180
  GGATAACAGG AACACAATG AAGGAATGTT GACTCGCTGC ATCATGAGG TCCTCTCAAA 240
```

5  
10  
15  
20  
25  
30  
35  
40

```

TGCCTTGTG AAGTCCAGCG CTCCACCCAT CACCCCTGAG TGCCGCCAAG TCCTGAAGAC 300
GAGTAGAAAA GACGTCAAAG ACAGAGAGAC AACTGAAAAA GAAAAACAA AGTTTGAAGT 360
AAGATTGTTA AGAGACCCAG CTGATGCCTC GGAAGCCAC GAGTCCTCCA GCAGGGGAGA 420
GGCAGGAGCC CCAGGGGAGG AGGACATCCA AGGCCCAACA AAGGCAGACA CAGAGAAATG 480
GCCAGAGGGA GCGGGGCACA GCGAGAGCG AGCGGATGAG CCCAGTGA GCCTCTATCC 540
CTCCGACAGC CAACTCTCTG AAGAAGTGAA GACAGGCCAT TCTGAGAAGA GCCAGAGAGA 600
GGATGAGAGG GAGGAGGAGG GAGAGAACTA TCAAAAAGGG GAGCGAGGGG AAGATAGCAG 660
TGAAGAGAAA CACCTTGAAG AGCCAGGAGA GACACAAAAC GCTTTTCTCA ATGAAAGAAA 720
GCAGGCTTCA GCTATAAAAA AAGAGGAGTT AGTGCCAGA TCGGAAACAC ATGCTGCCGG 780
GCATTCTCAG GAGAAGACAC ATAGCCGAGA GAAGAGTAGC CAGGAGAGTG GAGAGGAGGC 840
AGGGAGCCAG GAGAATCACC CCCAGGAGTC TAAAGGCCAA CCCGAGGCC AGGAAGAATC 900
TGAGGAAGGT GAGGAAGATG CCACCTCTGA GGTGACAAA CGACGCACGA GGCCAGACA 960
CCACCAGGG AGGAGCAGGC CGACAGGTC CTCTCAAGGA GGGAGTCTTC CCTCTGAGGA 1020
AAGGGACAC CCCAGGAGG AATCTGAGGA GTCAAAAGTC AGCATGGCCA GTTAGGGGA 1080
AAGAGGGAC CACATTCAA CCCACTACAG GCCTTCAGAG GAAGAACCTG AATATGAGA 1140
AGAAATAAAG GGTATCCAG GGTGCCAGGC CCCTGAGGAC CTGGAGTGGG AGCGCTATAG 1200
GGGCAGAGG AGTGAAGAAAT ACAGGGCTCC AAGACCTCAG AGTGAGGAGA GTTGGGATGA 1260
GGAGGACAG AGAAACTACC CCAGCTTAGA GCTTGATAAG ATGGCAGATG GATATGGTGA 1320
AGAAAGTGAG GAAGAGAGGG GCCTTGAGCC GGGAAAGGGA CGCATCACA GAGGCAGGGG 1380
AGGGGAGCCA CGTGCCTATT TCATGTCTGA CACCAGAGAA GAGAAAGGT TCTTGGGTGA 1440
AGGACACCCAG CGTGTCAGG AAAACAGAGT GGACAAAGGA AGGAGGCATC CACAAGGTGC 1500
GTGGAAAGAG CTGGACAGAA ATTATCTCAA CTACGGTGAG GAAGGAGCCC CAGGGAAAGT 1560
GCAGCAGCAG AGGAGCCTGC AGGACACTAA AGAAACAGG GAGGAAGCTA GGTTCAGAA 1620
TAAACAATAT AGCTCCCATC ACACAGCTGA AAGAGGAGAG AGATTAGGGG AACTGTTCAA 1680
CCCATACTAC GACCCCTCTC AGTGGAAAG CAGCCATTTT GAAAGAAGAG ACAACATGAA 1740
TGACAATTTT CTCGAGGGTG AGGAGGAAAA TGAGCTGACC TTGAACGAGA AGAATTTCTT 1800
CCCAGAATAC AACTATGACT GGTGGGAGAA AAGCCCTTTC TCTGAGGATG TGAAGTGGG 1860
GTATGAGAAG AGAAACCTGC CCAGGGTCCC CAACTGGAG CTGAAAAGGC AATATGACAG 1920
GGTGGCCCAA CTGGACAGC TCCTTCACTA CAGGAAGAG TCAGCTGAGT TTCCAGACTT 1980
CTATGATTTCT GAGGAGCCGG TGAGCACCCA CCAGGAGCCA GAAAATGAAA AGGACAGGGC 2040
TGACCAGACA GTCTGACAG AGGACGAGAA AAAAGAACTC GAAAACTTGG CTGCAATGGA 2100
TTTGGAACCTA CAGAAGATAG CTGAGAAATT CAGCCAAAGG GGCTGACTGT CATTTGAGCG 2160
GTGGGCACTG TTAAGAAGCA GCCATCACAT GATCTGTTT TCACCACTTC ACTGAAAGAC 2220
ACCATTTATA TACCAAGGG CAGAAAGTAG AACTTACTAT TCATTAAATG TTTGACACAA 2280
TTGGAATTGT CTTTAATTC TGTCAAGATG CTATTGAAA TGTGAATTGC ATGACTTGT 2340
GCATATCTCT TCTCTGAAAA TAGACATATT AACATGCTTA TGACAATGAC TGTGCTACTG 2400
TCTTTGAAAA AATGTTTGTG TCAGTTGGAA ATAATAAAG ATTCACTGA GACC 2454

```

Seq ID NO: C144 DNA Sequence  
Nucleic Acid Accession #: XM\_093082.1  
Coding sequence: 93..1988

45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
CTTCTGTGG TAGGACCTC TCCTCAGTAT TTGAACTAA CCAGCATCTG ACAGATTTCG 60
AATTTGTAAA AATACCCTC GAAGATTCAG GAATGAAGCT TCTGTGTGAA GGATTAAC 120
AGCCCACTG TGTATTACAG ACATTGAGGT GGTACCGGTG CCTTATCTCT TCTGCTTCT 180
TTGGGGCTCT AGCAGCTGTT CTAGCACCA GTCACTGGCT CACTGAAGTG GAATTTAGT 240
AGCAAACTT GGAAGCTTCA GCTTTGAAAT TGCTCTATGG AGGCTTAAAT GATCCAAAT 300
GCAAAATCA GAAGCTCAAC TTGCAGTTT CTATTCTGT AACCGCTGCA AAACCTCCAG 360
TTGGAATGTT TGGAAATTT TCTGTTTCT CGGATCATT GGTGCAATCT CAITTTGGCT 420
ACTGTCAAGA CAGTTCTTTC AATGTGATC TTTGTAAGCT GCTCTGCCCT TCCACAGAG 480
TTGCTGCTGC AAAGGATTGT GGGAGTCCTA AGTCTTCTC ATCAGAAAGG CTGAACTGGG 540
CAGGAAGACT TGAGGAGTG GAGGAGGTT TGGGGTTGGG GGTGCTTGTA CAGCCCGGTG 600
ACCCAGCATC TCAGGGTGGG GGGCAITGTG AAAACTATGG GTCITTTAGA GACTTGGTGG 660
ACTTAGAAGT CAAGGAGAG AAAGCCTGA GAAAGGTGG TATGGATCTC CAGAGACCCA 720
CCCTACAAGT TGTCTCTCT TGCAAAATCT TCTCCCTCAA ACTATTTCTC TTTATTGCAT 780
TGCTTAATTC TCTGTGTCAG GTTAGTGTGG TGCAAGTGAC CATCCAGAC GGTTTGTTGA 840
AOGTGAAGT TGATCTAAT GTCACTCTCA TCTGCATCTA CACCACTCT GTGGGCTCCC 900
GAGAACAGT TTCCATCCAG TGGTCTTCT TCCATAAGAA GGAGATGAG CCAATTTCTT 960
CTCCTTGGGA GAGGGGGAAG TGGCCAGATG TTGAGGCTGT GAAGGGCACT CTGTATGGAC 1020
AGCAGGCTGA ACTCCAGATT TACTTTTCTC AAGGTGGACA AGCTGTAGCC ATCGGGCAAT 1080
TTAAAGATCG AATTACAGGG TCCAACGATC CAGGTAATGC ATCTATCACT ATCTCGCATA 1140
TGCAGCCAGC AGACAGTGA ATTTACATCT GCGATGTTAA CAACCCCTCA GACTTTCTCG 1200
GCCAAAACCA AGGCATCTCT AACGTCAAGT TGTAGTGAA ACCTTCTAAG CCCCTTTGTA 1260
GGTTTCAAGG AAGACCAGAA ACTGGCCACA CTATTTCCCT TTCCTGTCTC TCTGGGCTTG 1320
GAACACCTTC CCCTGTGTAC TACTGGCATA AACTTGAGGG AAGAGACATC GTGCCAGTGA 1380
AAGAAAACCT CAACCCCAACC ACCGGGATTT TGGTCATTGG AAATCTGACA AATTTTGAAC 1440
AAGGTATTAT CAGTGTACT GCCATCAACA GACTTGGCAA TAGTTCTGCG GAAATCGATC 1500
TCACTTCTTC ACATCCAGAA GTTGGAAATCA TTGTTGGGGC CTGATTGGT AGCCTGGTAG 1560
GTGCCGCCAT CATCATCTCT GTTGTGTGCT TCGCAAGGAA TAAGGCAAAA GCAAAGGCAA 1620
AAGAAAGAAA TTCTAAGACC ATCGCGGAAC TTGAGCCAAT GACAAAGATA AACCAAGGG 1680
GAGAAAGCCA AGCAATGCCA AGAAGAGAGC CTACCCAAC AGAAGTAACT CTACCATCTT 1740
CCATTATCA GACTGGCCCT GATACCATCC AAGAACGAGA CTATGAGCCA AAGCCTACTC 1800
AGGAGCCTGC CCCAGGCTC GCCCAGGAT CAGAGCCTAT GGCAGTGCCT GACCTTGACA 1860
TOGAGCTGGA GCTGGAGCCA GAAACGAGT CGGAATTGGA GCCAGAGCCA GAGCCAGAGC 1920
CAGAGTCAGA GCCTGGGGTT GTAGTTGAGC CCTTAAGTGA AGATGAAAAG GGAGTGGTTA 1980
AGGCATAG

```

Seq ID NO: C145 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1242

1 11 21 31 41 51



5  
 10  
 15  
 20  
 25

ATGGTGTTCG	CATTTTGGAA	GGTCTTCTG	ATCCTAAGCT	GCCTTGCAAG	TCAGGTTAGT	60
GTGGTGCAAG	TGACCATCCC	AGACGGTTTC	GTGAACGTGA	CTGTTGGATC	TAATGTCACT	120
CTCATCTGCA	TCTACACCAC	CACGTGGGCC	TCCCGAGAAC	AGCTTTCCAT	CCAGTGGTCT	180
TTCTTCCATA	AGAAGGAGAT	GGAGCCAATT	TCTTCTCCTT	GGGAGGAGGG	GAAGTGGCCA	240
GATGTTGAGG	CTGTGAAGGG	CACCTTTGAT	GGACAGCAGG	CTGAATCCCA	GATTTACTTT	300
TCTCAAGGTG	GACAAAGTGT	AGCCATCGGG	CAATTTAAAG	ATCGAATTAC	AGGGTCCAAC	360
GATCCAGGTA	ATGCATCTAT	CACATCTCTG	CATATGCAGC	CAGCAGACAG	TGGAATTTAC	420
ATCTGCGATG	TTAAACAACC	CCCAGACTTT	CTCGGCCAAA	ACCAAGGCAT	CCTCAACGTC	480
AGTGTGTTAG	TGAACCTTTC	TAAGCCCTTT	TGTAGCGTTC	AAGGAAGACC	AGAACTGGC	540
CACACTATTT	CCCTTTCTGT	TCTCTCTGCG	CTTGGAAACAC	CTTCCCCTGT	GTACTACTGG	600
CATAAACTTG	AGGGAAGAGA	CATCGTGCCA	GTGAAAGAAA	ACTTCAACCC	AACCAACGGG	660
ATTTTGGTCA	TTGAAATCT	GACAAATTTT	GAACAAGGTT	ATTACCAGTG	TACTGCCATC	720
AACAGACTTG	GCAATAGTTC	CTGCGAAATC	GATCTCACTT	CTTCACATCC	AGAAGTTGGA	780
ATCATTGTTG	GGGCTTGTAT	TGGTAGCCTG	GTAGGTGCCG	CCATCATCAT	CTCTGTTGTG	840
TGCTTCGCAA	GGAAATAAGC	AAAAGCAAAG	GCAAAAGAAA	GAAATCTTAA	GACCATCGCG	900
GAACCTTGAGC	CAATGACAAA	GATAAACCCA	AGGGGAGAAA	GCGAAGCAAT	GCCAGAGAGAA	960
GACGCTAGCC	AAGTAGAATG	AACTCTACCA	TCTTCCATTC	ATGAGACTGG	CCCTGATAAC	1020
ATCCAAGAAC	CTAGCTATGA	GCCAAAGCCT	ACTCAGGAGC	CTGCCCCAGA	GCTTGCCCCA	1080
GGATCAGAGC	CTATGGCAGT	GCCTGACCTT	GACATCGAGC	TGGAGCTGGA	GCCAGAAACG	1140
CAGTCGGAAT	TGGAGCCAGA	GCCAGAGCCA	GAGCCAGAGT	CAGAGCTTGG	GGTTGTAGTT	1200
GAGCCCTTAA	GTGAAGATGA	AAAGGGAGTG	GTAAAGGCAT	AG		1242

Seq ID NO: C146 DNA Sequence

Nucleic Acid Accession #: NM\_003020.1

Coding sequence: 29..664

30  
 35  
 40  
 45  
 50

CGCTCCTCGG	GCTGCCCTTC	GGTTGACAAAT	GGTCTCCAGG	ATGGTCTCTA	CCATGCTATC	60
TGGCCTACTG	TTTGGGCTGG	CATCTGGATG	GACTCCAGCA	TTTGCTTACA	GCCCCCGGAC	120
CCCTGACCGG	GTCTCAGAAG	CAGATATCCA	GAGGCTGCTT	CATGGTCTTA	TGGAGCAATT	180
GGGCATGGCC	AGGCCCCGAG	TGGAATATCC	AGCTCACCAG	GCCATGAATC	TTGTGGGCCC	240
CCAGAGCATT	GAAGGTGGAG	CTCATGAAGG	ACTTCAGCAT	TTGGGTCTCT	TTGGCAACAT	300
CCCCAACATC	GTGGCAGAGT	TGACTGGAGA	CAACATTCTT	AAGGACTTTA	GTGAGGATCA	360
GGGTATCCCA	GACCCCTCCAA	ATCCCTGTCC	TGTTGGAAAA	ACAGATGATG	GATGTCTAGA	420
AAACACCCCT	GACACTGCAG	AGTTTCAGTC	AGAGTTCACG	TTGCACCAGC	ATCTCTTTGA	480
TCGGAACAT	GACTATCCAG	GCTTGGGCAA	GTGGAACAAG	AAACTCTCTT	ACGAGAAGAT	540
GAAGGGAGGA	GAGAGACGAA	AGCGGAGGAG	TGTCAATCCA	TATCTACAAG	GACAGAGACT	600
GGATAATGTT	GTTCGAAGA	AGTCTGTCCC	CCATTTTTC	GATGAGGATA	AGGATCCAGA	660
GTAAAGAGAA	GATGCTAGAC	GAAAACCCAC	ATTACCTGTT	AGGCCTCAGC	ATGGCTTATG	720
TGCACTGTGA	AATGGAGTCC	CTGTGAATGA	CAGCATGTTT	CTTACATAGA	TAATTTATGA	780
TACAAAGCAG	CTGTATGATG	ATAGTGTATT	GTCTTCACAC	CGATGATTTT	GCTTTTGTCT	840
AAATTAGAAAT	AAGAGCTTTT	TTGTTTCTTG	GGTTTTTAAA	ATGTGAATCT	GCAATGATCA	900
TAAAAATTAA	AATGTGAATG	TCAACAATAA	AAAGCAAGAC	TATGAAAGGC	TCAGATTTC	960
TGCAGTTTAA	AATGGTGTCT	GAGGTTGTAC	TATTTTGGCC	AAGTCTGTAG	AAAGCTGTCA	1020
TTTGATTTTG	ATTATGTAGT	TCATCCAGCC	CTTGGGCATT	GTTATACACC	AGTAAAGAAG	1080
GCTGTACTCA	AGAGGAGGAG	CTGACACATT	TCATTGGCTT	GCGTCTTAAT	AAACATGAAT	1140
GCAAGCATTG	GC					1152

Seq ID NO: C147 DNA Sequence

Nucleic Acid Accession #: NM\_024021.2

Coding sequence: 144..806

55  
 60  
 65  
 70  
 75  
 80

AACTTCTCTG	CAATGGTTT	CAATATATGC	AGATGTCTCG	ATATAGGAAT	GAAATTACGT	60
CTTTGGAAAC	ACTTAAATAA	GTCAATATA	CTTGGAGCTT	TAAAAATTAA	AAGGAGAGAG	120
ATTCCAGCAC	CTTTTCTGCT	GCCATGACAA	CCATGCAAGG	AATGGAACAG	GCCATGCCAG	180
GGGCTGGCCC	TGGTGTGCCC	CAGCTGGGAA	ACATGGCTGT	CATACATTCA	CATCTGTGGA	240
AAGGATTGCA	AGAGAAGTTC	TTGAAGGGAG	AAACCAAGT	CCTTGGGGTT	GTGCAGATTG	300
TGACTGCCCT	GATGAGCCCT	AGCATGGGAA	TAACAAATGAT	GTGTATGGCA	TCTAATACTT	360
ATGGAAGTAA	CCCTATTTC	GTGTATATCG	GGTACACAAT	TTGGGGGTCA	GTAATGTTTA	420
TTATTTTCAG	ATCCTTGTC	ATTGCAGCAG	GAATTAGAAC	TACAAAAGGC	CTGGTCCGAG	480
GTAGTCTAGG	AATGAATATC	ACCAGCTCTG	TACTGGCTGC	ATCAGGGATC	TTAATCAACA	540
CATTTAGCTT	GGGTTTTTAT	TCATTCCATC	ACCCTTACTG	TAACTACTAT	GGCAACTCAA	600
ATAATTGTCA	TGGGACTATG	TCCATCTTAA	TGGGTCTGGA	TGGCATGGTG	CTCCTCTTAA	660
GGTGTCTGGA	ATTCTGCATT	GCTGTGTCCC	TCTCTGCCTT	TGGATGTAAA	GTGCTCTGTT	720
GTACCCCTGG	TGGGTTTGTG	TTAATTCTGC	CATCACATTC	TCACATGGCA	GAACAGCAT	780
CTCCACACAC	ACTTAATGAG	GTTTGAGGCC	ACCAAAAGAT	CAACAGACAA	ATGCTCCAGA	840
AATCTATGCT	GACTGTGACA	CAAGAGCCCT	ACATGAGAAA	TTACCAAGAT	CCAACCTCGA	900
TACTGTATGA	CTTGTGTGTA	TTATTATTAT	ATGTAATCCA	ATTATGAATC	GTGTGTGAT	960
AGAGAGATAA	TAAATTCAAA	ATTATGTTCT	CATTTTTC	CCTGGAACCT	AATAACTCAT	1020
TTCACTGGCT	CTTATCGAG	AGTACTAGAA	GTTAAATTAA	TAAATAATGC	ATTATATGAG	1080
GCAACAGCAC	TTGAAAGTTT	TTCAATTCAT	ATAAGAATCT	TATATAAAGG	CATTACATTG	1140
GCAAAATAGG	TTTGAAGACA	GAAGAGCAAA	AAAAAGATAT	TGTTAAATATG	AGGCCTCCAT	1200
GCAAAACACA	TACTTCCCTC	CCATTTATTT	AACCTTTTTT	TTCTCCTACC	TATGGGGACC	1260
AAAGTCTTTT	TTCTTCCAGG	AAGTGGAGAT	GCAATGGCCAT	CTCCCCCTCC	CTTTTCTCTT	1320
CTCCGCTTTT	TCTTTCCCCA	TAGAAAGTAC	CTTGAAGTAG	CACAGTCCGT	CCTTGCAATG	1380
GCACAGGCTA	TCATTTGAGT	AAAAGTATAC	ATGGAGTAAA	AATCATATTA	AGCATCAGAT	1440
TCAACTTATA	TTTTCTATTT	CATCTTCTTC	CTTCCCCTTC	TCCACCTTTC	TACTGGGCAT	1500
AATTATATCT	TAATCATATA	TGGAAATGTG	CAACATATGG	TATTTGTATA	ATACGTTTGT	1560
TTTTATTGCA	GAGCAAAAT	AAATCAAAT	AGAAGCAATA	AAAAAATAAA	AAAAAATAAA	1619

Seq ID NO: C148 DNA Sequence  
Nucleic Acid Accession #: NM\_002091.1  
Coding sequence: 56..502

5  
10  
15  
20

1	11	21	31	41	51	
AGTCTCTGCT	CTTCCCAGCC	TCTCCGGCGC	GCTCCAAGGG	CTTCCCGTCG	GGACCATGCG	60
CGGCAGTGAG	CTCCCGCTGG	TCTGCTGGC	GCTGGTCTTC	TGCCTAGCGC	CCCGGGGGCG	120
AGCGGTCCCG	CTGCCTCGGG	GCGGAGGGAC	CGTGTCTGACC	AAGATGTACC	CGCGCGGGCAA	180
CCACTGGGGCG	GTGGGGCACT	TAATGGGGAA	AAAGAGCACA	GGGGAGTCTT	CTTCTGTTTC	240
TGAGAGAGGG	AGCCTGAAGC	AGCAGCTGAG	AGAGTACATC	AGGTGGGAAG	AAGCTGCAAG	300
GAATTGTCTG	GGTCTCATAG	AAGCAAAGGA	GAACAGAAAC	CACCAGCCAC	CTCAACCCAA	360
GGCCTTGGGC	AATCAGCAGC	CTTCGTGGGA	TTCAGAGGAT	AGCAGCAACT	TCAAAGATGT	420
AGTTTCAAAA	GGCAAAGTTG	GTAGACTCTC	TGCTCCAGST	TCTCAACGTG	AAGGAAGGAA	480
CCCCCAGCTG	AACCAGCAAT	GATAATGATG	GCCTCTCTCA	AAAGAGAAAA	ACAAAACCCC	540
TAAGAGACTG	AGTTCTGCAA	GCATCAGTTC	TACGGATCAT	CAACAAGATT	TCCTTGTCGA	600
AAATATTGTA	CTATTCTGTA	TCTTTCATCC	TTGACTAAAT	TCGTGATTTT	CAAGCAGCAT	660
CTTCTGGTTT	AAACTTGTGT	GCTGTGAACA	ATTGTGAAA	AGAGTCTTCC	AATTAATGCT	720
TTTTTATATC	TAGGTACTCT	GTTGGTTAGA	TTCAAGGCCC	CGAGCTGTGA	CCATTACAAA	780
TAAAAGCTTA	AACACAT					797

Seq ID NO: C149 DNA Sequence  
Nucleic Acid Accession #: NM\_012261.1  
Coding sequence: 203..1045

25  
30  
35  
40  
45  
50  
55  
60

1	11	21	31	41	51	
GATTGTCTCT	GCCAGCAGCT	GTGGGTGCGG	CGCTCGACAC	CGAGTCTTAG	CTAGGCGCTC	60
ACAGAATACG	CGCTCCCTCC	CTCCCCCTTC	TCTGTCCCCC	GCCTCTGCGT	CACCCCGGCC	120
CACTCCAGCG	GGCACTTTGA	GGGATTCCCT	CTCTGGCGGC	CTCTGCAGCA	GCAAGCCGG	180
CCTCATCGG	GGCACTGCGA	GTATGGATCT	CCAAGGAAGA	GGGGTCCCCA	GCATCGACAG	240
ACTTCAGATT	CTCTGTATGT	TGTTCCATAC	AATGGCTCAA	ATCATGGCAG	AACAAGAAAT	300
GGAAATCTCT	TCAGGCCTTT	CCACTAACCC	TGAAAAGAT	ATATTGTGG	TGCGGGAAAA	360
TGGGACGACG	TGTCTCATGG	CAGAGTTTGC	AGCCAAATTT	ATTGTACCTT	ATGATGTGTG	420
GGCCAGCAAC	TAGCTAGATC	TGATCACAGA	ACAGGCCGAT	ATCGCATTGA	CCCGGGGAGC	480
TAGAGTGAAG	GGCCGTGTGT	GCCACAGCCA	GTCGGAGCTG	CAAGTGTTC	GGGTGGATCG	540
CGCATATGCA	CTCAAAATGC	TCITTTGTAA	GGAAAGCCAC	AACATGTCCA	AGGGACCTGA	600
GGCGACTTGG	AGGCTGAGCA	AAGTGCAGTT	TGTCTAGCAC	TCCTCGGAGA	AAACCCACTT	660
CAAGAGCGCA	GTCACTGCTG	GGAGCACAC	AGCCAACTCG	CACCACTCT	CTGCCTTGGT	720
CACCCCGCT	GGGAAGTCC	ATGAGTGTCA	AGCTCAACAA	ACCATTTTCA	TGGCCTCTAG	780
TGATCCGCG	AAGACGGTCA	CCATGATCCT	GTCTCGGCTC	CACATCCAAC	CTTTTGACAT	840
TATCTCAGAT	TTTGTCTTCA	GTGAAGAGCA	TAAATGCCCA	GTGGATGAGC	GGGAGCAACT	900
GGAAAGAAAC	TTGCCCTTGA	TTTTGGGGCT	CATCTTGGGC	CTCGTCTATC	TGTAACACT	960
ATCCAGTTAC	CAGTCCACCC	ACAAAATGAC	TGCCAACCCAG	GTGCAGATCC	CTCGGGAGAC	1020
ATCCCAAGT	AAGCAGATGG	GCTAGAGGCC	GTTAGGCAGG	CACCCCTAT	TCTGTCTCCC	1080
CAAACCTGAG	CAGTAGAAG	AACAAAAGCA	CTTTTCCATC	TTGTACACGA	GATACACCAA	1140
CATAGCTACA	ATCAAAACAG	CCTGGGTATC	TGAGGCTTGC	TTGGCTTGTG	TCCATGCTTA	1200
AACCCACGGA	AGGGGGAGAC	TCTTTCCGAT	TTGTAGGGTG	AAATGCAAT	TATTCTCTCC	1260
ATGCTGGGGA	GGAGGGGAGG	AGGGTCTCAG	ACAGCTTTGC	TGCTCATGCT	GGCTTGGCTT	1320
TGACTCTCCA	AAGAGCAATA	AATGCCACTT	GGAGCTGTAT	CTGGCCCCAA	AGTTTAGGGA	1380
TTGAARACAT	GCTTCTTTGA	GGAGGAAACC	CCTTTAGGTT	CAGAAGAATA	TGGGGTGCTT	1440
TGCTCCCTTG	GACAGCTGCT	GCTTATCCTA	TACAGTTGTC	AATGCACACA	GAATACAAAC	1500
TCATGCTCCC	TGCAGCAAGA	CCCCTGAAAG	TGATTATGTC	TTCTGGCTGG	CATTCTGCAT	1560
GTTTAGTGAT	TGTCTTGGGA	ATGTTTCACT	GCTACCCGCA	TCCAGCGACT	GCAGCACCAG	1620
AAAACGACTA	ATGTAACATT	GCAGAGTTGT	TTGACTTCTC	TCTGTGCCCA	GGTCCAAGTC	1680
GGGGGACCTG	AAGAATCAAT	CTGTGTGAGT	CTGTTTTTCA	AAATGAAATA	AAACACACTA	1740
TTCTCTGGC						1749

Seq ID NO: C150 DNA Sequence  
Nucleic Acid Accession #: NM\_003226.1  
Coding sequence: 2..226

65  
70

1	11	21	31	41	51	
GATGCTGGGG	CTGGTCTTGG	CCTTGCTGTC	CTCCAGCTCT	GCTGAGGAGT	ACGTGGGCCT	60
GTCTGCAAA	CAGTGTGCGG	TGCCGGCCAA	GGACAGGGTG	GACTGCGGCT	ACCCCATGTT	120
CACCCCAAG	GAGTGCACAA	ACCGGGGCTG	CTGCTTTGAC	TCCAGGATCC	CTGGAGTGCC	180
TTGGTGTTC	AAGCCCTTGA	CTAGGAAGAC	AGAATGCACC	TTCTGAGGCA	CCTCCAGCTG	240
CCCCTGGGAT	GCAGGCTGAG	CACCTTGCC	CGGCTGTGAT	TGCTGCCAGG	CAGTGTTCAT	300
CTCAGTTTTT	CTGTCCCTTT	GCTCCCGGCA	AGCTTTCTGC	TGAAAGTTCA	TATCTGGAGC	360
CTGATGTCTT	AACGAATAAA	GGTCCCATGC	TCCACCCG			398

75  
80

Seq ID NO: C151 DNA Sequence  
Nucleic Acid Accession #: NM\_002993.1  
Coding sequence: 64..408

1	11	21	31	41	51	
GGCACGAGCC	AGTCTCCGGG	CCTCCACCCA	GCTCAGGAAC	CCGGAACCC	TCTCTTGACC	60
ACTATGAGCC	TCCCGTCCAG	CCGCGCGGCC	CGTGTCCCGG	GTCTTCCGGG	CTCCTTGTGC	120
CGCTCTCTCG	CGCTGCTGCT	CTGCTGACG	CGCGCGGGGC	CCCTCCCGAG	CGCTGGTCTT	180
GTCTCTGCTG	TGCTGACAGA	GCTGCGTTGC	ACTTGTTTAC	CGTTTACGCT	GAGAGTAAAC	240

5  
 10  
 15  
 20

```

CCCCAAACGA TTGGTAACT GCAGGTGTTT CCGGCAGGCC CGCAGTGCTC CAAGGTGGAA 300
GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
AAGAAAGTCA TCCAGAAAAT TTTGGACAGT GGAACAAGA AAAACTGAGT AACAAAAAAG 420
ACCATGCATC ATAAAATTGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
CAGTAAGAAT AAGAAGGAAG GGTGGTTTT TTTCCATTT CTACATGGAT TCCCTACTTT 540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCITTGG 660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCITTCAATG AATATTGAAT 720
TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCITTACGAA AAGGCTGTGG 780
ATTTCTGATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTTCTT 840
ACTCACTCTT CTCAATAAAT AGGAAATATT TTAGTTCTGT TTTCTGGGG AATATTGTAC 900
TCTTTACCTT AGGATGCTAT TTAAGTTGTA CTGTATTAGA AACTGGGTG TGTATACCG 960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
CTAATATATT CTCTTCTAT GGTTTTAGAT GTTGTATGTC TTCTTAGTAT GGCATAATGT 1080
CATGATTTAC TCATTAATAC TTGATTTTGT ATGCTATTTT TTCATATAG GATGACTATA 1140
ATTTCTGGCA CTAAATATAC ACTTTAGATA GATGAAGAAG CCAAAAAACA GATAAATTCC 1200
TGATTGCTAA TTTACATAGA AATGTATTCT CTGGTTTTT TAAATAAAG CAAAATTAAAC 1260
AATGATCTGT GCTCTGCAA GTTTGAAAA TATATTGAA CAATTTGAAT ATAAATTCAT 1320
CATTTAGTCC TCAAAATATA TACAGCAATT CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
AAATGCACT TTTATTTTTT CCGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500
TGGAGAAACA ATAAAGATT TCTAAACCA AAAAAAANA AAAAAA 1547
  
```

25  
 30

Seq ID NO: C152 DNA Sequence  
 Nucleic Acid Accession #: NM\_005242.2  
 Coding sequence: 148..1341

35  
 40  
 45  
 50  
 55

```

1 11 21 31 41 51
CGGCCCCGCC TGGGAGGCG CGCAGCAGAG GCTCCGATTC GGGGCAGGTG AGAGGCTGAC 60
TTTCTCTCGG TGCCTCCAGT GGAGCTCTGA GTTTCGAATC GGTGGCGGCG GATTCGCCGC 120
GCGCCCGGCG TCGGGGCTTC CAGGAGGATG CGGAGCCCCA GCGCGGCGTG GCTGCTGGGG 180
GCGCCCATCC TGCTAGCAGC CTCCTCTCC TGCAGTGSCA CCATCCAAGG AACCAATAGA 240
TCCCTCTAAG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCACGT CACTGGAAAA 300
GGAGTTACAG TTGAAACAGT CTTTCTGTG GATGAGTTT CTGCATCTGT CCTCACTGGA 360
AAACTGACCA CGGTCTTCTT TCCAATTGTC TACAATTTG TGTGTTGGT GGGTTTGCCA 420
AGTAACGGCA TGGCCCTGTG GGTCTTCTT TTCCGAATA AGAAGAAGCA CCCTGCTGTG 480
ATTACATGG CCATCTGGC CTTGGCTGAC CTCCTCTCTG TCATCTGGTT CCCTTGAAG 540
ATTGCTATC ACATACATGC CAACAACCTG ATTTATGGGG AAGCTCTTTG TAATGTGCTT 600
ATTGGCTTT TCTATGGCAA CATGTACTGT TCCATTCTCT TCATGACCTG CCTCAGTGTG 660
CAGAGGTATT GGGTCATCGT GAACCCCATG GGGCACTCCA GGAAGAAGGC AAACATTGCC 720
ATTGGCATCT CCTCGCAAT ATGGCTGCTG ATTCTGTGG TCACCATCCC TTTGTATGTC 780
GTGAAGCAGA CCATCTTCAT TCCTGCCCTG AACATCAGCA CCGTCTATGA TGTGTTGCTT 840
GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCTCT CTCTGGCCAT TGGGGTCTTT 900
CTGTTCCAG CCTTCTTCAC AGCCTCTGCC TATGTGCTGA TGATCAGAAAT GCTGCGATCT 960
TCTGCCATGG ATGAAAACTC AGAGAAGAAA AGGAAGAGGG CCATCAAATCT CATGTCACT 1020
GTCTGGGCA GTACCTGAT CTGCTTCACT CCTAGTAACC TTCTGCTTGG GTGTCATTAT 1080
TTTCTGATTA AGAGCCAGGG CCAGAGCCAT GTCTATGCC TGTACATTGT AGCCCTCTGC 1140
CTCTCTACCC TTAACAGCTG CATCGACCCC TTTGTCTATT ACTTTGTTTC ACATGATTTT 1200
AGGGATCATG CAAAGAAGCG TCTCCTTTG CGAAGTGTCC GCACGTGAAA GCAGATGCAA 1260
GTATCCCTCA CCTCAAAGAA ACACTCCAGG AAATCCAGCT CTTACTCTTC AAGTTCAACC 1320
ACTGTTAAGA CCTCTATTG AGTTTCCAG GTCCCTCAGAT GGAATTGCA CAGTAGGATG 1380
TGAACCTGT TTAATGTTAT GAGGACGTGT CTGTTATTTC CTAATCAAAA AGGTCTCACC 1440
ACATACCACC G 1451
  
```

60

Seq ID NO: C153 DNA Sequence  
 Nucleic Acid Accession #: NM\_003469.2  
 Coding sequence: 92..1945

65  
 70  
 75  
 80

```

1 11 21 31 41 51
GAAACGGCCC GAGAAGCTCG CCCGAGAAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60
CATATAAACA AAAAGAGGAA ATCTTTCAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG 120
AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAAAATG TCCAAAAGTT 240
TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCOGAC AACAGCTCA 300
TAAGGAAGAA AGCAGCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360
AAAAGAAAT GCGATGAAA GCCACTTGCC CGAGAGGGAT TCACGTAGTG AAGAAGACTG 420
GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGACCAAAA 480
AGAAAATAAG CCTATGCGCT TGAATTCAGA AAAGAACCTT CCAATGGACA TGAGTGATGA 540
TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA 600
TGAAGAGAA TCCAGGGATA ACCCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
TACTCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCAA GAGCTGGGGA AACTGACAGG 720
ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTATA CGGATGATGA 780
AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTGGGG GAGAAGACTG 840
GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900
GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGG AGCTTGGCAT 960
CCAGGAAGAA GATCTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020
AAATGGCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
AAATGGGGAA AGGGCCACCA GGCTTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGGAA GACTTAATTG AGATGCTCAA 1200
AACTGGGGAG AAGCCGAATG GATCAGTGA ACCGGAGCGG GAGCTTGACC TTCCTGTTGA 1260
CCTAGATGAC ATCTCAGAGG CTGACTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320
  
```

5 CTCCAAGAGT GGCTACCCTA AAACACCTGG TCGTGCTGGG ACTGAGGCC TACCAGACGG 1380  
 GCTCAGTGGT GAGGATATTT TAAATCTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAC 1440  
 GTCGTATTTT CCCAATCCAT ATAACCAGGA GAAAGTCTG CCAAGGCTCC CTATGGTGC 1500  
 TGGAAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCACATG TTGAAAACAG 1560  
 10 ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620  
 GATGCTAGTT AATATCCCTG AGATCATTAA TTCAAACCAA GTGAAGCGAG TTCTGGTCA 1680  
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAAGAGCA 1740  
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC 1800  
 15 TGTGGGGCCC CGAAGAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860  
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920  
 TAAGAGAGCA ATGGAAAATA TGTAAAGCTGC TTTCAATTAAT TACCCTACTT TCATTCTCC 1980  
 CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTGA CTCTATCCT GTTAACACTG 2040  
 TAATATCTTT AATGATGTA CAGGCAGATG AAACCAAGTC ACTGGGGAGT CTGCTTCATT 2100  
 20 TCCTCTGAGC TGTATCTTG TGTATGGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160  
 ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTAATAG TATATCTAAT 2220  
 GGCCTGGGCA TTGTTGATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280  
 TTTTAAATAT TTATTGAATT ATTTTGTTAC TGTCTGTAGC GTTTTGTGGA GTACTGGACC 2340  
 AAAAAATAA AGCATTATAA ATATA 2365

Seq ID NO: C154 DNA Sequence  
 Nucleic Acid Accession #: NM\_030955  
 Coding sequence: 327..5108

25 1 11 21 31 41 51  
 GAATTCGGGG AGCGGGGGGG CTGCGAGGCC GCGGGGCATG CGGGAGGCGG AGGGGTGGGA 60  
 CCGGGTGGCT GCGCCCATTC CACACCCGCC GAAAGCGGAC ACTGTGAGCT GAATCACTCC 120  
 CCTTTTAGGA GGAGGGAGGG GGAAGAGGTG TCTAGCTAAT TTCTGCTTAA AAAAGCACAG 180  
 30 GAGATCCGGG GTACAGCTTTG CAGTCGTGTC CTCTCGCGC CTGACCATGC ACCCTGTCAT 240  
 CTTCCTGCTG GGCACAGCGC AGCGCTTTAT TTCTGGAGCT GAGGGCTAAA ACTTTTTCAT 300  
 CTTTCTCTCT CCTCAACATC TGAATCATGC CATGTGCCCA GAGGAGCTGG CTTCGAAACC 360  
 TTTCCGTGGT GGCTCAGCTC CTAACTTTTG GGGCGCTTTG CTATGGGAGA CAGCCTCAGC 420  
 CAGGCCCGGT TCGCTTCCCG GACAGGAGGC AAGAGCATTT TATCAGGGC CTGCCAGAAT 480  
 35 ACCACGTGGT GGGTCCAGTC CGAGTAGATG CCACTGGGCA TTTTGTGTC TATGGCTTGC 540  
 ACTATCCCAT CACGAGCAGC AGGAGGAAGA GAGATTGGA TGGCTCAGAG GACTGGGTGT 600  
 ACTACAGAAAT TTCTCAGGAG GAGAAGGACC TGTTTTAA CTTCAGCGTC AATCAAGGAT 660  
 TTTCTTCCAA TAGCTACATC ATGGAGAAGA GATATGGGAA CCTCTCCCAT GTTAAGATGA 720  
 40 TGGCTTCTCT TGCCCTCTCT TGCCATCTCA GTGGCACGGT TCTACAGCAG GGCACAGAG 780  
 TTGGGAGCGC AGCCCTCAGT GCCTGCCATG GACTGACTGG ATTTTCCAA CTACCACATG 840  
 GAGACTTTTT CATTTGAACC GTGAAGAAGC ATCCACTGGT TGAGGGAGGG TACCACCCGC 900  
 ACATCGTTTA CAGGAGGCGAG AAGTTCCAG AAACCAAGGA GCCAACCTGT GGATTAAAGG 960  
 ACAGTGTAA CATCTCCAGC AAGCAAGAGC TATGGCGGGA GAAGTGGGAG AGGCACAACT 1020  
 TGCCAGAGTG AAGCTCTCT CGCGTCTCCA TCAGCAAGGA GAGATGGGTG GAGACACTGG 1080  
 45 TGGTGGCGGA CACAAGATG ATTGAATACC ATGGAGTGA GAATGTGGAG TCCTACATCC 1140  
 TCACCATCAT GAACATGGTC ACTGGGTGTG TCCATAACCC AAGCATGGC AATGCAATTC 1200  
 ACATTGTTGT GGTTCGGCTC ATTCTACTCG AAGAAGAAGA GCAAGGACTG AAAATAGTTC 1260  
 ACCATGCGAG AAGACACTG TCTAGCTTCT GCAAGTGCCA GAAGAGTATC AATCCCAAGA 1320  
 GTGACCTCAA TCGCTTCTAT CACGACGTGG CTGTCTCTCT CACCAGAAAG GACATCTGTG 1380  
 50 CTGTTTCAA TGCCCTCTGC GAGACCCCTG GCCTGTCTCA CCTTCCAGGA ATGTGTGAGC 1440  
 CTCACCCGAG TTGTAACATC AATGAAGATT CCGGACTCCC TCTGGCTTTC ACAATTGCC 1500  
 ATGAGCTAGG ACACAGCTTC GGCAATCCAG ATGATGGGAA AGAAATGAC TGTGAGCCTG 1560  
 TGGGAGAGCA TCCGTACATC ATGTCCCGCC AGCTCCAGTA CGATCCCATC COGCTGACAT 1620  
 55 GGTCCAAGTG CAGCGAGGAG TACATCACCC GCTTCTTGGA CCGAGGCTGG GGGTCTGTG 1680  
 TTGATGACAT ACCTAAAGAG AAGGCTTGA AGTCCAAGGT CATTCGCCCG GGAGTGATCT 1740  
 ATGATGTTCA CCACCAAGTC CAGCTACAAT ATGGACCCAA TGCTACCTTC TGCCAGGAAG 1800  
 TAGAAAAGCT CTGCAGACCA CTGTGGTGTG CGTGAAGGG CTTTGTCTGC TCTAAGCTGG 1860  
 ACGCTGTGTC AGATGGAATC CAATGTGGTG AGAAGAAGTG GTGTATGGCA GGCAAGTGCA 1920  
 TCACAGTGGG GAAGAAACCA GAGAGCATTC CTGGAGGCTG GGGCCGCTGG TCACCTGGT 1980  
 60 CCACTGTTC CAGGACCTGT GGGGCTGGAG TCCAGAGCGC AGAGAGGCTC TGCAACAAAC 2040  
 CCGAGCCAAA GTTTGGAGGG AATATTGCA CTGAGAAAG AAAACGCTAT CGCTTGTGCA 2100  
 ACGTCCACCC CTGTCGCTCA GAGGCACCAA CATTCGGA GATGAGTGC AGTGAATTTG 2160  
 ACATGTTCC CTACAAGAT GAATCTACC ACTGTTTCC CATTTTAAAC CCAGCACATC 2220  
 65 CTGTGAGTGT TACTGCGGA CCCATAGATG GCCAGTTTC TGAGAAAATG CTGGATGCTG 2280  
 TCATTGATGG TACCCCTGTC TTTGAAGCG GCAACAGCAG AATGTCTGT ATTAATGGCA 2340  
 TATGTAAGAT GGTGGCTGT GACTATGAGA TGSATTCCAA TGCCACCGAG GATGCTGGG 2400  
 GTGTGTGCTT GGGAGATGGC TCTTCTGCCC AGACTGTGAG AAAGATGTTT AAGCAGAAGG 2460  
 AAGGATCTGG TTATGTTGAC ATTTGGCTCA TTCCAAAAGG AGCAAGGGAC ATAAGAGTGA 2520  
 70 TGGAAATTTG GGGAGCTGGA AACTTCTGCG CCATCAGGAG TGAAGATCCT GAAAAATATT 2580  
 ACCGTAATGG AGGGTTTATT ATCCAGTGA ACGGGAACCA TAAGCTGGCA GGGACTGTCT 2640  
 TTCAGTATGA CAGGAAAGGA GACCTGGAAG AGCTGATGGC CACAGGTCCC ACCAATGAGT 2700  
 CTGTGTGGAT CCAGCTTCTA TTCCAGGTGA CTAACCTGG CATCAAGTAT GAGTACACAA 2760  
 TCCAGAAAGA TGGCCTTGAC AATGATGTTG AGCAGATGTA CTTCGCGAC TACGGCCACT 2820  
 75 GGAACAGAGT CAGTGTGACC TGCGGGACAG GTATCCGCGC CCAAACCTGC CATTGCATAA 2880  
 AGAAGGGCG CGGGATGGTG AAAGCTACAT TCTGTGACCC AGAAACACAG CCCAATGGGA 2940  
 GACAGAAGAA GTGCCATGAA AAGGCTTGT CACCCAGGTG GTGGGAGGG GAGTGGGAAG 3000  
 CATGCTCGGC GACATGCGGG CCCCACGGGG AGAAGAAGCG AACCGTGTCT TGCAATCCAGA 3060  
 CCATGTCTCT TGACGAGCAG GCTCTCCCGC CCACAGACTG CCAGCACCTG CTGAAGCCCA 3120  
 AGACCTCTCT TTCTGCAAC AGAGACATCC TGTGCCCTCT GGAAGTGACA GTGGGCAACT 3180  
 80 GGAATGAGTG TTCTGTTTCC TGTGTTGGTG GAGTGGGAT TCGCAGTGTG ACATGTGCCA 3240  
 AGAACCATGA TGAACCTTGC GATGTGACAA GGAACCCCAA CAGCCGAGCT CTGTGTGGCC 3300  
 TCCAGCAATG CCTTCTAGC CGGAGAGTTC TGAACCAAAA CAAAGGCACT ATTTCCAATG 3360  
 GAAAAACCC ACCAACACTA AAGCCCGTCC CTCCACCTAC ATCCAGGCCC AGAATGCTGA 3420  
 CCACACCCAC AGGCGCTGAG TCTATGAGCA CAAGCACTCC AGCAATCAGC AGCCCTAGTC 3480  
 CTACCAACGC CTCCAAAGAA GGAGACCTGG GTGGGAAACA GTGGCAAGAT AGCTCAACCC 3540

AACCTGAGCT GAGCTCTCGC TATCTCATTT CCACTGGAAG CACTTCCCAG CCCATCCTCA 3600  
 CTTCCTCAATC CTGAGCATT CAGCCAAAGT AGGAAAATGT TTCCAGTTCA GATACTGGTC 3660  
 CTACCTGGGA GGGAGGCCCTT GTAGCTACAA CAACAAGTGG TTCTGGCTTG TCATCTTCCC 3720  
 5 GCACCCCTAT CACTTGGCCT GTGACTCCAT TTTACAATAC CTTGACCAA GGTCCAGAAA 3780  
 TGGAGATTCA CAGTGGCTCA GGGGAAGAAA GAGAACAGCC TGAGGACAAA GATGAAAGCA 3840  
 ATCCTGTAAT ATGGACCAAG ATCAGAGTAC CTGGAAATGA CGCTCCAGTG GAAAGTACAG 3900  
 AAATGCACT TGCACTCCA CTAACACAG ATCTCAGCAG GGAGTCTGG TGGCCACCCT 3960  
 TCAGCACAGT AATGGAAGGA CTGCTCCCA GCCAAAGGCC CACTACTTCC GAAACTGGGA 4020  
 10 CACCCAGAGT TGAGGGGATG GTTACTGAAA AGCCAGCCAA CACTCTGCTC CCTCTGGGAG 4080  
 GAGACCACCA GCCAGAACCC TCAGGAAAGA CGGCAACCG TAACCACCTG AAACCTCCAA 4140  
 ACAACATGAA CCAACCAAAA AGTTCTGAAC CAGTCTGAC TGAGGAGGAT GCAACAAGTC 4200  
 TGATTACTGA GGGCTTTTGT CTAATGCTCT CCAATTACAA GCAGCTCACA AACGGCCACG 4260  
 GCTCTGCACA CTGGATGCTC GGAACCTGGA GCGAGTGCTC CACCACATGT GGCCTGGGGG 4320  
 15 CCTACTGAAA AAGGGTGGAG TGCACCAACC AGATGGATTG TGACTGTGCG GCCATCCAGA 4380  
 GAGCTGACCC TGCAAAAAGA TGCCACCTCC GTCCCTGTGC TGGCTGGAAA GTGGGAAACT 4440  
 GGAGCAAGT CTCCAGAAAC TGGAGTGGGG GCTTCAAGAT ACGCGAGATT CAGTGCCTGG 4500  
 ACAGCCGGGA CCACCCGAAC CTGAGGCCAT TTCACTGCCA GTTCTGTGCC GGCATTCTCT 4560  
 CCCCATGGAG CATGAGCTGT AACCCGGAGC CCTGTGAGGC GTGGCAGGTG GAGCCTTGGA 4620  
 20 GCCAGTGCTC CAGGTCTCTG TGAGGTGGAG TTCAGGAGAG AGGAGTGTC TGTCAGGAG 4680  
 GCCTCTGTGA TTGACAAAA AGACCCACAT CCACCATGTC TTGCAATGAG CACCTGTGCT 4740  
 GTCACTGGGC CACTGGGAAC TGGGACCTGT GTTCCACTTC CTGTGGAGGT GGCTTTTCA 4800  
 AGAGGATTGT CCAATGTGTG CCCTCAGAGG GCAATAAAAC TGAAGACCAA GACCAATGTC 4860  
 TATGTGATCA CAAACCCAGA CCTCCAGAA TCACAAAAATG CAACCAAGAG GCCTGCAAGA 4920  
 25 AAAGTGCCGA TTTACTTTGC ACTAAGGACA AACTGTGAGC CAGTTTCTGC CAGACACTGA 4980  
 AAGCCATGAA GAAATGTTCT GTGCCACCG TGAGGGCTGA GTGCTGCTTC TCGTGTCCCC 5040  
 AGACACACAT CACACACACC CAAAGGCAAA GAAGGCAACG GTTGCTCCAA AAGTCAAAAG 5100  
 AACTTAAGC CCAA 5115

Seq ID NO: C155 DNA Sequence  
 Nucleic Acid Accession #: NM\_001062.1  
 Coding sequence: 76..1380

1 11 21 31 41 51  
 35 | | | | |  
 GCTCTCATT CCTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCTATC AACATTCTGG 60  
 TACACTGTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTGT 120  
 TCTTTTATTC CAGGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAA CTACATCCGC 180  
 CTAACACCTC TGTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240  
 40 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AACCCCTGAT GCAAAAGATG 300  
 ATCCAACAAA TCAATACAAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAAAGCTG AGGAAAACIT AATATATGAT 420  
 TACCACCTGA CTGACAAAGT AGAAAAATAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480  
 CACAATGGCA CTGCTGAGT TAACCTACTC CAGCTCAGCC TGGACGTTTT GGCCTGTGT 540  
 45 CTGTTCATG GGAACACTCT AACCGCGGAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600  
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660  
 ACCTGTGTA AGAAGAGTCT AATAAATGGG CAGATCAAG CAGATGAAGG CAGTTTAAAG 720  
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATT TGTCTGAGAA AAAAGAAAAAT 780  
 GGTCTCATG CAGCAACATT TAGCAGGAG GAAGCCATGC AGGCCCTCTT TGTATCATCA 840  
 50 GACTATTATA ATGAAATGTA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCACGGAA 900  
 ATTTCTCAG GAGCATTGAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960  
 GGAAAGACCT TCTTGGATAT TAACAAGAC TCTTCTTGG TCTCTGCTTC AGGTAACTTC 1020  
 AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080  
 GTCAATTACT CTGTGAGAT CAATGAAACA TATTTACCA ATGTCACTGT GCTAAATGGT 1140  
 55 TCTGTCTTCC TCACTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200  
 ACAATGGAG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260  
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320  
 GGTAGTTAG TTTGTCGCAA TGGAGAAAAC TTGGAGGTTG GCTGGAGCAA ATACTAATAA 1380  
 GCCCAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCCATG TTTATTGTCC 1440  
 60 TTATGCTTTC TTCTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500  
 TTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC 1537

Seq ID NO: C156 DNA Sequence  
 Nucleic Acid Accession #: NM\_004591  
 Coding sequence: 59..349

1 11 21 31 41 51  
 65 | | | | |  
 CACTCCAAA GAACCTGGTA CTCAACACTG AGCAGATCTG TTCCTTGAGC TAAAAACCAT 60  
 GTGCTGTACC AAGAGTTTGC TCCGGCTGCG TTTGATGTC GTGCTGTAC TCACCTCTG 120  
 70 CGGGAATCA GAAGCAGCAA GCAACTTTGA CTGCTGTCTT GGATACACAG ACGTATTCT 180  
 TCATCTTAAA TTTATTGTGG GCTTCACACG GCAGCTGGCC AATGAAGGCT GTGACATCAA 240  
 TGCTATCATC TTTACACAA AGAAAAAGTT GTCTGTGTGC GCAAAATCAA AACAGACTTG 300  
 GGTGAAATAT ATTTGTGGCT TCCTCAGTAA AAAAGTCAAG AACATGTAAG AACTGTGGCT 360  
 75 TTTCTGGAAT GGAATTTGAG ATAGCCCAAG AACAGAAAGA ACCTTGCTGG GGTGGAGGT 420  
 TTCCTTGCA CATCATGGAG GGTTTAGTGC TTATCTAATT TGTGCTCAC TGGACTTGTC 480  
 CAATTAATGA AGTTGATTCA TATTGCATCA TAGTTTGCTT TGTTAAGCA TCACATTAAA 540  
 GTTAACTGT ATTTATGTTT ATTTATAGCT GTAGGTTTTC TGTGTTAGC TATTTAATAC 600  
 TAAITTTCCA TAAGCTATTT TGGTTAGTG CAAAGTATAA AATTATATT GGGGGGGAAT 660  
 80 AAGATTATAT GCACCTTTTG GCAAGCAACA AGCTATTTT TAAAAAATC ATTTAACATT 720  
 CTTTGTGTTA TATTGTTTGT TCTCCTAAAT TGTGTGAATT GCATTATAAA ATAAGAAAAA 780  
 CATTAAATAG ACAATATT 799

Seq ID NO: C157 DNA Sequence  
 Nucleic Acid Accession #: NM\_013271.1

Coding sequence: 27..809

```
1      11      21      31      41      51
5      |      |      |      |      |
TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCGCGGC 120
TCTGCGCGCG GCGCGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
AGACTGGCGC TCCTCGCGCG TTCCGGCGGT CAGTGCCCGG AGGTGAGGCG GCGGGGGCGG 240
TGCAGGAGCT GCGCGGGGCG CTGCGGCATC TGCTGGAGGC CGAACGTGAG GAGCGGGGCG 300
GGGCGGAGGC GCAGGAGGCT GAGGATCAGC AGGCGGCGGT CCTGGGCGAG CTGCTGCGCG 360
TCTGGGGGCG CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGAAGACGAC CCCGACGCGC 420
CTGACGCGCG GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCTGCGC GCGCTAGCAG 480
CCCAGCTTGT CCOCGCGGCC GTCCCGCGCG CGGCGCTCCG ACCCGGGCCC CCGTCTACG 540
ACGACGGCCC CGCGGGCCCC GATGCTGAGG AGGCAGGCGA CGAGACACCC GAGCTGGACC 600
CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGGGGG AAGCGCGGAC TCCGAGGGGG 660
TGGCAGCCCG GCGCGGCGCT CGCCGTGCGC CGCAACACGA TGTGGGCTCT GAGCTGCCCC 720
CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACGCGCT AGACCCCGCG GCGCCCCAGG 780
TGCTGTCAGC CCGCGTCTTG CCACCTGAGC ACTGCGCGG ATCCCGTGCA CCCTGGGACC 840
CAGAAGTGCC CCGCGCATCC CGCCACGAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900
TTACCCCGCG CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCCCTGGCCC ACAATAACAT 969
GATCTGAGC
```

Seq ID NO: C158 DNA Sequence  
Nucleic Acid Accession #: NM\_002245.2  
Coding sequence: 183..1193

```
1      11      21      31      41      51
30     |      |      |      |      |
GGGCAGGAAG ACGGCGCTGC CCGGAGGAGC GGGGCGGGCG GGCAGCGCGG GGAGCGGGCG 60
GCGGGGCGGA GCCAGGCCCG GCGGGGGGCG GGGGCGGGCG GGCCAGAAGA GGCAGCGGGC 120
CGCGCTCCGG CCGGCTGCGC CGCTTGGCCT TGGCTTTGGC TTTGGCGCGC GCGGTGGAGA 180
AGATGCTGCA GTCCCTGGCC GGCAGCTCGT CGCTGCGCCT GGTGGAGCGG CACCGCTCGG 240
CCTGTGCTCT CGGCTTCTTG GTGCTGGGCT ACTTGCTCTA CCTGGTCTTC GGCGCAGTGG 300
TCTTCTCTCT GGTGGAGCTG CCCTATGAGG ACCTGCTGCG CCAGGAGCTG CGCARGCTGA 360
AGCGAGCTGT CTGGGAGGAG CACGAGTGCC TGTCTGAGCA GCAGCTGGAG CAGTTCTCTG 420
GCGGGTGCTT GGAGGCCACG AACTACGCGC TGTGGGTGCT CAGCAACGCC TCGGGCAACT 480
GGAAGTGGGA CTTCACCTCC GCGCTCTTCT TCGCCAGCAC CGTGCTCTCC ACCACAGGTT 540
ATGGCCACAC CGTGCCCTTG TCAGATGGAG GTAAGGCCTT CTGCATCATC TACTCGTCA 600
TTGGCATTCC CTTCACCTTC CTGTTCTCTG CCGCTGTGGT CCAGCGCATC ACCGTGCAAG 660
TCACCCGCGA GCGGCTCTCT TACTTCCACA TCCGCTGGGG CTCTCCAAG CAGGTGGTGG 720
CCATCGTCCA TGCGGTGCTC CTGGGTTTG TCACTGTGTC CTGCTTCTTC TTCTATCCCG 780
CCGCTGTCTT CTAGTCTCTG GAGGATGACT GGAATCTTCT GGAATCTTCT TATTTTGT 840
TTATTTCTCT GAGCACCATT GGCCTGGGGG ATTATGTGCC TGGGAAGGC TACAATCAAA 900
AATTCAGAGA GCTCTATAAG ATTGGGATCA CGTGTACCT GCTACTTGGC CTATTTGCCA 960
TGTTGGTAGT TCTGGAAACC TTCTGTGAAC TCCATGAGCT GAAAAAATTC AGAAAAATGT 1020
TCTATGTGAA GAAGGACCAAG GACGAGGATC AGGTGCACAT CATAGAGCAT GACCAACTGT 1080
CCTTCTCTCT GATCACAGAC CAGGACAGCT GCATGAAAGA GGACCAAGAG CAAATAGAGC 1140
CTTTTGTGGC CACCCCTCTG TCTGCTGCGG TGGATGGGCC TGCAAAACAT TGAGCGTAGG 1200
ATTGTTGCA TTATGCTAGA GCACCAGGT CAGGCTGCAA GGAAGAGGCT TAAGTATGTT 1260
CATTTTATC AGAATGCAAA AGCGAAAATT ATGTCACITT AAGAAATAGC TACTGTTTGC 1320
AATGCTTAT TAAAAACAA CAAAAAAGA CACATGGAAC AAAGAAGCTG TGACCCAGC 1380
AGGATGTCTA ATATGTGAGG AAATGAGATG TCCACCTAAA ATTATATGT GACAAAATTA 1440
TCTGACCTT ACATAGGAGG AGAATACTTG AAGCAGTATG CTGCTGTGGT TAGAAGCAGA 1500
TTTTATACTT TAACTGGAA ACTTTGGGT TTGCATTAG ATCATTAGC TGATGGCTAA 1560
ATAGCAAAAT TTATATTAG AAGCAAAAAA AAAAAGCATA GAGATGTGTT TTATAAATAG 1620
GTTTATGTG ACTGGTTTGC ATGTACCCAC CCAAAATGAT TATTTTGGGA GAATCTAAGT 1680
CAAACTCACT ATTATATAG CATAGGTAAC CATTAACTAT GTACATATAA AGTATAAATA 1740
TGTTTATAT CTGTACATAT GGTTTAGGTC ACCAGATCCT AGTGTAGTTC TGAATAAAG 1800
ACTATAGATA TTTTGTCTCT TTTGATTCTT CTTTATACTA AAGAATCCAG AGTTGCTACA 1860
ATAAATAAAG GGAATAAATA AACTTGAGAG TGAATAACCA T 1901
```

Seq ID NO: C159 DNA Sequence  
Nucleic Acid Accession #: NM\_005472.1  
Coding sequence: 93..404

```
1      11      21      31      41      51
65     |      |      |      |      |
AAAGGGACTC CTGAAACTG ATTGAGAGCC CAGTGGATTG GCCAGCAGTT TGAGCTTCTA 60
CCGAGTCTTC CCCCACCTCA ATCCCTGTG CTATGGAGAC TACCAATGGA ACGGAGACCT 120
GGTATGAGAG CCTGCATGCC GTGCTGAAGG CTCTAAATGC CACTCTTCAC AGCAATTGTC 180
TCTGCGCGCC AGGGCCAGGG CTGGGGCCAG ACAACAGAGC TGAAGAGAGG GGGGCCAGCC 240
TAACCTGGCG TGATGACAA TCCTACATGT ACATTCTCTT TGTCATGTTT CTATTTGCTG 300
TAACTGTGGG CAGCCTCATC CTGGGATACA CCGCTCCCG CAAAGTGGAC AAGCGTAGTG 360
ACCCCTATCA TGTGTATATC AAGAACCCTG TGTCTATGAT CTAACACGAG AGGGCTGGGA 420
CGGTGGAAGA CCAAGACACC TGGGGATTGC GTCTGGGGCC TCCAGAACTC TGCTGTGGAC 480
TGATCAGGT CT
```

Seq ID NO: C160 DNA Sequence  
Nucleic Acid Accession #: NM\_005245.1  
Coding sequence: 187..13959

```
1      11      21      31      41      51
80     |      |      |      |      |
CTGGGCGGCC GGGCGGGGGG AGAGGGCGCG GGAGCGGCTC GTGCGGCAGG TACCATGCGG 60
```

	ACGCGCGAGC	CGCGCGAGGC	CCCGCGAGGC	CGTCCCTGC	TCGGGGGCGC	GCTGAGACGG	120
	CGGGTGAGCT	CCAGCAGAGC	GGCGTCGCCA	CTTCGGGCCA	ACTTTGCGAT	TCCCGACAGT	180
	TAAGCAATGG	GGAGACATTT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCAACATTTT	240
5	GGAGACAGTG	ATGGCAGCCA	ACGACTTGAA	CAGACTCTCT	TGCAGTTTAC	ACACCTCGAG	300
	TACAACGTCA	CGSTGCAGGA	GAACCTCTGA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAAGTAAGGT	ACAAAATTGT	TTCGGGAGAC	420
	AGTGAAGAAC	TGTTCAAAGC	TGAAGAGTAC	ATTCTCGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
10	ATAGTGAAG	CACTTGAAAA	AAATACTAAT	GTGGAGGCGC	GAACAAAGGT	CAGGCTGCAG	600
	GTGCTGGATA	CAATGACTT	GAGACCGTTA	TTCTCACCCA	CCTCATACAG	CGTTTCTTTA	660
	CCTGAAAAACA	CAGCTATAAG	GACCAGTATC	GCAAGAGTCA	GCGCCACGGA	TGCAGACATA	720
	GGAAACCAAG	GGGAATTTTA	CTACAGTTT	AAAGATCGAA	CAGATATGTT	TGCTATTTCAC	780
	CCAACCAAGT	GTGTGATAGT	GTTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
15	GAGATGGAAA	TCTCGCTGTC	GGACCGTGGC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
	AGCATGGCCA	AGCTAACCGT	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	GCAGTGACAT	TGTACCATTC	AGAACTGGAC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGACTCGC	ATCAGGGTGC	CAATGGTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTAGAAC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
20	GCCATCGGTG	ACATTGATTG	GGACAGTCAT	CCTTTCGGCT	ACAATCTCAC	ACTACAGGCT	1200
	AAAGATAAAG	GAACCTCGCC	CCAGTTCTCT	TCTGTTAAAG	TCATTACAGT	GACTTCTCCA	1260
	CAGTTCAAAG	CCGGGCCAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGCTCTCT	CCAACACACC	TGTGGTCATG	GTAAGGGCCA	TTCTGCTCTA	TTCCCATTTG	1380
	AGGTATGTTT	TTAAAGGAGC	ACCTGGAAAA	GCTAAATTCA	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTTAGAAC	AGTTAAAGAA	CAGCAGGCAG	CCCATTITGA	ACTTGAAGTA	1500
	ACRACAGTGG	ACAGAAAAGC	GTCCACCAAG	GTCTTGGTGA	AAGTCTTAGG	TGCAAAATAGC	1560
	AATCCCCCTG	AATTTACCCA	GACAGCGTAC	AAAGCTGCTT	TTGATGAGAA	CGTGCCCAT	1620
	GGTACTACTA	TGATGAGCCT	GAGTGCCGTA	GACCCGTATG	AGGGTGAGAA	TGGGTACGTG	1680
	ACATACAGTA	TGCAAAATTT	AAATCATGTG	CCGTTTGCGA	TTGACCATTT	CACTGGTGCC	1740
30	GTGAGTACGT	CAGAAAACCT	GGACTACGAA	CTGATGCCTC	GGGTTTATAC	TCTGAGGATT	1800
	CGTGACATCAG	ACTGGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCCPTGC	TACATTAAT	1860
	CTCAATAACT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTTGTA	AGGGACAATT	1920
	CCCAGAGATC	TAGGCGTGGG	AGAGCAAAAT	ACCAGTCTTT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAGTTGG	TACAGTATCA	GATTGAAGCT	GGAAATGAAC	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCAACTCGG	GGGTATTGTC	ATTAAGCGA	TCGCTAATGG	ATGGCTTAGG	TGCAAAAGGTG	2100
	TCTTTCCACA	GTCGTAGAAT	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCATTATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAAG	CTGGTAAACT	TGCACTGTGA	AGAGACTGGT	2220
	GTGCCCCAAA	TGCTGGCAGA	GAAGCTCCTG	CAGGCAAAAT	AATTACACAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTTCTCGA	TTCTCACTCT	GTCAATGCTC	ACATACCGCA	GTTTAGAAGC	2340
40	ACTCTTCCGA	CTGTATTTC	GGTAAAGGAA	AACACGCTG	TGGTTCCAG	TGTAATTTTC	2400
	ATGAACCTCA	CTGACCTTGA	CAGTGGCTTC	AATGGAAAAC	TGGTCTATGC	TGTTCTGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCTCTTGACC	GTGAAAACAC	AGACAAATAC	ACCCTGAATA	TTACCGTCTA	TGACCTTGGG	2580
	ATACCCGAGA	AGGCTCGGTG	GGCTCTTCTA	CATGTGTTGG	TTGTGATGTC	CAATGATAAT	2640
45	CCACCCGAGT	TTTTACAGGA	GAGCTATTTT	GTGGAAGTGA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAAATCA	TCCAGGTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACGG	ACACGTGACG	2760
	TACTCAATTC	TTACAGACAC	AGACACATTT	TCAATTGACA	GCGTGACGGG	TGTTGTTAAC	2820
	ATCGCAGGCC	CTCTGGATCG	AGAGCTGCAG	CATGAGCACT	CCTTAAAGAT	TGAGGGCCAGG	2880
	GACCAAGCCA	GAGGAGAGCC	TCAGCTGTTC	TCCACTGTGG	TTGTGAAAGT	ATCACTAGAA	2940
50	GATGTTAATG	ACAACCCACC	TACATTTATT	CCACCTAATT	ATCGTGTGAA	AGTCCGAGAG	3000
	GATCTTCCAG	AAGGAACCGT	CATCATGTGG	TTAGAAAGCC	ACGATCTCTA	TTTAGTCTAG	3060
	TCGTGTCAGG	TGAGATACAG	CCTTCTGGAC	CACGGAGAAG	GAACCTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAAGAAGCA	AGTGTATAAT	3180
	CTCACTGCGA	CGGCCAAAGA	CHAGGGAAAG	CCAATTTCTC	TGCTTCTTAC	TTGCTATGTT	3240
55	GAAGTTGAGG	TGGTTGATGT	GAATGAGAAC	CTGCACCCAC	CCGTGTTTTT	CAGCTTTGTG	3300
	GAAGAGGGGA	CAGTGAAAGA	AGATGCACCT	GTTGGTTTCT	TGGTAATGAC	GGTGCGGCT	3360
	CATGATGAGG	ACGCCGGAGG	AGATGGGGAG	ATCCGATACT	CCATTAGAGA	TGGCTCTGGC	3420
	GTGTGTGTTT	TCAAAATAGG	TGAAGAGACA	GGTGTCTAGG	AGAGCTCAGA	TGCACTGGAC	3480
	CGTGAATCGA	CCTCCCAITTA	TTGGCTAACA	CTCTTTGCAA	COGATCAGGG	TGCTGTCCT	3540
60	CTTTTATGTT	TATAGAGAT	CTACATAGAG	GTTGAGGATG	TCAATGACAA	TGCACCAACG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAAATTT	CTCCTAAAGA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTTGA	TCCAGATTGG	AGCTCTAATG	ACAAGCTCAT	GTACAAAATT	3720
	ACAAGTGGA	ATCCACAAGG	ATTCTTTTCA	ATACATCTTA	AAACAGGTCT	CATCACAATT	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACATATGTA	GTCCCCCAA	ATCAACCAT	GCAAGAGTCA	TTGTGAAAT	CCTTGATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTCTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACGG	GAGCGCTCT	ATCGGCTCAT	AGCCACCGAC	4020
	AAGGATGAGG	GCCCAATGCA	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTTCA	TGCAACCGAA	AACTGGAGTG	GTTTGTGCTA	AGAGGTTTTT	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAAGT	GACAATGGTC	GCCCTCAAAA	GTCACTCAAC	4200
	ACCAGACTCC	ATATTGAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTCATTT	4260
	GAAGAATCAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CGSTGCTCA	CATGATTGGA	4320
	GTAATATCTG	TGGAGCCTCC	TGGCATACCC	CTTTGGTTTG	ACATCACTGG	TGGCAACTAC	4380
	GACAGTCACT	TGATGTGGA	CAAGGGAAC	GGAACCATCA	TTGTTGCCAA	ACCTCTGTAT	4440
75	GCAGAACAGA	AGTCARAATA	CAACCTCACA	GTCCAGGCTA	CAGATGGAAC	CACCACTATC	4500
	CTCACTCAGG	TATTCATCAA	AGTAATAGAC	ACAAATGACC	ATCGTCTCTA	GTTTCTACA	4560
	TCAAAGTATG	AAGTTGTTAT	TCCTGAAGAT	ACAGCGCCAG	AAACAGAAAT	TTTGCAAAATC	4620
	AGTGTGTGG	ATCAGGATGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
80	CCACTGATC	TCAAGAAAT	TCGTCTTGAT	CCTGCAACCG	GCTCTCTCTA	TACTTCTGAG	4740
	AAACTGGATC	ATGAAGCTGT	TTCAACGACA	CACCTCACGG	TCAATGGTACG	AGATCAAGAT	4800
	GTGCTGTGAA	AACGCAACTT	TGCAAGGATT	GTGGTCAATG	TCAGCGACAC	GAATGAACAC	4860
	GCCCGTGGT	TCACCGCTTC	CTCCTACAAA	GGGCGGGTTT	ATGAATCGGC	AGCCGTTGGC	4920
	TCACTGTGTG	TGCAGGTGAC	GGCTCTGGAC	AAGGACAAAG	GGAAAAATGC	TGAAGTGTCTG	4980
	TACTCTGCTG	AGTCAGGAAA	TATTGGAAAT	ATTGGAAAT	CTTTTATGAT	TGATCTGCTC	5040
	TTGGCTCTTA	TTAAACTGTC	CAAGGAATTA	GATCGAAGTA	ACCAAGCGGA	GTATGATTTA	5100

	ATGGTAAAAG	CTACAGATAA	GGGCAGTCCA	CCAATGAGTG	AAATAACTTC	TGTGGGTATC	5160
	TTTGTACAAA	TTGCTGACAA	CGCTCTCCG	AAGTTTACAT	CAAAAGAATA	TTCTGTTGAA	5220
	CTTAGTGAAA	CTGTGAGCAT	TGGGAGTTTC	GTTGGGATGG	TTACAGCCCA	TAGTCAATCA	5280
	TCAGTGGTGT	ATGAAATAAA	AGATGGAAAT	ACAGGTGATG	CTTTTGATAT	TAATCCACAT	5340
5	TCTGGAACCTA	TCATCACTCA	GAAAGCCCTG	GACTTTGAAA	CTTTGCCCAT	TTACACATTG	5400
	ATAATACAAAG	GAACATAACAT	GGCTGGTTTG	TCCACTAATA	CAACGGTTCT	AGTTCACTTG	5460
	CAGGATGAGA	ATGACAACGC	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
	GAATCAGCCT	CAATTAACAG	CGTGGTCTTA	ACAGACAGGA	ATGTCCCACT	GGTGATTGGA	5580
10	GCAGCTGATG	CTGATAAAGA	CTCAATGCT	TTGCTTGAT	ATCACATTGT	TGAACCATCT	5640
	GTACACACAT	ATTTTGCTAT	TGATTCTAGC	ACTGGTGCTA	TTCATACAGT	ACTAAGTCTG	5700
	GACTATGGAAG	AAACAAGTAT	TTTTCACTTT	ACCGTCCAAG	TGCATGACAT	GGGAACCCCA	5760
	CGTTTATTTG	CTGAGTATGC	AGCGAATGTA	ACAGTACATG	TAATTGACAT	TAATGACTGC	5820
	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAAGTCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
	TACTCCATCA	CCGAAGGCCA	CATCGGGGAG	AAGTTTCTTA	TGGACTACAA	GACTGGTGCT	6000
	CTCACTGTCC	AAACAACAAC	TCAGTTAAGA	AGCGCTACG	AGCTAACCGT	TAGAGCTTCC	6060
	GATGGCAGAT	TTGCGGCCCT	TACCTCTGTC	AAAAATTAAT	TGAAAGAAAG	CAAGAAAGT	6120
	CACCTAAGCT	TTACCCAGGA	TGTCTACTCT	CGCGTAGTGA	AAGAGAATTTC	CACCGAGGCC	6180
	GAAACATTAG	CTGTCAATTAC	TGCTATTGGG	AGTCCAATCA	ATGAGCCTTT	GTITTTATCAC	6240
20	ATCCTCAACC	CAGATCGCAG	ATTTAAAAATA	AGCCGCACTT	CAGGGGTTCT	GTCAACCACT	6300
	GGCAGCGCCT	TCGATCGTGA	GCAGCAGGAG	CGGTTTGATG	TGGTTGTAGA	AGTGATAGAG	6360
	GAACATAAGC	CTTCTGCACT	GGCCCAAGTT	GTCTGGAAGG	TCAATTGTAGA	AGACCAAAAT	6420
	GATAATGCGC	CGGCTGTTGT	CAACCTTCCC	TACTACGCGG	TGTTTAAAGT	GGACACTGAG	6480
	GTGGGCCCATG	TCATTGCGTA	TGTCACTGCT	GTAGACAGAG	ACAGTGGCAG	AAACGGGGAA	6540
25	GTGCATTACT	ACCTCAAGGA	ACATCATGAA	CACCTTCAAA	TTGACCCCTT	GGGTGAAATT	6600
	TCACGTGAAA	AGCAATTGGA	GCTTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCAAAAGATG	GAGGGAACCC	GGCCTTTTCA	GCGGAAGTTA	TGCTTCCGAT	CACGTGCTATG	6720
	AATAAAGCCA	TGCTGTGTTT	TGAAAAACCT	TTCTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
	CAGGTGACCA	GCCCTGTGGT	CCACGTGCAG	GCTAACAGCC	CGGAAGGCCCT	GAAAGTGTTC	6840
30	TACAGCATCA	CAGACGGAGA	CCCTTTCAGC	CAGTTCACTA	TTAACTTCAA	TACTGGAGTT	6900
	ATCAATGTCA	TAGCTCTCTT	GGACTTTGAG	GCCACCCCGG	CATATAAGCT	GAGCATACGC	6960
	GCAACTGACT	CCTTGACGGG	CGCTCATGCT	GAAGTATTTG	TGGACATCAT	AGTAGACGAC	7020
	ATCAATGATA	ACCTCTCTGT	GTTTGTCTAG	CAGTCTTATG	CGGTGACCCCT	GCTGAGGCA	7080
	TCTGTAATTG	GAACTGTCTG	TGTTCAAGTT	AGAGCCACCG	ATTCTGATTC	AGAACCATAAT	7140
35	AGAGGAATCT	CATACCAGAT	GTITGGGAAT	CACAGCAAGA	GTCTATGATCA	TTTTCATGTA	7200
	GACAGCAGCA	CTGGGCTCAT	CTCACTACTC	AGAACCCCTG	ATTACGAGCA	GTCCCGGCAG	7260
	CACAGGATTT	TTGTGAGGGC	AGTTGATGGT	GGTATGCCCA	CGCTGAGCAG	TGATGTGATT	7320
	GTCAAGGTGG	AGCTTACCGA	CCTCAATGGT	AATCCACCA	TCTTTGAACA	ACAGATTAT	7380
40	GAAGCCAGAA	TTAGCGAGCA	CGCCCTCAT	GGGCATTGCG	TGACCTGTGT	AAAAGCCTAT	7440
	GATGCAGACA	GTTCAAGAT	AGACAAGTTG	CAGTATTCCA	TTCTGTCTGG	CAATGATCAT	7500
	AAACATTTTG	TCATTGACAG	TGCAACAGGG	ATTATCACCC	TCTCAACCT	GCACCGGCAC	7560
	GCCCTGAAGC	CATTTTACAG	TCTTAACCTG	TCACTGTCTG	ATGGAGTTT	TAGAAGTTC	7620
	ACCCAGTTTC	ATGTAACCTG	AATTGGAGGC	AATTTGCACA	GTCTCTGTTT	CCTTCAGAAC	7680
	GAATATGAAG	TGGAATAGC	TGAAAACGCT	CCCTACATA	CCCTGTGTAT	GGAGGTGAAA	7740
45	ACTACGGATG	GGGATTCTGG	TATTTATGGT	CAGTTTACTT	ACCATTATTG	AAATGACTTT	7800
	GCCAAAGACA	GATTTTACAT	AAATGAGAGA	GGACAGATAT	TTACTTTTGA	AAACTTGTAT	7860
	CGAGAAACCC	CGGCGGAGAA	AGTGATCTCA	GTCCGTTTAA	TGGCTAAGGA	TGCTGGAGGA	7920
	AAAGTTGGGT	TCTGCACCGT	GAATGTCTATC	CTTACAGATG	ACAATGACAA	TGCAACCAAA	7980
50	TTTGGAGCAA	CCAATAACGA	AGTGAATATC	GGGTCCAGTG	CTGCTAAAGG	GACTTCAGTC	8040
	GTAAAGTCTG	CAAGTATGTC	CGATGAGGGC	TCCAATGCCG	ACATCACCTA	TGCCATTGAA	8100
	GCAGACTGTC	AAAGTGTAAA	AGAGAATTTG	GAAATTAACA	AACTGTCCGG	CGTAATCACT	8160
	ACAAAGGAGA	GCCTCATTTG	CTTGGAATAA	GAATCTTCTA	CTTCTTTTGT	TAGAGCTGTG	8220
	GATAATGGTG	TCCTCATCAA	AGAACTCTGT	GTCTTGTCT	ATGTTAAAT	CCTTCCACCG	8280
55	GAAATGCAAG	TTCCAAATAT	TTCAAGACCT	TTCTATACCT	TTACAGTGTG	AGAGGACGTG	8340
	CCTGTTGGAA	CAGAGATAGA	TCTCATCCGA	GCAGAACATA	GTGGGACTGT	TCTTTACAGC	8400
	TGCTGTAAG	GGAACTACTC	AGAAAGCAAT	AGGGATGAGT	CCTTTGTGAT	TGACAGACAG	8460
	AGCGGAGAGC	TGAAGTTGGA	GAAGAGTCTT	GATCATGAGA	CAACTAAGTG	GTATCAGTTT	8520
	TCCATAGTTC	CCAGGTGCAC	TCAAGATGAC	CATGAGATGG	TGGCTTCTGT	AGATGTTAGT	8580
60	ATCCAAGTGA	AAGATGCAAA	TGACAAACGC	CCGCTCTTGG	AATCTAGTCC	ATATGAGGCA	8640
	TTCTATTGTT	AAAACCTGCC	AGGGGAAGT	AGAGTAATTC	AGATCAGGGC	ATCTGATGCT	8700
	GACTCAGGAA	CCAAAGGCCA	AGTTATGTAT	AGCCTGGATC	AGTCACAAAG	TGTGGAAGTC	8760
	ATTGAATCCT	TTGCCATTAA	CATGGAAAAC	GGCTGGATTA	CAACTTTAAA	GGAACTTGAC	8820
	CATGAAAAGA	GAGACAATTA	CCAGATTAAA	GTGGTTGCAT	CAGATCATGG	TGAAAAGATC	8880
65	CAGCTATCCT	CCACAGCCAT	TGTGGATGTT	ACCGTCAACG	ATGTCAACGA	TAGTCCACCA	8940
	CGATTCAACG	CCGAGATCTA	TAAAGGGACT	GTGAGTGAGG	ATGACCCCCA	AGGTGGGGTG	9000
	ATTGCCATCT	TAAGTACCA	GGATGCTGAT	TCTGAAGAGA	TCAACAGACA	AGTTACATAT	9060
	TTCTATACAG	GAGGGGATCC	TTTAGGACAG	TTTGCCGTTG	AAACTATACA	GAATGAATGG	9120
	AAGGTATATG	TGAAGAAACC	TCTAGACAGG	GAAAAAAGGG	ACAATTACCT	TCTTACTATC	9180
70	ACGGCAACTG	ATGGCACTTT	CTCATCAAAA	GCGATAGTTG	AAGTGAAGT	TCTGGATGCA	9240
	AATGACACAA	GTCCAGTTTG	TGAAAAGACT	TTATATTACG	ACACTATTCC	TGAAGACGTC	9300
	CTTCTGGAAA	AATTGATCAT	GCAGATCTCT	GCTACAGACG	CAGACATCCG	CTCTAACGCT	9360
	GAAATTACTT	ACAAGTTATT	GGGTTACAGT	GCAGAAAAAT	TCAAACTAAA	TCCAGACACA	9420
	GGTGAATCTG	AAAGCTCAAC	CCCCCTTGAT	CGTGAGGAGC	AAGCTGTTTA	TCATCTTCTC	9480
75	GTCAAGGCCA	CAGATGGAGG	AGGAAGATTC	TGCCAAGCCA	GTATTGTGCT	CACGCTAGAA	9540
	GATGTGAACG	ATAACGCCCC	CGAATTCTCT	CGCATCTCT	ATGCCATCAC	CGTGTGTTGA	9600
	AACACGAGGC	CGGGAACGCT	GCTGACAAGA	GTGCAGGCCA	CAGATGCCGA	CGCAGGATTA	9660
	AATCGGAAGA	TTTTATACTC	ACTGATTGAC	TCTGCTGATG	GGCAGTTCTC	CATTAAACGAA	9720
	TTATCTGGAA	TATTCTAGTT	AGAAAAACCT	TTGGACAGAG	AACTCCAGGC	AGTATACACC	9780
	CTCTCTTTGA	AAGCTGTGGA	TCAAGGCTTG	CCAAGGAGGC	TGACTGCCAC	TGGCACTGTG	9840
80	ATTGTATCAT	TTCTTGACAT	AAATGACAAC	CCCCCTGTGT	TTGAGTACCG	TGAATATGGT	9900
	GCCACCGTGT	CTGAGGACAT	TCTTGTGGA	ACTGAAGTTC	TTCAAGTGTG	TGCAGCAAGT	9960
	CGGGATATTT	AAGCAATATG	AGAAATCAC	TACTCAATAA	TAAGTGGAAA	TGAACATGGG	10020
	AAATTACAGA	TGATTCTTAA	AACAGGGGCC	GTATTTATCA	TTGAGAATCT	GGATTATGAG	10080
	AGCTCTCATG	AGTATTACCT	AACAGTAGAG	GCCACTGATG	GAGGCACGCC	TTCACTGAGC	10140



	GACGTTGCCA	CTGTGAACGT	TAATGTAACA	GATATCAACG	ATAATACCCC	TGTGTTTCAGC	10200
	CAAGACACCT	ACACGACAGT	CATCAGTGAA	GATGCCGTTT	TTGAGCAGTC	TGTCATCACG	10260
	GTATATGGCG	ATGATGCCGA	TGGACCTTCC	AACAGCCACA	TCCACTACTC	AATTATAGAT	10320
	GGCAACCAAG	GAAGCTCGTT	CACAAATTGAC	CCCGTCAGGG	GAGAAGTCAA	AGTGACCAAA	10380
5	CTTCTCGACC	GAGAAACGAT	TTCAGGTTAC	ACGCTCACGG	TTCAGCTTTC	TGATAATGGC	10440
	AGTCCACCCA	GAGTCAACAC	GACGACCGTG	AACATCGATG	TGTCGGATGT	CAATGACAAC	10500
	GCGCCCGTCT	TCTCCAGGGG	AAACTACAGT	GTCAATTATC	AGGAAAATAA	GCCAGTGGGC	10560
	TTCAGCGTGC	TGCAGCTGGT	AGTAACAGAT	GAGGATTCTT	CCCATAACGG	TCCACCCCTC	10620
	TTCTTTACTA	TTGTAACTGG	AAATGATGAG	AAGCTTTTGG	AAGTTAACCC	GCAAGGAGTC	10680
10	CTCTTGACAT	CATCTGCGAT	CAAGAGGAAG	GAGAAAGATC	ATTACTTACT	GCAGGTGAAG	10740
	GTGGCAGATA	ATGGAAGCC	TCAGTTGTCA	TCTTTGACAT	ACATTGACAT	TAGGGTAATT	10800
	GAGGAGAGCA	TCTATCCGCG	TGCGATTTTG	CCCCCTGGAG	TTTTCATCAC	CTCTCTGGGA	10860
	GAAGAATACT	CAGGTGGCGT	CATTGGGAAG	ATCCATGCCA	CAGACCAGGA	CGTGTATGAT	10920
	ACTCTAACCT	ACAGTCTCGA	CCCTCAGATG	GACAACCTGT	TCTCTGTTTC	CAGCACAGGG	10980
15	GGCAAGCTGA	TAGCACACAA	AAAGCTAGAC	ATAGGGCAAT	ACCTTCTCAA	TGTCAGCGTA	11040
	ACAGATCGGA	AGTCAACGAC	GGTGGCCGAC	ATCACAGTGC	ATATCAGACA	AGTCACACAG	11100
	GAGATGTTGA	ACCAACCAT	CGCGATCCGC	TTTGCCAACC	TCACTCCGGA	AGAATTCTGT	11160
	GGTGACTACT	CGCGCACTT	CCAGCGAGCT	TTACGGAACA	TCTTGGGTGT	GAGGAGGAAC	11220
	GACATACAGA	TTGTTAGTTT	GCAGTCTCTT	GAACCTCACC	CACATCTGGA	CGTCTTACTT	11280
20	TTTGTAGAGA	AACCAAGTAG	TGCTCAGATC	TCAACAAAAC	AACCTTCTGA	CAAGATTAAC	11340
	TCTTCGCTGA	ATGGAATCTG	GGAAATCATT	GGAGTTAGGA	TACTGAATGT	ATTCAGAAAA	11400
	CTCTGCGCGG	GACTGGAAGT	CCCTTGGGAG	TTCTGCGATG	AAAAGGTGTC	TGTGGATGAA	11460
	AGTGTGATGT	CAGACACAG	CACAGCCAGA	CTGAGTTTGT	TGACTCCCGG	CCACCAACAG	11520
	GCAGCGGTGT	GTCTCTGCAA	AGAGGGAAGG	TGCCCCACCT	TCCACCATGG	CTGTGAAGAT	11580
25	GATCCGTTGC	CTGAGGAGTC	CGAATGTGTG	TCTGATCCCT	GGGAGGAGAA	ACACACCTGT	11640
	GTCTGTCCCA	GCGGCAGGTT	TGCTCAGTGC	CCAGGGAGTT	CATCTATGAC	ACTGACTGGA	11700
	AACAGCTACG	TGAATACCG	TCTGACGGAA	AATGAAAACA	AATTAGAGAT	GAAACTGACC	11760
	ATGAGGCTCA	GAACTATTC	CACGCATCG	GTTGTCTATG	ATGCTCGAGG	AACTGACTAT	11820
	AGCATCTTGG	AGATTATCA	TGGAAGGCTG	CAGTACAAGT	TTGACTGTGG	AAGTGGCCCT	11880
30	GGAAATGTCT	CTGTTTCAGG	CATTGAGTGC	AATGATGGGC	AGTGGCAGCG	AGTGGCCCTG	11940
	GAAGTGAATG	GAACTATGTC	TCGCTTGGTT	CTAGACCAAG	TTTACTACTG	ATCGGGCACA	12000
	GCCCCAGGGA	CTCTGAAAC	CCTGAACTGT	GATAACTATG	TGTTTTTTGG	TGGCCACATC	12060
	CGTCAGCAGG	GAACAAGGCA	TGGAAGAAGT	CCTCAAGTTG	GTAATGGTTT	CAGGGGTTGT	12120
	ATGGACTCCA	TTTATTGAA	TGGSCAGGAG	CTCCCTTTAA	ACAGCAAAAC	CAGAAGCTAT	12180
35	GCACACATCG	AAGATCTGGT	GGATGTATCT	CCAGGCTGCT	TCTTGACGCG	CAGGGAAGAC	12240
	TGCGCCAGCA	ACCTTGGGAC	GAATGGAGGC	GTTTGCAATC	CGTCACCTGC	TGGAGTTATG	12300
	TACTGCAAA	CGAGTGCCTT	GTACATAGGG	ACCCACTGTG	AGATAAGCGT	CAATCCGTGT	12360
	TCTTCCAACT	CATGCTCTTA	TGGGGSCACG	TGTGTTGTGC	ACAACCGAGG	CTTTGTTTGC	12420
	CAGTGTAGAG	GATTATATAC	TGCTCAGAGG	TGTCAGCTTA	GTCCATACCT	CAAAGATGAA	12480
40	CCCTGTAAGA	ATGGCGGAAC	ATGCTTTGAC	AGTTTGGATG	GCGCCGTTTG	TCAGTGTGAT	12540
	TGGGCTTTTA	TGGGAGAAAG	GTGTACAGAT	GATATGACG	AGTGTCTGCG	AAACCCCTGC	12600
	CTGCACGGGG	CCCTCTGTGA	GAACAACGAC	GGCTCTTATC	ACTGCAACTG	CAGCCACGAG	12660
	TACAGGCGAG	GAACATGCGA	GGATGCTGCG	CCCAACCACT	ATGTGTCCAC	GCGCTGGAAC	12720
	ATTGGGTTGG	CGGAAGGAAT	TGGAATCGTT	GTGTTTGTGT	CAGGGATATT	TTTACTGGTG	12780
45	GTGGTGTGTT	TTCTCTGCGG	TAAGATGATT	AGTCGGAATA	AGAAGCATCA	GGCTGAACCT	12840
	AAAGACAAGC	ACCTTGGGAC	CGCTACGGCT	TTCTTGCAAA	GACCGTATTT	TGATTCCAAAG	12900
	CTAAATAGAA	ACATTACTCT	AGACATACCA	CCCCAGGTGC	CTGTCCGGCC	TATTTCTCTC	12960
	ACCCCGAGAG	TTCCAAAGTA	CTCAAGAAAC	AATCTGGACC	GAAATTCCTT	CGAAGGATCT	13020
	GCTATCCAG	AGCATCCCGA	ATTCAGCACT	TTTAACCCCG	AGTCTGTGCA	CGGGCACCGA	13080
50	AAAGCAGTGG	CGGTCTGCAG	CGTGGGCGCA	AACCTGCCTC	CCCCACCCCG	TTCAAACCTC	13140
	CCCTCTGACA	GCGACTCCAT	CCAGAAGCCT	AGCTGGGACT	TTGACTATGA	CACAAAAGTG	13200
	GTGGATCTTG	ATCCCTGTCT	TTCCAAGAAG	CCTCTAGAGG	AAAAGCCTTC	CCAGCCATAC	13260
	AGTGCCCGGG	AAAGCCTGTC	TGAAGTGCAG	TCCCTGAGCT	CCTTCCAGTC	CGAATCGTGC	13320
	GATGACAATG	GGTATCACTG	GGATACATCA	GATTGGATGC	CAAGCGTTCC	TCTGCCGAGC	13380
55	ATACAAGAGT	TCCCACTACT	TGAGGTGATT	GATGAGCAGA	CACCCCTGTA	CTCAGCAGAT	13440
	CCAAAGCCCA	TGATATCGGA	CTATTACCTT	GGAGGCTACG	ACATOGAAAG	TGATTTTCCT	13500
	CCACCCCCAG	AAGACTTCCC	CGCAGCTGAT	GAGCTAACAC	CGTTACCGCC	CGAATTCCAG	13560
	AATCAGTTTG	AATCCATCCA	CCCTCCTAGA	GACATGCCCT	CGCGGGGTGA	CTTGGGTTCT	13620
60	TCATCAAGAA	ACCGGAGAG	GTTCAACTTG	AATCAGTATT	TGCCCAATTT	TTATCCCTCT	13680
	GATATGTCTG	AACCTCAAAC	AAAAGGCAC	GGTGAGAATA	GTAATCTGTG	AGAACCCCAT	13740
	GCCCCCTTAC	CGCCAGGGTA	TCAAAGACAC	TTCGAGGCGC	CGCTGTGCGA	GAGCATGCCC	13800
	ATGTCTGTGT	ACGCTCCAC	CGCTCTCTGC	TCTGACGTGT	CAGCTGCTGT	CGAAGTGGAG	13860
	TCCGAGGTCA	TGATGAGTGA	CTATGAGAGC	GGGACGAGCG	GCCACTTCGA	AGAGGTGACG	13920
	ATCCCGCCCC	TGGATTCCCA	CGACGACACG	GAAGTCTGAC	TCTCAACTCC	CCCCAAAGTG	13980
65	CCTGACTTTA	GTGAACCTAG	AGGTGATGTG	AGTAATCCGC	GCCTGTTCTT	GCAGCAGTGC	14040
	TTCCAAGCTT	TTTTTGGTGA	GCCGAATGGG	CATGGCTGCG	CTGAGTCTTG	CGCTCTGGA	14100
	CGTGCTAGCC	ATTTCCAGTG	TCCCAACTAC	TGTCATCGTG	AGGTTTTCAT	CGCTGTGCCC	14160
	ATTTCCCAAC	GTCTTTTGGG	ATTTACATCT	GTCTGTGTTA	AAATAATCAA	ACGAAAAATC	14220
70	AGTCTGTGTG	TGTCAGCATG	ATTCACTGAT	TTATATAGAT	TTGATTATTT	TAATTTTCTT	14280
	GTCTCTTTTT	TTTGTAATTT	TTATGTACAG	ATTTGATTTT	TCATAGTTTT	AACTAGATTT	14340
	CAAAGATATT	TTTGCAATTT	GTTCACACTG	AATTTTGGTG	GTGTCAGTGC	CATTATCTAG	14400
	CACCTGATT	TTTTTTTTTT	TACTATAACC	AGGTTTTCAT	TCTGTCTTTT	TCCACTGAAG	14460
	TGTGACATT	TGTTAGTACA	TTTCAGTGA	GTCAATTCAT	CTAGCTGTA	CATAGGATGA	14520
	AGGAGAGATC	AGATACATGA	ACATGCTTAA	CATGGGTGCG	TGTAATTTAGA	ATTATAAACA	14580
75	TTTTTCATTA	TTGAAAGTG	TAAACGGGAC	CTTCTGCATA	CCTGTTTAGA	ACCAAAACCA	14640
	CCATGACACA	GTTTTATAG	TGTCGTGATA	TTTGATGATC	AATGGTCTTG	TAAAGGTTTT	14700
	TAATGAAAC	TACCAATAGC	CAGTCTTCT	TACTGACAA	AAATATTAA	TAAAT	14756

80 Seq ID NO: C161 DNA Sequence  
Nucleic Acid Accession #: NM\_014220.1  
Coding sequence: 102..710

1 11 21 31 41 51  
| | | | |

5 GTGGTGTGTTG CTTTCTCCAC CAGAAGGGCA CACTTTCATC TAATTTGGGG TATCACTGAG 60  
 CTGAAGACAA AGAAGAGGGG GAGAAAACCT AGCAGACCAC CATGTGCTAT GGAAGTGTG 120  
 CAOGATGCAT CGGACATTCT CTGGTGGGGC TGGCCTCCT GTGCATCGCG GCTAATATTT 180  
 TGCTTTACTT TCCCAATGGG GAAACAAAGT ATGCCCTCGA AAACCAACCTC AGCCGCTTCG 240  
 TGTGGTTCCT TTCTGGCCTC GTAGGAGGTG GCCTGCTGAT GCTCCTGCCA GCATTGTGCT 300  
 TCATTGGGCT GGAACAGGAT GACTGCTGTG GCTGCTGTGG CCATGAAAAC TGGGGCAAAC 360  
 GATGTGGGAT GCTTCTCTCT GTATTGGCTG CTCTCATTTG AATTGCAGGA TCTGGCTACT 420  
 GTGTCACTTT GGCAGCCCTT GGCTTAGCAG AAGGACCACT ATGTCTTGAT TCCCTCGGCC 480  
 AGTGGAACTA CACCTTTGCC AGCACCAGG GGCAGTACCT TCTGATACCC TCCACATGGT 540  
 10 CGAGTGCAC TGAACCCAAG CACATTGTGG AATGGAATGT ATCTCTGTTT TCTATCCTCT 600  
 TGGCTCTTGT TGGAAATTGA TTCATCTTGT GTCTTATTC AATGAATAAT GGAGTGTCTT 660  
 GAGGCATATG TGGCTTTTGC TGCTCTCACC AACAGCAATA TGACTGTAA AAGAACCAC 720  
 CCAGGACAGA GCCCAATCT TCCTCTATTT CATTTGAATT TATATATTTT ACTTGTATTC 780  
 15 ATTTGTAATA CTTTGTATTA GTGTAACTA CTCCCAACAG TCTACTTTTA CAAAGCCCTG 840  
 TAAAGACTGG CATCTTCACA GGATGTCAGT GTTTAAATTT AGTAAACCTC TTTTGTGTTT 900  
 GTTTATTTGT TTTTGTGTTT TTTTAAAGAA TGAGGAAACA AACCAACCTC TGGGGGTAGT 960  
 TTACAGACTG AGTACAGTA CTCAGTATAT CTGAGATAAA CTCTATAATG TTTTGGATAA 1020  
 AAATAACTAT CCAATCACTA TTGTATATAT GTGCATGTAT TTTTAAATTT AAAGATGTCT 1080  
 20 AGTTGCTTTT TATAAGACCA AGAAGGAGAA AATCCGACAA CCTGGAAGAA TTTTGTGTTT 1140  
 CACTGCTTGT ATGATGTTTC CCATTACATC ACCTATAAAT CTCTAACAG AGGCCCTTTG 1200  
 AACTGCCCTG TGCTCTGTGA GAAACAAATA TTTACTTAGA GTGGAAGGAC TGATTGAGAA 1260  
 TGTTCCAACT CAAATGAATG CATCAACTA TACAATGCTG CTCAATGTGT TGAGTACTAT 1320  
 GAGATTCAAT TTTTCTAAC ATATGGAAG CCCTTGTGTC TCCAAAGATG AGTACTAGGG 1380  
 25 ATCATGTGTT TAAAAAAGA AAGGCTACGA TGACTGGGCA AGAAGAAAGA TGGGAAACCTG 1440  
 AATAAGCAG TTGATCAGCA TCATTGGAAC ATGGGGACGA GTGACGGCAG GAGGACCACG 1500  
 AGGAATATCC CTCAAAATA ACTTGTATTAC AACAAAATAA AGTATTCACT ACGAAAAAAA 1560  
 AAAAAAATAA AAAAAAATA AAA 1583

30 Seq ID NO: C162 DNA Sequence  
 Nucleic Acid Accession #: NM\_003759.1  
 Coding sequence: 150..3257

35 1 11 21 31 41 51  
 | | | | |  
 GTTCTTTTGT ACACATCACA CAGAATTGGA GTGCTGTCCT TCTGGAGAGT GGTGGAGAAC 60  
 CAAGATACAG TTCAGAACCA AAGGAATAGA GAAGGGCTTT GATTCTTTT TGGCTTTAGA 120  
 TTGGGGATTG GGGAGGCTTA GCAGGAAAGA TGTCCTACTG AATGTGGAA GGGAAAGCCA 180  
 GTAACTCTGG GAGAGAGGGA AGAGCCCGGA GCTCCACTTT CCTCAGGTT GTCCAGCCAA 240  
 40 TGTTTAAACA CAGTATTTTC ACTTCTGCAG TCTCTCTGCG TGCAGAACGC ATCCGATTCA 300  
 TCTTGGGAGA GGAGGATGAC AGCCCGAGCTC CCCCTCAGCT CTTCACGAA CTGGATGAGC 360  
 TGCTGGCCGT GGTGCGGAGC GAGATGGAGT GGAAGGAAAC AGCCAGGTGG ATCAAGTTTG 420  
 AAGAAAAGT GGAACAGGCT GGGGAAAGAT GGAGCAAGCC CCATGTGGCC ACATTGTCCC 480  
 TTCAATGTTT ATTTGAGCTG AGGACATGTA TGGAGAAAGG ATCCATCATG CTTGATCGGG 540  
 45 AGGCTTCTTC TCTCCACAG TTGGTGGAGA TGATTGTGA CCATCAGATT GAGACAGGCC 600  
 TATTGAAACC TGAACCTAAG GATAAGGTGA CCTATACTTT GCTCCGGAAG CACCGGCATC 660  
 AAACCAAGAA ATCCACCTT CGGTCCCTGG CTGACATTGG GAAGACAGTC TCCAGTGCAA 720  
 GTAGGATGTT TACCAACCTC GATAATGGTA GCCCAGCCAT GACCCATAGG AATCTGACTT 780  
 CCTCCAGCTT AATGACATT TCTGATAAAC CGAGAAAGGA CCAGCTGAAG AATAAGTTCA 840  
 50 TGAATAAATT GCCACGTGAT GCAGAACTT CCAACGTGCT TGTGGGGAG GTTGACTTTT 900  
 TGGATACTCC TTTCAATGCC TTTGTTAGGC TACAGCAGGC TGTCTGCTG GGTGCCCTGA 960  
 CTGAAGTTTC TGTGCCACA AGGTTCTTGT TCATTCTCT AGTCTCTAAG GGGAAAGCCA 1020  
 AGTCTTACCA CGAGATTGGC AGAGCCATTG CCACCTCTGAT GTCTGATGAG GTGTTCCATG 1080  
 ACATTGCTTA TAAAGCAAAA GACAGGCAAG ACCTGATTGC TGTGATTGAT GAGTTCCTAG 1140  
 55 ATGAAGTCAT CGTCTTCCA CTGGGGAAAT GGGATCCAGC AATTAGGATA GAGCTCCTA 1200  
 AGAGTCTTCC ATCTCTGAC AAAAGAAAGA ATATGTACT AGGTGGAGAG AATGTTTACA 1260  
 TGAATGGAGA TGCACCCAT GATGGAGGTC ACGGAGGAGG AGGACATGGG GATTGTGAAG 1320  
 AATTGCAAGG AACTGGAAGG TTCTGTGGTG GACTAATTA AGACATAAAG AGGAAAGGCC 1380  
 CATTTTGTGC CAGTGAATTT TATGATGCTT TAAATATTC AGCTCTTTC GCAATTTCTT 1440  
 60 TCATTATCTT GGCACCTGTA ACTAATGCTA TCATTTTGG AGGACTGCTT GGGGATGCCA 1500  
 CTGACAACAT GCAGGGCGTG TTGGAGAGTT TCCTGGGCAC TGCTGTCTCT GGAGCCATCT 1560  
 TTTGCCCTTT TGCTGGTCAA CCATCACTA TTCTGAGCAG CACCGGACCT GTCCTAGTTT 1620  
 TTGAGAGGCT TCTATTATAT TTCAGCAAGG ACAAATAATT TGACTATTG GAGTTTCGCC 1680  
 TTTGGATTGG CCTGTGCTCC GCCTTCTAT GTCTCATTTT GGTAGCCACT GATGCCAGCT 1740  
 65 TCTTGGTTCA ATACTTACA CGTTTACGG AGGAGGGCTT TTCTCTCTG ATTAGCTTCA 1800  
 TCTTTATCTA TGATGCTTTC AAGAAGATGA TCAAGCTTGC AGATTACTAC CCCATCACT 1860  
 CCAACTTCAA AGTGGGCTAC AACACTCTCT TTTCTGTAC CTGTGTGCCA CCTGACCCAG 1920  
 CTAATATCTC AATATCTAAT GACACCAAC TGGCCCCAGA GTATTTGCCA ACTATGTCTT 1980  
 CTACTGACAT GTACCATAAT ACTACCTTTC ACTGGGCATT TTTGTGGAAG AAGGAGTGT 2040  
 70 CAAATAACGG AGGAACCTT GTGGGAACA ACTGTAATTT TGTCTCTGAT ATCACACTCA 2100  
 TGTCTTTTCT CCTCTTCTG GGAACCTACA CCTCTTCCAT GGTCTGAAA AAATTCAAAA 2160  
 CTAGTCTCTA TTTTCCAAAC ACAGCAAGAA AACTGATCAG TGATTTTGCC ATTATCTTGT 2220  
 CCAATCTCAT CTTTGTGTA ATAGATGCC TAGTAGGCTG GGACACCCCA AAATAATTG 2280  
 TGCCAAAGTA GTTCAAGCCA ACAAGTCCAA ACCGAGGTTG GTTGTGTTCA CGTTTGGAG 2340  
 75 AAAACCCCTG GTGGGTGTGC CTGTGCTG CTATCCCGGC TTTGTGGTC ACTATACTGA 2400  
 TTTTCATGGA CCAACAAAT ACAGCTGTGA TGTAAACAG GAAAGAACAT AAATCAAGA 2460  
 AAGGAGCAGG GTATCACTTG GATCTCTTT GGGTGGCCAT CCTCATGGTT ATATGCTCCC 2520  
 TCATGCTCT TCGTGGTAT GTAGCTGCTA CGTCACTCT CATGCTCAC ATGACAGTT 2580  
 TGAAGATGA GACAGAGAT TCTGCACTG GAGAACAAAC AAAGTTTCTA GGAGTGAAG 2640  
 80 AACAAAGAGT CACTGGAAC CTGTGTGTTA TTCTGACTGG TCTGCTAGTC TTTATGCTC 2700  
 CCATCTTGAA GTTTATACCC ATGCTGTAC TCTATGGTGT GTTCTGTAT ATGGAGTAG 2760  
 CATCCCTTAA TGGGTGTCAG TTCATGGATC GTCTGAAGCT GCTTCTGAT CCTCTGAAGC 2820  
 ATCAGCCTGA CTCTATCTAC CTGCTCATG TTCTCTGCG CAGAGTCCAC CTGTTCACTT 2880  
 TCCTGCAGGT GTGTGTGCTG GCCCTGCTT GGCATCTCAA GTCAACGGTG GCTGCTATCA 2940  
 TTTTCCAGT AATGATCTTG GCATGTGAG CTGTCAAGAA AGCATGGAC TACCTCTTCT 3000

	CCCAGCATGA	CCTCAGCTTC	CTGGATGATG	TCATTCCAGA	AAAGGACAAG	AAAAAGAAGG	3060
	AGGATGAGAA	GAAAAAGAAA	AAGAAGAAGG	GAAGTCTGGA	CAGTGACAAT	GATGATTCTG	3120
	ACTGCCCAT	CTCAGAAAAA	GTTCCAAGTA	TTAAAAATCC	AATGGACATC	ATGGAACAGC	3180
	AACCTTTCCT	AAGCGATAGC	AAACCTTCTG	ACAGAGAAAG	ATCACCACA	TTCTTGAAC	3240
5	GCCACACATC	ATGCTGATAA	AATTCCCTTC	CTTCAGTCAC	TCGGTATGCC	AAGTCTCCT	3300
	AGAACTCCAG	TAAAAGTTGC	CTCAAATTAG	ACTAGAACTT	GAACCTGAAG	ACAATGATTA	3360
	TTTCTGGAGG	AGCAAGGGAA	CAGAAACTAC	ATTGTAACCT	GTTTGTCTTT	CTTAAAACCTG	3420
	ACATTITGTT	TTAATGTCAT	TTGTTTTTGT	TTGGCTGTTT	GTTTATTTT	TAACTTTTAT	3480
10	TTGCTCTCAG	TTTTTGGTCA	CAGGCCAAAT	AATACAGCGC	TCTCTCTGCT	TCTCTCTTGC	3540
	ATAGATACAA	TCAAGACAAT	AGTGCAACCGT	TCCTTAAAAA	CAGCATCTGA	GGAATCCCCC	3600
	TTTTGTTCCT	AAACTTTCAG	ATGTGTCCTT	TGATAACCAA	ATTCTGTAC	TCAAGACACA	3660
	GACACCCACA	GACCTGTGCC	TTTGCTCTTA	TTAAGCAGAG	GATGGAAAGTA	TTAAGGATTT	3720
	TGTAACACCT	TTAATGAAAA	TGTTGAAGGA	ACTTAAAACT	TTAGCTTTGG	AGCTGTGCTT	3780
15	ACTGGCTTGT	CTTTGTCTGG	TAGAACAAC	CTTGACCTCC	AGACAGAGTC	CCTTCTCACT	3840
	TATAGAGCTC	TCCAGGACTG	GAAAAAGTGC	TGCTATTTTA	ACTTGTCTTT	GCTTGTAAAT	3900
	CCTAATCTTA	GAGTTATCAA	AAGAAGAAAA	AACCTGAAGGT	ACTTTACTCC	CTATAGAGAA	3960
	ACCATTGCCA	TCATTGTAGC	AAGTGCTGGA	ATGTCCCTTT	TTTCTATGCG	AACCTTTTTTA	4020
	TAACCCCTTA	TTGAATCTAT	CTGTGGAGTA	CATTGAAGAA	TATTTTCTTT	CCTAGATTTT	4080
20	GTGTTTAA	TTATGGGGCC	TAACTGCCA	CTTATTTTTT	GTCAAATTTT	AAAACCTTTT	4140
	TTTAATTACT	GTAAAGAAAA	TGAATTTTTT	CTGSCAGCAG	GAAACATAGT	TTTCAGTAGT	4200
	TCTACCTCTT	ATTGTAGCT	GCCAGGCTTT	CTGTAAAAAT	TGTATTGTAT	ATAATGTGAT	4260
	TTTTACACAT	ACATACACAC	ACAAATACAC	AATCTCTAGG	GTAAGCCAGA	AGGCAAGATC	4320
	AGATTAAAA	CACCATGTTT	CTAAGCATCC	ATTTTCCCTT	TTCTTTAAAA	GAAACTTAAC	4380
25	TGTTCTATGA	AGGAGATTGA	GGGAGAAGAG	ACAACTCCTT	ATGTCTAGAG	AATAACCGAT	4440
	GTTCGTATA	TAGTAGCATC	TAGGTACAGA	TGCTGGTTGT	ATTACCACTG	CAATGTCTTA	4500
	TGCAGTATTG	TTAGACATTT	TCTCATTTTG	AAATATTGTG	GTGTTTGTGT	ATGTGCTCTG	4560
	TGCCATGGCT	GGTGTATATA	TGTGCAATGT	TAGAAGGCAA	AAGAGTGATG	GTAGGCGAGAG	4620
	GGCAAGTCA	TGAAATCTCT	TATGCCAGTT	TTCAATAAAC	CCAAACCACA	TATGAAAAAA	4680
30	TCCATTAAAG	GTCCAAAGAG	TCTGTCCATA	TGAAATAGAG	GGTAAATATA	GTTTATTTCC	4740
	CAGGTATCAG	TCATTATAAT	TGATATAATA	GCTCAACAT	GCAATATAAA	ATTCATAGGA	4800
	GTATTAAATAG	CCCATTTACA	CATCTATAAA	ATGTAATGGG	ATTGCAGAGC	TGCAGAGTAC	4860
	AGTGTAAACAG	TACTCTCATG	CAATTTTTTT	CAGGATGCAA	AGGCAATTAT	TCTTTGTAAAG	4920
	CGGGACATTT	AGATATATTT	GTGTACATAT	TATATGTATG	TATATTTCAA	AGTACCACAC	4980
35	TGAAATATAG	ACATTATTTA	ACCAAAATTA	ACGTGGTATT	TAAAGGTAAT	ATTTTATAAT	5040
	TGATACATTA	CATATTGTGA	ATGTATACTA	AAAAAACATT	TAAATGTGTA	AAATTATAAT	5100
40	TTCAGATTCA	TATAACCACA	ACTGTGATAT	ATCCTAACTA	TAACCACTTG	TTGAGGGGTA	5160
	TACTACAGAG	AGAATGAAAC	CACATTTTTT	GGTTTGATAA	TATGCACCTA	TTGACTCCCA	5220
	CTCATTGTTA	TGTAAATTTA	GTTATTATTC	TGCTCTCTTG	TAATTTTGAT	TACAAAAAAT	5280
	TTATTATCCT	GAGTTAGCTG	TTACTTTTAC	AGTACCTGAT	ACTCCTAAAA	CTTTTAACTT	5340
45	ATACAAATTA	GTCAATAATG	ACCCCAATTT	TTTCATTAAA	ATAATAGTGG	TGAATTATAT	5400
	GTATTGTGTT	TAAAACTCA	CTTGCCAAAT	TCTGGCTTCA	CATTTGTATT	TAGGGCTATC	5460
	CTTAAATGTA	TGAGTCTATA	TTATCTAGCT	TTCTATTACC	CTAATATAAA	CTGGTATAAG	5520
	AAGACTTTCC	TTTTTCTTTT	ATGCATGGAA	GCATCAATAA	ATTGTTTAAA	AACCATGTAT	5580
50	AGTAAATTC	GCTTAACCCG	TGATCTTCTT	AAGTTAAAGG	TACTTTTGGT	TTATAAAGC	5640
	TCTAGATAAA	ACTTCTTTTT	CTGATCATGA	ATCAAGTATC	TGTGGTTTCA	TGCCCCCTCT	5700
	TATACCTTTC	AAAGAACTCC	TGAAGCAACT	TAACCTCATCA	TTTCAGGCTC	TGAGTAGAGG	5760
	TAAACCTAT	GTGTACTTCT	GTTTATGATC	CATATTGATA	TTTATGACAT	GAACACAGAA	5820
	TAGTACCTTA	CATTGTCTAA	ACAGACAGTT	AATATCAAAT	CCTTTCAATA	TTCTGGGAAC	5880
55	CCAGGGAAGT	TTTTAAAAAT	GTCTTACTT	TCAAAGGAAC	AGAAGTAGTT	AACCAAACTA	5940
	ACAAGCAAAA	CCTGAGGTTT	ACCTAGTGAC	ACCAAAATTA	CGGTATTTTA	ACTGAATTTA	6000
	CCCATTGACT	AGAATGAAC	CGGATTGGT	GGTGGTTTGG	TTTCTATGCA	AACTGGACAC	6060
	AAATTACAAC	AGTAAATTTT	TTTATAAGTG	CTTCTCCCTT	CTCCATGATG	TGACTTCCGG	6120
	AGATAAGAGA	TTCAAAAGAT	AAAGACAAAG	TACGCTCAGA	GTGTTAAACC	AGAAAGTCTT	6180
60	GGCTGTGGTT	GCAGAAACAC	TGTTGGAAGA	AAAGAGATGA	CTAAGTCAAG	TGCTGCTCCT	6240
	ATCAAAAGAG	CAAAAATGCC	TCTGGTTTTG	TGTTTGGGAG	AAAAATATCT	TGGACGCACT	6300
	GTTTTCTCTG	ATAAAAGTCA	TCTTCTCTAC	TGTGTGAAAT	GAATACTTGG	AATTCTAATT	6360
	GTTTTGTGTG	CCAGGGGCG	TAAATGCCCT	GCCTCTCTCT	CCAATCAAGG	TTGAGGAGTG	6420
	GGGCTGGGGA	GAGGACTTAA	CTGACTTAAG	AAGTAGGAAA	ACAAAAACCT	CTCTCTCAG	6480
65	CCTTCCACCT	CCAAGAGAGT	AGGAAAAACA	GTGTCTGCT	GTCTGTAAAT	CAGTTTGCCT	6540
	GTATTTTATG	CTCATGCAAC	AACCCATACA	GAGTAAATCT	TTTATCAACT	ATATACTGGT	6600
	GTTTAATAGA	GAATGATTGT	CTTCCGAGTT	TTTTGGTTCC	TTTTTTAACT	GTGTTAAAGT	6660
	ACTTGAAATG	TATTGACTGC	TGACTATATT	TTAAAAACAA	AATGAAATAA	TTTGTAGTTG	6720
	ATTACAGAGG	TTGACATTGT	TCAGGGATGG	GACAAAGCCT	TCTTCAATCC	TTTTCATACT	6780
70	ACTTAATGAT	TTTGGTCAG	GAACCTGAGA	TTTTCTGATT	TATATTTCAT	GATATTTCAC	6840
	ATTTGCTCTT	CCACAGATGA	GCATGAAGCC	CAGTGGCACC	AAATGGCTGG	GTCAATCAAA	6900
	GTGATATTTT	GTAGCACCTC	ACTATCTGAA	AGGCCATGAG	TTTTTCAGATG	ATTTCAATTGA	6960
	GCTTCATTCG	AGCCTGAAAT	TTTAAAAAAG	TTGTGTAATA	CGCCAACAG	TCAAGTTGTG	7020
	TTTTGGCCAG	AGATTAGAT	ATGTCCAATT	TCCTGGCTCA	TTTCATTGTG	CTCTATGGGT	7080
75	ACGTATAAAA	AGCAAGAATT	CTGTTCCTTA	GGCAACATT	GCAACTCAGG	GCTAAAGTCA	7140
	TCCAGTGAAA	CTTTTAGAGC	CAGAAGTAAC	TTTGTCCAG	TCCTACAATG	TGAAAAGAGT	7200
	GAATAGTTGC	CTCTTTTTAG	CCATTTTCAT	GGCTGGTACA	TATTCGTACG	CATTACTTTT	7260
	CAGAAATCAAT	ACGCATTTTC	AGATATTTCT	ATTTTTATTC	TCTTAAGTCT	TTATTAACTT	7320
	TGGAGAGAGA	AATGATGCAT	CTTTTTATTT	TAAATGAAGT	AGATCAACAT	GGTGGAAACAA	7380
	AATGATAAAG	AACAGAAAC	ATTTCAATAT	ATTACTAATA	ACTTTTTCCA	ATATAAATCC	7440
80	TAAAATTCCT	ATAACATAGT	ATTTTACAGT	TTTATGAAGC	TTTCTATTGT	GACTTTTATG	7500
	GAATTAAGAG	ATGAAGAAGA	TGAGATATTT	TAGCATTTAT	ATTTTTCAAA	ATTATATGTA	7560
	TACTTAAAAA	TAAAGTAACT	TTATGC				7586

Seq ID NO: C163 DNA Sequence  
Nucleic Acid Accession #: NM\_000958  
Coding sequence: 389..1855

1 11 21 31 41 51  
| | | | |  
1301

5  
10  
15  
20  
25  
30  
35

```

CGGCACAGCC TCACACCTGA ACGCTGTCTT CCCGACAGCG AGACCGGCGG GCACTGCAAA 60
GCTGGGACTC GTCTTTGAAG GAAAAAATAA AGCGAGTAAG AAATCCAGCA CCATTCTTCA 120
CTGACCCATC CGCTGACACC TCTTGTTCCT CAAGTTTITG AAAGCTGGCA ACTCTGACCT 180
CGGTGTCCAA AAATGCACAG CCACTGAGAC CGCTTTTGAG AAGCCGAAGA TTTGGCAGTT 240
TCCAGACTGA GCAGGACAAG GTGAAAGCAG GTTGGAGGCG GTTCCAGGAC ATCTGAGGSC 300
TGACCCCTGGG GGCTGTGTAG GCTGCCACCG CTGCTGCCGC TACAGACCCA GCCTTGCACT 360
CCAAGGCTGC GCACCGCCAG CCACTATCAT GTCCACTCCC GGGGTCAATT CGTCCGCTCT 420
CTTGAGCCCC GACCGGCTGA ACAGCCCACT GACCATCCCG GCGGTGATGT TCATCTTCGG 480
GGTGGTGGCG AACCTGGTGG CCATCGTGGT GCTGTGCAAG TCGCGCAAGG AGCAGAAGGA 540
GACGACCTTC TACACGCTGG TATGTGGGCT GGCTGTCAAC GACCTGTTGG GCATTGTGTT 600
GGTGAGCCCG GTGACCATCG CCACGTACAT GAAGGGCCAA TGGCCCGGGG GCCAGCCGCT 660
GTGCGAGTAC AGCACCCTCA TTCTGCTCTT CTTCAGCCCTG TCGGCTCTCA GCATCATCTG 720
CGCCATGAGT TCGAGCGCTT ACCTGGCCAT CAACCATGCC TATTTCTACA GCCACTACCT 780
GGACAAGCGA TTGGCGGGCC TCAOGCTCTT TGCAGTCTAT GGTCCCAACG TGCTCTTTTG 840
CGCGCTGCCC AACATGGGTC TCGGTAGCTC GCGGCTGCAG TACCAGACA CCTGGTGTCT 900
CATCGACTTG ACCACCAACG TGACGGCGCA CGCGCCCTAC TCCTACATGT ACGCGGGCTT 960
CAGCTCCTTC CTCTTCTGCG CCACCGTCTT CTGCAACCTG CTGTGTGTCG GCGCGCTGCT 1020
CGCATGCGCC CGCCAGTTCA TGCGCCGCGC CTGCTGGGCG ACCGAGCAGC ACCACGCGGC 1080
CGCGCGCCCG TCGGTTCGCT CCCGGGGCCA CCCGCTGCGC TCCCGAGCCT TGCGCGGCTT 1140
CAGCGACTTT CGCGCGCGCC GGAGCTTCCG CCGCATCGCG GCGCGCGAGA TCCAGATGGT 1200
CATCTTTACTC ATTGCCACTC CCCTGGTGGT GCTCATCTCG TCCTATCCCG TCCTGGTGGG 1260
AGTATTCTGC AACCACTTAT ATCAGCCAAAG TTTGGAGCGA GAAGTCAGTA AAAATCCAGA 1320
TTTGAGGCCC ATCCGAATTG CTCTGTGAA CCCCCTCTTA GACCCCTGGA TATATATCT 1380
CCTGAGAAAG ACAGTGTCTA GTAAAGCAAT AGAGAAGATC AAATGCTCTT TCTGCGCAT 1440
TGGCGGGTCC CGCAGGGAGC GCTCCGGACA GCACTGCTCA GACAGTCAAA GGACATCTTC 1500
TGCCATGTCA GGCCACTCTC GCTCCTTCAT CTCCCGGGAG CTGAAGGAGA TCAGCAGTAC 1560
ATCTCAGACC CTCTCGCCAG ACCTCTCACT GCCAGACCTC AGTGAAATAG GCCTTGGAGG 1620
CAGGAATTTC CTTCAGGTG TGCTGGCAT GGGCTGGGCC CAGGAAGACA CCACCTCACT 1680
GAGGACTTTG CGAATATCAG AGACCTCAGA CTCTTCACAG GGTGAGGACT CAGAGAGTGT 1740
CTTACTGGTG GATGAGGCTG GTGGGAGCGG CAGGGCTGGG CCTGCCCTTA AGGGGAGCTC 1800
CCTGCAAGTC ACATTTCCCA GTGAAACACT GAACCTATCA GAAAAATGTA TATAATAGGC 1860
AAGGAAAGAA ATACAGTACT GTTCTGGAC CCTTATAAAA TCCTGTGCAA TAGACACATA 1920
CATGTACATC TTAGCTGTGC TCAGAAGGGC TATCATCA 1958

```

Seq ID NO: C164 DNA Sequence  
Nucleic Acid Accession #: NM\_002659.1  
Coding sequence: 427..1434

40  
45  
50  
55  
60  
65  
70

```

1 11 21 31 41 51
| | | | |
CAGTATCCCT CCTGACAAAA CTAACAAAAA TCCTGTAGC CAAATAATCA GCCACATTCA 60
TATTTACCGT CAAAGTTTTT ATCTCATTT TACAGCAGTG GAGAGCGATT GCCCGGGTGC 120
CCACGTTAGG AAGAGAGAGA ACTGGGATTT GCACCCAGGC AATCTGGGGA CAGAGCTGTG 180
ATCACAACTC CATGAGTCAG GGCCGAGCCA GCGCTTCAC CACCAGCCGG CCGCGCCCCG 240
GGAAGGAAGT TTTGGGCGGA GGAGGTTCTG ACGGAGGAGG GGGGAGGCGC CCACGCATCT 300
GGGGCTGACT CGCTCTTTTG CAATAACGTCT GGGAGGAGTC CCTGGGGCCA CAAAACCTGC 360
TCCTTCTCTG GGCCAGAAAG AGAGAAGACG TGCAGGGACC CCGCGCACAG GAGCTGCCCT 420
CGCGACATGG GTACCCCGCC GCTGCTGCGG CTGCTGCTGC TGCTCCACAC CTGOGTCCCA 480
GCCCTCTGGG GCCTCGGGTG CATGCAGTGT AAGACCAACG GGGATTGCGG TGTGGAAGAG 540
TGCGCCCTTG GACAGGACCT CTGAGGAGCC ACGATCGTGC GCTTGTGGGA AGAAGGAGAA 600
GAGCTGGAGC TGGTGGAGAA AAGCTGTACC CACTCAGAGA AGACCAACAG GACCTGTAGC 660
TATCGGACTG GCTTGAAGAT CACCAGCCTT ACCGAGGTTG TGTGTGGGTT AGACTTGTGC 720
AACCAGGGCC ACTCTGGCGG GGCTGTCACT TATTTCCGAA GCGTTTACCT CGAATGCAAT 780
TCCTGTGGCT CATCAGACAT GAGCTGTGAG AGGGGCGCGC ACCAGAGCCT GCAGTCCGCG 840
AGCCCTGAAG AACAGTGCCT GGATGTGGTG ACCCACTGSA TCCAGGAAGG TGAAGAAGGG 900
CGTCCAAAGG ATGACCGGCA CCTCGGTGGC TGTGGCTACC TTCCGGCTG CCGGGGCTCC 960
AATGGTTTCC ACACAACAGA CACCTTCCAC TTCTGAAAT GCTGCAACAC CACCAATGTC 1020
AACGAGGGCC CAATCTGGGA GCTTGAATAA CTGCGCGAGA ATGGCCGCGA GTGTACAGC 1080
TGCAAGGGGA ACAGCACCCA TGGATGCTCC TCTGAAGAGA CTTTCTCAT TGACTGCCGA 1140
GGCCCCATGA ATCAATGTCT GGTAGCCACC GGCACCTACG AACCGAAAAA CCAAGCTAT 1200
ATGGTAAGAG GCTGTGCAAC CGCTCAATG TGCCAACTG CCCACCTGGG TGACGCTTTC 1260
AGCATGAACC ACATGTAGT CTCTGTCTGT ACTAAAAGTG GCTGTAAACA CCCAGACCTG 1320
GATGTCCAGT ACCGAGTGG GGCTGTCTCT CAGCCTGGCC CTGCCCATCT CAGCCTCACC 1380
ATCACCTTGC TAATGACTGC CAGACTGTGG GGAGGCATCT TCCTCTGGAC CTAAACCTGA 1440
AATCCCCCTC TCTGCCCTGG CTGGATCGGG GGGACCCCTT TGCCCTTCCC TCGGCTCCCA 1500
GCCCTACAGA TTTGCTGTGT GACCTCAGGC CAGTGTGGCG ACCTCTCTGG GCCTCAGTTT 1560
TCCCAGCTAT GAAACAGCT ATCTCACAAA GTTGTGTGAA GCAGAAGAGA AAGCTGGAG 1620
GAAGGCGGTG GGCAATGGGA GAGCTCTTGT TATTATTAAT ATTGTGCGG CTGTGTGTGT 1680
GTTGTATTA ATTAATATTC ATATTATTTA TTTTATACT ACATAAGAT TTTGTACCAG 1740
TGG

```

Seq ID NO: C165 DNA Sequence  
Nucleic Acid Accession #: AK027843.1  
Coding sequence: 193..1731

75  
80

```

1 11 21 31 41 51
| | | | |
TTGCTTGAGT CATCTTCTGA AGCTTTAAAA ACAATTGATG AATTGGCCTT CAAGATAGAC 60
CTAAATAGCA CATCACATGT GAATATTACA ACTGGAACT TGGCTCTCAG CGTATCATCC 120
CTGTTACCAG GSAACAATGC AATTTCAAAT TTTAGCATGT GTCCTTCAAG CAATAATGAA 180
TCGTATTTCC AGATGGATTT TGAGAGTGGG CAAGTGGATC CACTGGCATC TGTAATTTTG 240
CCTCCAACTC TACTTGAGAA TTTAAGTCCA GAAGATTCTG TATTAGTTAG AAGAGCACAG 300
TTTACTTTCT TCAACAAAAC TGGACTTTTC CAGGATGTAG GACCCCAAGG AAAAATTTTA 360
GTGAGTTATG TGATGGCGTG CAGTATTGGA AACATTACTA TCCAGATCT GAAGGATCCT 420

```

GTTCAAAATAA AAATCAAACA TACAAGAACT CAGGAAGTGC ATCATCCCAT CTGTGCCTTC 480  
 TGGGATCTGA AAAAAACAA AAGTTTGGGA GGATGGAACA CGTCAGGATG TGTGACACAC 540  
 AGAGATTGAG ATGCAAGTGA GACAGTCTGC CTGTGTAACC ACTTCACACA CTTTGGAGTT 600  
 CTGATGGACC TTCCAAGGAG TGCCCTCAGG TTAGATGCAA GAAACACTAA AGTCTCACT 660  
 5 TTCATCAGCT ATATTGGGTG TGGAAATCTCT GCTATTTTTT CAGCAGCAAC TCTCTGACA 720  
 TATGTTGCTT TTGAGAAATT GCGAAGGGAT TATCCCTCCA AAATCTTGAT GAACCTGAGC 780  
 ACAGCCCTGC TGTTCCTGAA TCTCCTCTTC CTCTAGATG GCTGGATCAC CTCTTCAAT 840  
 GTGGATGGAC TTGCAATGTC TGTTCAGTCT CTGTGCAAT TCTTCTTCT GGCAACCTTT 900  
 10 ACCTGGATGG GGCTAGAAGC AATTCACATG TACATTGCTC TAGTTAAAGT ATTTAACTACT 960  
 TACATTCGCC GATACATCTT AAAATTCTGC ATCATTGGCT GGGGTTTGGC TGCCTTAGTG 1020  
 GTGTCACTTG TTCTAGCGAG CAGAAACAAC AATGAAGTCT ATGGAAGAAG AAGTTATGGG 1080  
 AAAGAAAAGG GTGATGAATT CTGTGGGATT CAAGATCCAG TCATATTTTA TGTGACCTGT 1140  
 GCTGGGTATT TTGGAGTCAT GTTTTTCTG AACATTGCCA TGTTCATTGT GGTAATGGTG 1200  
 15 CAGATCTGTG GGAGGAATGG CAAGAGAAGC AACCGGACCC TGAGAGAAGA AGTGTAAAGG 1260  
 AACCTGCGCA GTGTGGTTAG CTTGACCTTT CTGTGGGCA TGACATGGGG TTTTGCATTG 1320  
 TTTGCTGGGG GACCTTAAAT TATCCCTTTC ATGTACCTCT TCTCCATCTT CAATTCACTA 1380  
 CAAGGCTTAT TTATATTCAT CTTCACATGT GCTATGAAGG AGAATGTTCA GAAACAGTGG 1440  
 CGGCGGCATC TCTGCTGTGG TAGATTTCGG TTAGCAGATA ACTCAGATTG GAGTAAGACA 1500  
 20 GCTACCAATA TCATCAAGAA AAGTTCTGAT AATCTAGGAA AATCTTTGTC TTCAAGCTCC 1560  
 ATTGGTTCCA ACTCAACCTA TCTTACATCC AATCTAAAT CCAGCTCTAC CACCTATTTC 1620  
 AAAAGGAATA GCCACACAGA TAATGCTCTC TATGAGCATT CCTTCAACAA AAGTGGATCA 1680  
 CTCAGACAGT GCTTCCATGG ACAAGTCTCT GTCAAACTG GCCCATGCTG ATGGAGATCA 1740  
 AACATCAATC ATCCCTGTCC ATCAGGTCTAT TGATAAGGTC AAGGGTTATT GCAATGCTCA 1800  
 25 TTCAGACAAC TTCTATAAAA ATATTATCAT GTCAGACACC TTCAGCCACA GCACAAAGTT 1860  
 TTAATGTCTT TAAGAAAAAG AAATCAATCT GCAGAAATGT GAAGATTGTC AAGCAGTGTA 1920  
 AACTGCAACT AGTGATGTAA ATGTGCTATT ACCTAGGTAA CTGCATATAT ATAAGGAATG 1980  
 TATTTTGTGA AGAAGGCTTT TGTGAAATTC AGAATTTTTC TTTTAAATAT ATTTCTTCCA 2040  
 TGGAAAGATC GTGATCACTA AAATCTCAGT ACTGAGAGTA ACATGACTCA GTAGCCACAG 2100  
 30 AAGCTATGAT TTGTAATAA TATAATTGAA TCAGAGTAAT CATAATGACG GGGAGACATT 2160  
 CAAATTAGAG ACAAGGGAGA AGCAATGCTG AGGAAGACCC TAGATAGAGC TCATTTTACT 2220  
 CCACCTAATC GTTATATCTG GATATACCCA TTTCTGTCAT CTTCTTTCTC AACATAAAC 2280  
 TGTCTTGCTT TTGGAGACTT TAAGACATTT CCTAAAGCAC AAATAAAGC CTGATTTTC 2340  
 CCCATTGAGA GTTTTGTTC AAGGAATATG AAGTGAGACA TATGGGTGAG TCATAATAAT 2400  
 35 CAAATAAATT TATGAAGAGC TGGGTCTGCA ATAGCTAGTC TAAAACTAC TTGTGTGTCA 2460  
 GTCTCTCGT TATAGTATAT AAGAGCCTGA GAGGTCTGCG CAAGATAGAT GGTGATTAT 2520  
 TTATGGATCA GGCTGCTGCA TACAAACCTT GCATACTATT ATGCAGCTTA CCTAATCTCT 2580  
 AGACTATTCT GAGTAATGCT TGCTTGCTAA TGAATGTATA GGAGACCACA TTGTAATTGT 2640  
 40 TCTTAGATGA TGGAGTCCAT GCACTTTCTT AGAAATCGGT CTCAGTGCAAT GCTGTGCTTT 2700  
 TTCACATTGT CTCTGGGTTA TCTGGGAAGT ATCAGGTTCT GGGAGGCCAC AGCATTAAAT 2760  
 GATAAGAAAA GGAGACATTC TGGCAAAGCC AATCTGCTTA AAGGCAAGT CCAGAACCTG 2820  
 GAACCTAGAG GCCTTTCTCT CTGCACGAAA AACAGGTAGT TTGCAGTCTG AGATATGGGA 2880  
 GAGCTTTTGA GCTACACAGC AACCACAGGG ACCTCTCACC TTTTGTGAG CTTCAATCAG 2940  
 45 GAAGCTATTG GCTGTGCTCC AGCAGATGAT GAGATAATGA GGTAGTGGGT TTTTATTAC 3000  
 TGTTCATTTT TGCAACATCC TGCAACACCA TCCTGGGAGA CAAGAGCAAT ACCCAGCTTG 3060  
 GCCTTACCGG GGGAGGGTTG TATTCACT 3088

Seq ID NO: C166 DNA Sequence  
 Nucleic Acid Accession #: NM\_000574.1  
 Coding sequence: 66..1211

50  
 1 11 21 31 41 51  
 CCGCTGGGCG TAGTGCAGC TCGGCGGAGT CCGGCGGCG GCTCCTTGT TAAACCCGGC 60  
 GCGCCATGAC CGTGGCGCG CGAGCGGTGC CCGGCGGCGT GCCCTCCTC GGGGAGCTGC 120  
 55 CCCGCTGCT GCTGCTGGT CTGTTGTGCC TCGCGGCGT GTGGGTGAC TGTGGCCTTC 180  
 CCCAGATGT ACCAATGTC CAGCCAGCTT TGGAAAGCCG TACAAGTTT CCCGAGGATA 240  
 CTGTAATAAC GTACAATGT GAAGAAAGCT TTGTGAAAT TCTTGGCGAG AAGGACTCAG 300  
 TGAATGCTCT TAAGGGGAGT CAATGCTCAG ATATTGAAGA GTTCTGCAAT CGTAGCTGCG 360  
 60 AGGTGCCAAC AAGGCTAAAT TCTGCATCCC TCAACAGGCC TTATATCACT CAGAATTATT 420  
 TTCCAGTCGG TACTGTTGTG GAATATGAGT GCGTCCAGG TTACAGAAGA GAACCTTCTC 480  
 TATCACCAAA ACTAATCTGC CTTCAAGATT TAAATGGTC CACAGCAGTC GAATTTTGT 540  
 AAAAGAAATC ATGCCCTAAT CCGGAGAGAA TACGAATGG TCAGATTGAT GTACCAGGTG 600  
 GCATATTATT TGGTGCAACG ATCTCCTTCT CATGTAAAC AGGGTACAAA TTATTGGCT 660  
 65 CGACTTCTAG TTTTGTCTT ATTTCAAGCA GCTCTGTCCA GTGGAGTGAC CCGTGGCCAG 720  
 AGTGACAGGA AATTTATTGT CCAGCACCAC CACAAATTGA CAATGGAATA ATTCAGGGG 780  
 AACGTGACCA TTATGGATAT AGACAGTCTG TAACGTATGC ATGTAATAAA GGATTACCA 840  
 TGATTGGAGA GCATCTTATT TATTGTACTG TGAATAATGA TGAAGGAGAG TGGAGTGGCC 900  
 70 CACCACTGTA ATGCAGAGGA AAATCTCTAA CTTCAGAGT CCCACCAACA GTTCAGAAAC 960  
 CTACCAAGT AAATGTTCCA ACTACAGAAG TCTCACCAC TTCTCAGAAA ACCACCACAA 1020  
 AAACCAACAC ACCAATGCTC CAAGCAACAC GAGATACACC TGTTCAGG ACAACCAAGC 1080  
 ATTTTCATGA AACAACCCCA AATAAAGGAA GTGGAACCC TCCAGTACT ACCCGTCTTC 1140  
 TATCTGGGCA CAGGTGTTTC ACGTTGACAG GTTGTCTTGG GACGCTAGTA ACCATGGGCT 1200  
 TGCTGACTTA GCGAAAGAG AGTTAAGAG AAAATACACA CAAGTATACA GACTGTTCTC 1260  
 75 AGTTTCTTAG ACTATCTGC ATATTGGATA AAATAAATGC AATTGTGCTC TTCAATTAGG 1320  
 ATGCTTTTAA GTCTTTTAA ATGTGTTAGG AATGTCAACA GAGCAAGGAG AAAAAGGCA 1380  
 GTCTTGAAT CACATTCTTA GCACACCTAC ACCTCTTGAA AATAGAACA CTGTCAGAT 1440  
 TGAGAGTGAT TCTTTCTCTA AAGTGTAAAG AAGCATAGA GATTGTTGCT TATTAGAAT 1500  
 80 GGGATCAGCA GGAAGAGAGA AGGAAGTGA TTTTCTTCCA CAAGATCTGT AATGTTATT 1560  
 CCACCTATAA AGGAATATAA AATGAAGAAA CATTATTGG ATATCAAAG CAAATAAAAA 1620  
 CCAATTCAG TCTCTTCTAA GCAAAATTGC TAAAGAGAGA TGAACCATAT TATAAAGTAA 1680  
 TCTTTGGCTG TAAGGCATTT TCACTTTTCC TTGGGTTGG CAAAATATT TAAAGGTAAA 1740  
 ACATCTCGGT GAACAGGGGG TGTGTATGGT GATAAGGGAG GAATATAGAA TGAAGAGCTG 1800  
 AATCTTCTGT TGTGCAACA ATAGAGTTTG GAAAAAGCCT GTGAAGGTG TCTTCTTGA 1860  
 CTTAATGTCT TAAAGATAT CCAAGAGATAC TACAATATTA ACATAAGAAA AGATTATATA 1920

TTATTTCTGA ATCGAGATGT CCATAGTCAA ATTTGTAAAT CTTATTCITT TGTAATATTT 1980  
 ATTTATATTT ATTTATGACA GTGAACATTC TGATTTTACA TGTAAACAA GAAAAGTTGA 2040  
 AGAAGATATG TGAAGAAAAA TGTATTTTTC CTAAATAGAA ATAAATGATC CCAATTTTGT 2100  
 GT 2102

Seq ID NO: C167 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2651

10 1 11 21 31 41 51  
 | | | | |  
 ATGGACACCT CCCGCTCGG TGTGCTCCTG TCCTTGCCCTG TGCTGCTGCA GCTGGCGACC 60  
 GGGGGCAGCT CTCACAGGTC TGGTGTGTG CTGAGGGGCT GCCCACACA CTGTCATTGC 120  
 GAGCCCGAAG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTGGGAGCTG 180  
 15 CCTTCCAACC TCAGGCTCTT CACCTCTTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240  
 CTGCTCCCGA ATCCCTCGCC CAGTCTCCGC TTCCTGGAGG AGTTAGCTCT TCGGGGAAAC 300  
 GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCCTTATG 360  
 CTGCAGAATA ATCAGTAAAG ACACGTACCC ACAGAAGCTC TGCAGAATTT GCGAAGCCTT 420  
 CAATCCCTGC GTCTGGATGC TAACCATATC AGCTATGTGC CCCAAGCTG TTTCACTGGC 480  
 20 CTGCAATCCC TGAGGCACCT GTGGCTGGAT GACAATGGGT TAACAGAAAT CCCGTCAG 540  
 GCTTTTAGAA GTTTATGGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC 600  
 ATACCAAGAT ATGCTTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT 660  
 AGAATCCACT CCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT 720  
 TTAATATACA ATAACTTGA TGAATTCCTC ACTGCAATTA GGACACTCTC CAACCTTAAA 780  
 25 GAACATCAAT TCATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA 840  
 CCTGAATCAA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACGAATT TCCTGATTTA 900  
 ACTGGAACCTG CAAACCTGGA GAGTCTGACT TTAACCTGGAG CACAGATCTC ATCTCTTCTC 960  
 CAAACCTGCT GCAATCAGTT ACCTAATCTC CAAGTGTAG ATCTGTCTTA CAACCTATTA 1020  
 GAAGATTAC CCAGTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT 1080  
 30 GAAATCTACG AAATTAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATGCTGAAAT 1140  
 TTGGCTTGGG ACAAAATGTC TATTATTCAC CCCAATGCAT TTCCACTTT GCCATCCCTA 1200  
 ATAAAGCTGG ACCTATCGTC CAACCTCTG TCGTCTTTTC CTATACTGG GTTACATGGT 1260  
 TTAACCTACT TAAATTAAC AGGAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC 1320  
 TTTCCAGAAC TCAAGGTTAT AGAATGCCT TATGCTTACC AGTGTGTGC ATTTGGAGTG 1380  
 35 TGTGAGAAAT CTAATAAGAT TTCTAATCAA TGGAAATAAG GTGACAAACAG CAGTATGGAC 1440  
 GACCTTCATA AGAAAGATGC TGAATGTTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT 1500  
 TTCTGCTTG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC 1560  
 CCAGGCCCTC TCAACCCCTG TGAACACCTG CTTGATGGCT GGCTGATCAG AATTGGAGTG 1620  
 40 TGGACATAGC CAGTCTGCGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA 1680  
 TCCCTCTGT ACATTTCCTC CATTAAACTG TTAATTGGGG TCATGCTGAG AGTGAACATG 1740  
 CTCAGGGAG TCTCAGTGC CGTGTGGCT GGTGTGGATG GGTTCACITT TGGCAGCTTT 1800  
 GCACGACATG GTGCTGTGTG GGAGAAATGG GTTGGTTGCC ATGTCAATGG TTTTGTCTCC 1860  
 ATTTTGTCT CAGAAATCAT TGTTTTCTG CTTACTCTGG CAGCCCTGGA GCGTGGGTTT 1920  
 45 TCTGTGAAT ATCTGCAAA ATTTGAAAGC AAGCTCCAT TTCTAGCCT GAAAGTAATC 1980  
 ATTTTGTCT GTGCTCTGCT GGCCTTGACC ATGGCCGAG TTCCCTGCT GGGTGGCAGC 2040  
 AAGTATGGCG CCTCCCTCT CTGCTGCTT TGCCCTTTG GGGAGCCAG CACCATGGGC 2100  
 TACATGGTGC CTCTCATCT GCTCAATCC CTTTGCTTTC TCATGATGAC CATTGCTTAC 2160  
 ACCAAGCTCT ACTGCAATTT GGACAAAGGA GACCTGGAGA ATATTGGGA CTGCTCTATG 2220  
 50 TTAAACACAA TTGCTCTGT GCTCTTACC AACTGCATCC TAAACTGCC TGTGGCTTTC 2280  
 TGTCTCTCT CCTCTTAAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC 2340  
 CTCTGTGTG TAGTCCACT TCTGTGATG CTCAATCCCT TTCTCTACAT CTGTGTTCAAT 2400  
 CTCACITTA AGGAGGATCT GGTGAGCCTG AGAAAGCAAA CCTACCTCTG GACAGATCA 2460  
 AAACACCCAA GCTTGTATGC AATTAACTCT GATGATGTGC AAAACAGTC CTGTGACTCA 2520  
 55 ACTCAAGCCT TGTAAACCTT TACAGCTCC AGCATCACT ATGACCTGCC TCCAGTTCC 2580  
 GTGCCATCAC CAGCTTATCC AGTGAATGAG AGCTGCCATC TTTCTCTGT GGCATTTGTC 2640  
 CATGTCTTA A 2651

Seq ID NO: C168 DNA Sequence  
 Nucleic Acid Accession #: NM\_003667.2  
 Coding sequence: 49..2772

60 1 11 21 31 41 51  
 | | | | |  
 TGCTGCTCTC GCGCCGCTG CGGCTCGTGG CCCCTACTT CGGGCACCAT GGACACCTCC 60  
 CGGCTCGGTG TGCTCCTGTC CTTGCTGTG CTGCTGCAGC TGGGACCGG GGGCAGCTCT 120  
 CCCAGGCTCTG GTGTGTGTGCT GAGGGGCTGC CCCACACACT GTCAATGGGA GCCCGAGCGC 180  
 AGGATGTTGC TCAGGGTGA CTGCTCGAC CTGGGGCTCT CGGAGCTGCC TTCCAACCTC 240  
 AGGCTCTTCA CCTCTACCT AGACCTCAGT ATGAACRACA TCAGTCAGCT GCTCCCGAAT 300  
 70 CCCCTGCCCA GTCTCGCTT CTTGGAGGAG TTACGTCTTG CGGGAAACGC TCTGACATAC 360  
 ATTCCCAAGG GAGCATTAC TGGCCTTAC AGTCTTAAAG TTCTTATGCT GCAGAATAAT 420  
 CAGCTAAGAC ACCTACCCAC AGAAGCTCTG CAGAATTTGC GAAGCCTTCA ATCCCTCGGT 480  
 CTGGATGCTA ACCACATCAG CTATGTGCC CCAAGCTGTT TCAGTGGCCT GCATTCCCTG 540  
 AGGCACCTGT GGTCTGGATG CAATGCGTTA ACAGAAATCC CCGTCCAGGC TTTTAGAAGT 600  
 75 TTATCGGATC TGAAGCCAT GACCTTGGCC CTGAACAAA TACACCACAT ACCAGACTAT 660  
 GCCTTTGGAA ACCTCTCCAG CTTGGTAGTT CTACATCTCC ATAACATAG AATCCACTCC 720  
 CTGGGAAGA AATGCTTTGA TGGGCTCCAC AGCCTAGAGA CTTTAGATT AAATTACAAT 780  
 AACCTTGAAT AATTCCCACT TGCAATTAGG ACATCTCCA ACCTTAAAG ACTAGGATT 840  
 CATAGCAACA ATATCAGGTC GATACCTGAG AAAGCATTTG TAGGCAACCC TTCTCTTAT 900  
 80 ACAATACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA 960  
 CTGAACATAA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACGAATT TCCTGATTTA 1020  
 ACTGGAACCTG CAAACCTGGA GAGTCTGACT TTAACCTGGAG CACAGATCTC ATCTCTTCTC 1080  
 CAAACCTGCT GCAATCAGTT ACCTAATCTC CAAGTGTAG ATCTGTCTTA CAACCTATTA 1140  
 GAAGATTAC CCAGTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT 1200  
 GAAATCTACG AAATTAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGTGAAT 1260

5	TTGGCTTGGG	ACAAAATTGC	TATTATTCAC	CCCAATGCAT	TTTCCACTTT	GCCATCCCTA	1320
	ATAAAGCTGG	ACCTATCGTC	CAACCTCCTG	TCGTCTTTTC	CTATAACTGG	GTTACATGGT	1380
	TTAACTCACT	TAAAATTAA	AGGAATCAT	GCCTTACAGA	GCTTGATATC	ATCTGAAATC	1440
	TTTCAGAAC	TCAAGGTTAT	AGAAATGCCT	TATGCTTACC	AGTGCTGTGC	ATTTGGAGTG	1500
	TGTGAGAATG	CCTATAAGAT	TTCTAATCAA	TGGAATAAAG	GTGACACACG	CAGTATGGAC	1560
10	GACCTTCATA	AGAAAGATGC	TGGAATGTTT	CAGGCTCAAG	ATGAACGTGA	CCTTGAAGAT	1620
	TTCTGCTTGG	ACTTTGAGGA	AGACCTGAAA	GCCCTTCATT	CAGTGCAGTG	TTACCTTTCC	1680
	CCAGGCCCTT	TCAAACCTTG	TGAACACCTG	CTTGATGGCT	GGCTGATCAG	AATTGGAGTG	1740
	TGGACCATAG	GAGTTCTGGC	ACTTACTTGT	AATGCTTTGG	TGACTTCAAC	AGTTTTCAGA	1800
	TCCCTCTGT	ACATTTCCCC	CATTAAACTG	TTAATTGGGG	TCATCGCAGC	AGTGAACATG	1860
15	CTCAGGGGAG	TCTCCAGTGC	CGTGCTGGCT	GGTGTGGATG	CGTTCACTTT	TGGCAGCTTT	1920
	GCACGACATG	GTGCCTGGTG	GGAGAAATGG	GTGGTTGGCC	ATGTCACTTG	TTTTTGTGCC	1980
	ATTTTGTCTT	CAGAATCATC	TGTTTTCTGT	CTTACTCTGG	CAGCCCTGGA	GCCTGGGTTT	2040
	TCTGTGAAT	ATTCTGCAAA	ATTGAAACG	AAAGCTCCAT	TTTCTAGCCT	GAAAGTAATC	2100
	ATTTTGTCTT	GTGCCCTGCT	GGCCTTGACC	ATGGCCGACG	TTCCCTGCT	GGGTGGCAGC	2160
20	AAGTATGGCG	CCTGCCCTCT	CTGCCCTGCT	TTGCCCTTTG	GGGAGCCGAG	CACCATGGGC	2220
	TACATGGTCT	CTCTCATCTT	GCTCAATTCC	CTTTGCTTCC	TCATGATGAC	CATTGCCCTAC	2280
	ACCAAGCTCT	ACTGCAATTT	GGACAAGGGA	GACCTGGAGA	ATATTGGGGA	CTGCTCTATG	2340
	GTAACAACAC	TGCCCCGTGT	GCTCTTCAAC	AACCTGATCC	TAAACTGCCC	TGTGGCTTTC	2400
	TTGTCTTCT	CCTCTTTAAT	AAACCTTACA	TTTATCAGTC	CTGAAGTAAT	TAAGTTTATC	2460
25	CTTCTGGTGG	TAGTCCCACT	TCCTGCATGT	CTCAATCCCC	TTCTCTACAT	CTTGTTCAT	2520
	CCTCACTTTA	AGGAGGATCT	GGTGAGCCTG	AGAAAGCAAA	CCTACGCTCG	GACAAAGATCA	2580
	AAACACCCAA	GCTTGATGTC	AATTAACTCT	GATGATGTCC	AAAAACAGTC	CTGTGACTCA	2640
	ACTCAAGCCT	TGTAACCTTT	TACCAGCTCC	AGCATCACTT	ATGACCTGCC	TCCCAAGTCC	2700
	GTGCCATCAC	CAGCTTATCC	AGTGACTGAG	AGCTGCCATC	TTTCTCTGT	GGCAITTTGTC	2760
30	CCATGTCTCT	AATTAAATATG	TGAAGGAAAA	TGTTTTCAAA	GTTTGAGAAC	CTGAAATGT	2820
	GAGATTGAGT	ATATCAGAGC	AGTAATTAAT	AAGAAGAGCT	GAGGTGAAAC	TCGGTTTAAA	2880
	Seq ID NO: C169 DNA Sequence						
	Nucleic Acid Accession #: NM_003506.1						
	Coding sequence: 259..2379						
35	1	11	21	31	41	51	
	GCAGCTCCAG	TCCCGGAGCG	AACCCCGGAG	CCGTCTCAGG	TCCCTGGGGG	GAACGGTGGG	60
	TTAGACGGGG	ACGGGAAGGG	ACAGCGGCCT	TCGACCGCCC	CCCGAGTAAT	TGACCCAGGA	120
	CTCATTTTCA	GGAAAGCCTG	AAAATGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
	ATCTTTGGAT	GGGATCTTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
40	ATCAGGAATT	TGAAGAAAT	GGAGATGTTT	ACATTTTGT	TGACGTGTAT	TTTTCTACCC	300
	CTCCTAAGAG	GGCACAAGCT	CTTCACTGT	GAACCAATTA	CTGTCCCGAG	ATGATGAAA	360
	ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
	GGCGTGGAAA	TGGAGCATTT	TCTTCTCTCT	GCAAACTCTG	AATGTTCAAC	AAACATTGAA	480
	ACTTTCTCT	GCAAGCAATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GGTTCCACCT	540
45	TGTCGTAAC	TTTGTGAGAA	AGTATATTCT	GATTGCAAAA	AAATTAATGA	CACCTTTGGG	600
	ATCCGATGGC	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTTCTT	660
	GTAACCTTTG	ATCCACACAC	AGAAATTTCT	GGTCTCAGA	AGAAAACAGA	ACAAGTCCAA	720
	AGAGACATTG	GATTTTGGTG	TCCAAAGCAT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
	TTTCTGGGAA	TGACCAAGTG	TGCGCCTCCA	TGCCCAACA	TGTATTTTAA	AAGTGATGAG	840
50	CTAGAGTTTG	GAAGAAAGTT	TATTGGAACA	GTTTCAATAT	TTTGTCTTTG	TGCAACTCTG	900
	TTCACTTCC	TTACTTTTTT	AATTGATGTT	AGAAGATTCA	GATACCCAGA	GAGACCAATT	960
	ATATATTACT	CTGTCTGTTA	CAGCAATTGA	TCCTTATGTT	ACTTCAATGG	ATTTTGTCTG	1020
	GGCGATAGCA	CAGCCTGCAA	TAAGGCAGAT	GAGAAGCTAG	AACTTGGTGA	CACGTGTTGC	1080
	CTAGGCTCTC	GAAGTAAGGC	TGCAACCGTT	TTGTTCACTG	TTTTGTATTT	TTTCACAATG	1140
55	GCTGGCACTG	TGTGTGGGTT	GATTCCTACC	ATTACTTGTT	TCTTAGCTGC	AGGAAGAAAA	1200
	TGGAGTTGTG	AAGCATGCGA	GCAAAAAGCA	GTGTGGTTTC	ATGCTGTTGC	ATGGGGAAAC	1260
	CCAGGTTTCC	TGACTGTTAT	GCTTCTTGCT	CTGAACAAAG	TTGAAGGAGA	CAACATTAGT	1320
	GGAGTTTGCT	TTGTGGGCTT	TTATGACCTG	GATGCTTCTC	GCTACTTTGT	ACTCTTGCCA	1380
	CTGTGCTCTT	TGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTAAAT	1440
60	CATGTTCCAG	AAGTCATACA	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAAATTTATG	1500
	ATTGGAATTG	GAGTCTTCAG	CGGCTTGAT	CTTGTGCCAT	TAGTGACACT	TCTGGGATGT	1560
	TACGCTATG	AGCAAGTGAA	CAGGATTACC	TGGAGATATA	CTTGGGTCTC	TGATCATTGT	1620
	CGTCAGTACC	ATATCCCATG	TCCTTATCAG	GCAAAAAGCAA	AAGCTCGAOC	AGAATTGGCT	1680
	TTAATTATGA	TAAATATCT	GATGACATTA	ATTGTTGGCA	TCTCTGCTGT	CTTCTGGGTT	1740
65	GGAGCAAAAA	AGACATGCAC	AGAATGGGCT	GGGTTTTTAA	AACGAAATCG	CAAGAGAGAT	1800
	CCAATCAGTG	AAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCACAAAT	1860
	TCTAAAGTTA	AACACAAAAA	GAAGCACTAT	AAACCAAGTT	CACACAGCT	GAAGGTCAAT	1920
	TCCAAATCCA	TGGGAACCCG	CACAGGAGCT	ACAGCAATTC	ATGGCACTTC	TGCAGTAGCA	1980
	ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAAC	CTCACCAGAA	2040
70	ACATCAATGA	GAGAGGTGAA	AGCGGACCGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
	TGTGGTGAAC	CTGCTCGGCC	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTGAC	2160
	GGGAAGGGCC	AGGCAGGACG	TGTATCTGAA	AGTGGGGGGA	GTGAAGGAAG	GATTAGTCCA	2220
	AAGAGTGATA	TTACTGACAC	TGGCCTGGCA	CAGAGCAACA	ATTTGACAGT	CCCCAGTTCT	2280
	TCAGAACCAA	GCAAGCTCAA	AGGTTCACCA	TCTCTGCTTG	TTACCCAGT	TTACGGAGTG	2340
75	AGAAAGAGGC	AGGGAGGTTG	TTGTCTTCA	GATACCTGAA	GAACATTTTC	TCTCGTTACT	2400
	CAGAAGCAA	TTTGTGTTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
	TACGTTCTTC	TTTTGCACCT	AAAGTTGCAT	TGCCCTACTGT	TATACTGGAA	AAATAGAGT	2520
	TCAGAATATA	TATGACTCAT	TTCAACAAAA	GGTTAATGAC	AACAATATAC	CTGAAAACAG	2580
	AAATGTGCAG	GTTAATAATA	TTTTTTTAAT	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
80	CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTAAGATGT	ACTATGCTAT	2700
	TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTTAA	TCTTATCCTT	2760
	GTATCTTTTT	ATACATATTT	GAAATAAGC	TTATATGTAT	TTGAACTTTT	TTGAAATCCT	2820
	ATTCAAGTAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTACACTGA	2880
	ATTTCTAAGA	AAATGTGAAA	ATAGTCTTCT	TTTATCTGT	AAAAAAGAT	ATACCAAAAA	2940
	GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTTATTG	ATACCTTACC	ATCTAAAAATG	3000



5 TGTGATTTTT ATAGTCTCGT TTTAGGAATT TCACAGATCT AAATTATGTA ACTGAAATAA 3060  
 GGTGCTTACT CAAAGAGTGT CCACTATTGA TTGTATTATG CTGCTCACTG ATCCTTCTGC 3120  
 ATATTAAAA TAAATGTGCC TAAAGGGTTA GTAGACAAAA TGTAGTCTTT TTGTATATTA 3180  
 GGCCAAGTGC AATTGACTTC CCTTTTTTAA TGTTCATGA CCACCCATTG ATTGTATTAT 3240  
 AACCACTTAC AGTTGCTTAT ATTTTGTGTT TTAACCTTGG TTTCTTAACA TTTAGAATAT 3300  
 TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG 3342

Seq ID NO: C170 DNA Sequence  
 Nucleic Acid Accession #: NM\_000582  
 Coding sequence: 88..990

10  
 15  
 20  
 25  
 30  
 35  
 40  
 1 11 21 31 41 51  
 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60  
 AACGCGACC AAGGAAAAC CACTACCATG AGAATTGCAG TGATTTCCTT TTGCTCCTTA 120  
 GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG 180  
 CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240  
 CAGAATCTCC TAGCCGCCA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300  
 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360  
 AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420  
 TCTGATGAAT CTGATGAAC TGTCACTGAT TTTCCACCG ACCTGCCAGC AACCGAAGTT 480  
 TTCATCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540  
 GGACTGAGGT CAAATCTAA GAAGTTTCGC AGAAGTGAACA TCCAGTACCC TGATGCTACA 600  
 GAGCAGGACA TCACCTCACA CATGGAAGC GAGGAGTTGA ATGGTGACATA CAAGGCCATC 660  
 CCGTGTGCC AGGACCTGAA CGGCCCTTCT GATTGGGACA GCCGTGGGAA GACAGATTAT 720  
 GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780  
 TATAAGCGGA AAGCCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA 840  
 CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTTT ACAGCCATGA AGATATGCTG 900  
 GTTGTAGACC CCAAAAGTAA GGAAGAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA 960  
 TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCATTTCG 1020  
 ATTTAGTCAA AAGAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080  
 CTCAGTTTAT TGGTTGAATG TGTATCTAT TTAGTCTGGA AATAACTAAT GTGTTTGATA 1140  
 ATTAGTTTAG TTTGTGGCTT CATGGAACCT CCCTGTAAAC TAAAGCTTC AGGGTTATGT 1200  
 CTATGTTTAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTAATATT TGTATTCTC 1260  
 TCATGAATAG AATTTATGTG AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320  
 ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380  
 TATCTTTTGG TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAAAT TGGTGGTGTG 1440  
 AATTGCTTAT TTGTTTCCCG ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTTACT 1500  
 GCCTAAAAAA AAAAAAAAAA AAAA 1524

Seq ID NO: C171 DNA Sequence  
 Nucleic Acid Accession #: NM\_002821  
 Coding sequence: 150..3362

45  
 50  
 55  
 60  
 65  
 70  
 75  
 80  
 1 11 21 31 41 51  
 AACTCCGCCC TCGGGAGCCC TCGGGGTCGG GCTCCGCGCTG CGGCTGCTGC TGCGGGCGCC 60  
 GCGCTCCGGT GCGTCCGCTT CCTGTGCCCG CCGCGGAGCA GTCTGCGGCC CGCGGTGGCG 120  
 CTTCAAGCTC TTTTCTGAG CCGCGCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCACAG 180  
 CCGCGCGGTT GCGTCTGCTC AGCGTCTCTG TGCTGCCGCT GCTGGGCGGT ACCCAGACAG 240  
 CCATGTCTTT CATCAAGCAG CGTCTCTCCC AGGATGCAC TCAAGGCGCG CCGGCGCTGC 300  
 TTGCTGTGA GGTGTAGGCT CCGGGCCCGG TACATGTGTA TGGCTGCTC GATGGGCGCC 360  
 CTGTCCAGGA CAGCGAGCGG CGTTTGGCCC AGGACAGCAG CCTGAGCTTT GCAGCTGTGG 420  
 ACCGCGTGA GAGCTCTGGC ACCTTCCAGT GTGTGGCTCG GATGATGTC ACTGGAGAAG 480  
 AAGCCCGCAG TCGCAAGCCC TCCTTCAACA TCAATGATG TGAGGAGAGT CCGTGTGGTCC 540  
 TGAAGCAGT AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGTTCACA CTTCGTGCCC 600  
 ACATTGATGG GCACCTCCGG CCCACCTACC AATGGTCCG AGATGGGACC CCGCTTCTTG 660  
 ATGGTCAGAG CAACCCACACA GTCCAGCAGC AGGAGCGGAA CCTGAGCTTC CCGCCAGCTG 720  
 GTCTGAGCA TAGTGGGCTG TATTCTGTCT GCGCCACAGC TGCTTTTGGC CAGGCTTGCA 780  
 GCAGCCAGAA CTTCACTCTG AGCATGTCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840  
 CCCAGGAGCT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900  
 AGCCACCCCC GAGCCTCGAG TGGCTCTTTG AGGATGAGC TCCCATCACT AACCGCAGTC 960  
 GCGCCCCACA CCTCGCAGAG GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020  
 TCCGCGCAAG CCGTCTCAGG ATCTACCGCT GCATTGGCCA GGGGAGAGG GCGCCACCCA 1080  
 TCATCTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTAGGCCAC 1140  
 GGGTGTTCAT AGCTGGCAGC GAGGAGCGTG TGACCTGCGT TCCGCCCAAG GGTCTGCCAG 1200  
 AGCCAGCGCT GTGCTGGGAG CAGCGGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260  
 AGAAGGGCCA CGAGCTGGTG TTGGCCAAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT 1320  
 GCCAGCGGCG CAACCTGGCT GGTCAAGCGA GACAGGATGT CAACATCACT GTGGCCACTG 1380  
 TGCCCTCTCT GCTGAAGAAG CCCCAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440  
 TGGATGTGCT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACCATATGC 1500  
 TCATCTCAGA GGACTCACGG TTCGAGGTCT TCAAGATGG GACCTTGCGC ATCAACAGCG 1560  
 TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGCC GGCAGCATCG 1620  
 AGGCGCAAGC CCGTGTCCAA GTGCTGAAA AGCTCAAGTT CACACCAACA CCGCAGCCAC 1680  
 AGCAGTGCAT GGAATTTGAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GCGCGAGAGA 1740  
 AGCCCTACT TAAGTGGGAA OGGCAGATG GAGGAGCGCT CCAGAGTGG GTGACAGACA 1800  
 ACGCTGGGAC CCGTCAATTT GCCCGGTGA CTGAGATGA CGCTGGCAAC TACACTTGCA 1860  
 TTGCTTCCA CCGGCGCGAG GGCAGATTTC GTGCCATGT CCAGCTCACT GTGGCAGTTT 1920  
 TTATCACTTT CAAAGTGGAA CAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980  
 TGCACTGCGA GGCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAAGGC AAGGACCGCA 2040  
 TCTGTGACCC CACCAAGCTG GACCCAGGA TGACATCTT CCAGAAATGGC TCCTGTGTGA 2100  
 TCCATGACGT GGCCCTGAG GACTCAGGCC GCTACACCTG CATTGCAGGC AACAGCTGCA 2160  
 ACATCAAGCA CAGGAGGCC CCGCTCTATG TCGTGGACAA GCCTGTGCGG GAGGAGTCGG 2220  
 AGGCGCTCG CAGCCCTCCC CCGTACAAGA TGATCCAGAC CATTGGGTTG TGGTGGGTTG 2280  
 CCGCTGTGCG CTACATCATT GCGGTGCTGG GCCTCATGTT CTACTGCAAG AAGCGCTGCA 2340



5	AAGCCAAGCG	GCTGCAGAAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCTTT	GCAGAAACGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCACCGGTC	TAGCCTGTCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCCCTGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAGCTGAA	CCAGCCCAAC	GTGGTGGGCT	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCTCT	AGGATTTCCA	2820
10	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTAGGC	ATGGAGCACC	TGTCCAACAA	CGCTTTGTGT	CATAAGGACT	2940
	TGGCTGCGCG	TAACCTGCTG	GTCACTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCTTGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCCTTCCG	CCAGCCCTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTGGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
15	CAGATGATG	ATGTTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCTC	CAGCCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAAGT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCGCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
20	CAGCATGATG	GGCAAGATCC	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
	TTGCTGAGGT	AGCTCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCCCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCTGCCAC	3600
	CTCTTCTCTG	ATCAGGGACA	GTGTGGGTGC	CACAGTAAAC	CCCAATTCTT	GGCCTTCAAC	3660
	TTCTCCCTTT	GACCGGGTCC	AACCTCGCCA	CTCATCTGCC	AACCTTGCCT	GGGAGGGGCT	3720
25	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTTAAATA	TTCTCAAGTT	CTGGGCACAC	3780
	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAAG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCCAAGTCTT	3900
	CCCCACCCCT	CTCTCTCTTC	CTCATCTCTA	GTGCCCTGGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAAC	GCCCTTTTGT	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
30	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
	GCCATCCTTA	CCCCACACTT	TTATTTGTGT	CGTTTTTGT	TTGTTTGTGT	TTTTTGTGTT	4140
	TGTTTTGTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTTA		4187

Seq ID NO: C172 DNA Sequence

Nucleic Acid Accession #: NM\_002309.2

Coding sequence: 65..673

35	1	11	21	31	41	51	
	ATGAACCTCT	GAAAACTGCC	GGCATCTGAG	GTTTCTCTCA	AGGCCCTCTG	AAGTGCAGCC	60
40	CATAATGAAG	GTCTTGGCGG	CAGGAGTTGT	GCCCTGCTGT	TTGGTTCTGC	ACTGGAAACA	120
	TGGGGCGGGG	AGCCCCCTCC	CCATCACCCC	TGTCAACGCC	ACCTGTGCCA	TACGCCACCC	180
	ATGTCAACAC	AACCTCATGA	ACCAGATCAG	GAGCCAACCT	GCACAGCTCA	ATGGCACTGC	240
	CAATGCCCTC	TTTATTCTCT	ATTACACAGC	CCAGGGGGAG	CCGTTCCCCA	ACAACTCGGA	300
45	CAGCTATGAT	GGCCCAACG	TGAOGGACTT	CCGCCCCCTC	CACGCCAACG	GCACGGAGAA	360
	GGCCAAGCTG	GTGGAGCTGT	ACCGCATAGT	CGTGTAACCT	GGCACTCTCC	TGGGCAACAT	420
	CACCGGGGAC	CAGAAGATCC	TCAACCCAG	TGCCCTCAGC	CTCCACAGCA	AGCTCAACGC	480
	CACCGCCGAC	ATCCTGCGAG	GCTCCTTAG	CAACGTGCTG	TGCCGCTGT	GCAGCAAGTA	540
	CCAAGTGGGC	CATGTGGACG	TGACCTACGG	CCCTGACACC	TCGGGTAAAG	ATGTCTTCCA	600
50	GAAGAGAGAG	CTGGGCTGTC	AACCTCTGGG	GAAGTATAAG	CAGATCATCG	CCGTGTGGGC	660
	CAGCGCTTTC	TAGCAGGAGG	TCTTGAAGTG	TGCTGTGAAC	CGAGGGATCT	CAGGAGTTGG	720
	GTCCAGATGT	GGGGCGCTGT	CCAAGGGTGG	CTGGGGCCCA	GGGATCGCT	AAACCCAAAT	780
	GGGGCTCTCT	GGCAGACCCC	GAGGGTGCCT	GGCCAGTCCA	CTCCACTCTG	GGCTGGGCTG	840
	TGATGAAGCT	GAGCAGAGTG	GAAACTTCCA	TAGGGAGGGA	GCTAGAAGAA	GGTGCCCTTT	900
55	CCTCTGGGAG	ATTGTGGACT	GGGGAGCGTG	GGCTGGACTT	CTGCTCTTAC	TTGTCCCTTT	960
	GGCCCCCTTG	TCACTTTTGT	CAGTGAACAA	ACTACACAAG	TCATCTACAA	GAGCCCTGAC	1020
	CACAGGGTGA	GACAGCAGGG	CCCAAGGGAG	TGGACCAAGC	CCAGCAAAAT	TATCACCATC	1080
	TGTGCTCTTG	CTGCCCTTTA	GGTTGGGACT	TAGGTGGGCC	AGAGGGGCTA	GGATCCCAAA	1140
	GGACTCCTTG	TCCCTTAGAA	GTITGATGAG	TGGAAGATAG	AGAGGGGCTT	CTGGCATGGA	1200
60	AGGCTGTCTT	CTTTTGAGGA	TGATCAGAGA	ACTTGGGCAT	AGGAACAATC	TGGCAGAAGT	1260
	TTCCAGAAGG	AGGTCACTTG	GCATTCAAGC	TCTTGGGGAG	GCAGAGAAGC	CACCTTCAGG	1320
	CCTGGGAAGG	AAGACACTGG	GAGGAGGAGA	GGCCTGGAAA	GCTTTGGTAG	GTCTCTCGTT	1380
	CTCTTCCCCG	TGATCTTCCC	TGCAGCCTGG	GATGGCCAGG	GTCTGATGGC	TGGACCTGCA	1440
	GCAGGGGTTT	GTGGAGGTGG	GTAGGGCAGG	GGCAGGTTGC	TAAGTCAGGT	GCAGAGGTTT	1500
65	TGAGGGACCC	AGGCTCTTCC	TCTGGGTAAA	GGTCTGTAA	AAGGGGCTGG	GGTAGCTCAG	1560
	AGTAGCAGCT	CACATCTGAG	GCCCTGGGAG	GTCTTGTGAG	GTACACACAG	GGTACTTGAG	1620
	GGGGACTGGA	GGCGTCTCT	GGTCCCCAGG	GCAAGGGAA	AGCAGAACTT	AGGGTCAGGG	1680
	TCTCAGGGAA	CCCTGAGCTC	CAAGGTGCT	GTGCGTCTGA	CCTGGCATGA	TTTCTATTTA	1740
	TTATGATATC	CTATTTATAT	TAACCTTATT	GTGCTTTCAG	TGGCCAAAGT	AATTCCTCCT	1800
70	TCCTTGGTCC	CTACTCAACA	AAATATGATG	ATGGCTCCCC	ACACAAGGCC	CAGGGCCAGG	1860
	GCTTAGCAGG	GCCTGCTCTG	GAAGTCGACA	ATGTTACAAG	TGGAATAAGC	TTACGGGTGA	1920
	AGCTCAGAGA	AGGGTCGGAT	CTGAGAGAAT	GGGGAGGCCT	GAGTGGGAGT	GGGGGGCCTT	1980
	GCTCACCCCG	CATCCCTTAC	TGTGACTTGC	TTTAGCGTGT	CAGGGTCCAG	GCTGCAGGGG	2040
	CTGGGCCAAT	TTGTGGAGAG	GCCGGGTGCC	TTTCTGTCTT	GCTTCCAGGG	GGCTGGTTCA	2100
75	CACGTGTTCT	GGGGGCCCCA	GCATTGTGTT	GTGAGGGGCA	CTGTTCTCTG	CAGATATTGT	2160
	GCCCCCTGGA	GCAGTGGGCA	AGACAGTCC	TGTGGCCAC	CCTGTCTCTG	TTTCTGTGTC	2220
	CCATGCTGTC	CTCTGAAATA	GCGCCCTGGA	ACAACCCCTG	CCCTGCACCC	AGCATGTCTC	2280
	GACACAGCAG	GGAAGCTCCT	CCTGTGGCCC	GGACACCCAT	AGACGGTGGG	GGGGGCTGG	2340
	CTGGGCCAGA	CCCCAGGAAG	GTGGGGTAGA	CTGGGGGAT	CAGCTGCCCA	TTGCTCCCAA	2400
80	GAGGAGGAGA	GGGAGGCTGC	AGAGCCCTGG	GACTCAGACC	AGGAAGCTGT	GGGCCCTCCT	2460
	GCTCCACCCC	CATCCGCTCT	CCACCCATGT	CTGGGCTCCC	AGGCAGGGAA	CCCGATCTCT	2520
	TCCTTTGTGC	TGGGGCCAGG	CGAGTGGAGA	AAOCCCTTCC	AGTCTGAGAG	CAGGGGGAGG	2580
	AAGGAGGCG	CAGAGTTGGG	GCAGCTGCTC	AGAGCAGTGT	TCTGCTTCT	TCTCAAAACC	2640
	TGAGCGGGCT	GCCGCGCTCC	AAGTTCTCTC	GACAAGATGA	TGGTACTAAT	TATGGTACTT	2700
	TTCACTCACT	TTGCACCTTT	CCCTGTGCTG	CTCTAAGCAC	TTTACTGGA	TGGCGCGTGG	2760

	GCAGTGTGCA	GGCAGGTCTC	GAGGCCTGGG	GTTGGGGTGG	AGGGTGCAGC	CCGGAGTTGT	2820
	CCATCTGTCC	ATCCCAACAG	CAAGACGAGG	ATGTGGCTGT	TGAGATGTGG	GCCACACTCA	2880
	CCCTTGTCCA	GGATGACAGG	ACTGCCCTCT	CCTTCTCTGT	TCATCCGGCT	TAGCTTGGGG	2940
5	CTGGCTGCAT	TCCCCAGGA	TGGGCTTGA	GAAAGACAAA	CTTGTCTGGA	AACCAGAGTT	3000
	GCTGATTCCA	CCCGGGGGGC	CGGGCTGACT	CGCCCATCAC	CTCATCTCCC	TGTGGACTTG	3060
	GGAGCTCTGT	GCCAGGCCCA	CCTTGCAGCC	CTGGCTCTGA	GTCGCTCTCC	CACCCAGCCT	3120
	GGACTTGGCC	CCATGGGACC	CATCCTCAGT	GCTCCCTCCA	GATCCCGTCC	GGCAGCTTGG	3180
	CGTCCACCTT	GCACAGCATC	ACTGAATCAC	AGAGCCTTTG	CGTGAACAG	CTCTGCCAGG	3240
	CCGGAGAGCT	GTTTTCTCTT	CCCTTTTAT	CTGCTGGTGT	GGACCACACC	TGGGCTTGGC	3300
10	CGGAGGAAGA	GAGAGTTTAC	CAAGAGAGAT	GTCTCCGGGC	CCTATTATTAT	TATTTAAACA	3360
	TTTTTTTAAA	AAGCACTGCT	AGTTTACTTG	TCTCTCCTCC	CCATOGTCCC	CATCGTCTCT	3420
	CTTGCTCCCTG	ACTTGGGGCA	CTTCCACCCCT	GACCCAGCCA	GTCAGCTCT	GCCTTGGCGG	3480
	CTCTCCAGAG	TAGACATAGT	GTGTGGGGTT	GGAGCTCTGG	CACCCGGGGA	GGTAGCATTT	3540
	CCCTGCAGAT	GGTACAGATG	TTCTTGCCTT	AGAGTCACTT	CTAGTTCCCC	ACCTCAATCC	3600
15	CGGCATCCAG	CTTCACTGCT	CGCCACGCTG	CTAGCTCCGT	GGGCCACCGC	TGCGGCTTGA	3660
	GAGGTTTCCC	TCCTTCTCTT	CACTGAAAA	GCACATGGCC	TGGGTGACA	AATCTCTCTT	3720
	TGATGAATGT	ACCTGTGGG	GATGTTTCAT	ACTGACAGAT	TATTTTATAT	TATTCATGT	3780
	CATATTTAAA	ATATTTATTT	TTTATACCAA	ATGAATCACT	TTTTTTTTTA	AGAAAAAAA	3840
20	GAGAAATGAA	TAAAGAACT	ACTCTTCG				3868

Seq ID NO: C173 DNA Sequence  
Nucleic Acid Accession #: XM\_097508  
Coding sequence: 44..2788

25	1	11	21	31	41	51	
	TGAAAGGCGG	TTTGTGGTGA	AAGGAAAACC	CACAGGCCAA	GGAATGGGAA	GACCAAGGTT	60
	GACACTTGT	TGTCACTGT	CAATAATCAT	CTCTGCCCGG	GACCTCAGCA	TGAACAACCT	120
30	CACAGAGCTT	CAGCCTGGCC	TCTTCCACCA	CCTGCGCTTC	TTGGAGGAGC	TGCGTCTCTC	180
	TGGGAACCAT	CTCTCACACA	TCCCAGGACA	AGCATTCTCT	GGTCTCTACA	GCCTGAAAAA	240
	CCTGATGCTG	CAGAACATTC	AGCTGGGAGG	AATCCCCGCA	GAGGCGCTGT	GGGAGCTGCC	300
	GAGCCTGCAG	TCGCTGCGCC	TAGATGCCAA	CCTCATCTCC	CTGGTCCCGG	AGAGGAGCTT	360
	TGAGGGGCTG	TCCTCCCTCC	GCCACCTCTG	GCTGGAGGAC	AATGCATCTA	CGGAGATCCC	420
	TGTCAAGGCC	CTCAACAACC	TCCCTGCCCT	CGAGGCCATG	ACCCTGGCCC	TCAACCGCAT	480
35	CAGCCACATC	CCCGCTACG	CGTTCCAGAA	TCTCACCAGC	CTTGTGGTGC	TGCATTGACA	540
	TAAACAACGC	ATCCAGCATC	TGGGAGCCCA	CAGCTTCGAG	GGGCTGCACA	ATCTGGAGAC	600
	ACTAGACCTG	AATTATAACA	AGCTGCAGGA	GTTCCTGTG	GCCATCCGGA	CCCTGGGCGG	660
	ACTGCAGGAA	CTGGGGTTCC	ATAACAACAA	CATCAAGGCC	ATCCCAGAAA	AGGCCCTCAT	720
	GGGGAACCC	CTGCTACAGA	CGATACACTT	TTATGATAAC	CCAATCCAGT	TTGTGGGAAG	780
40	ATCGGCACTC	CAGTACCTGC	CTAAACTCCA	CACACTATCT	CTGAATGGTG	CCATGGACAT	840
	CCAGGAGTTT	CCAGATCTCA	AAGGCACCAC	CAGCCTGGAG	ATCCTGACCC	TGACCGCGGC	900
	AGGCATCCGG	CTGCTCCCAT	CGGGGATGTG	CCAACAGCTG	CCCAGGCTCC	GAGTCTCTGA	960
	ACTGTCTCAC	AATGCAATTT	AGGAGCTGCC	CAGCGTCGAC	AGGTGTGAGA	AATTGGAGGA	1020
	AATCGGCTCC	CAACACAACC	GCATCTGGGA	AATTGGAGCT	GACACCTTCA	GCCAGCTGAG	1080
45	CTCCCTGCAA	GCCTTGGATT	TTAGCTGGAA	CGCCATCCGG	TCCATCCACC	CCGAGGCTTT	1140
	CTCCACCTCG	CATCTCCCTG	TCAAGCTGGA	CCTGACAGAC	AACCAGCTGA	CCACACTGCC	1200
	CCTGGCTGGA	CTTGGGGGCT	TGATGCATCT	GAAGCTCAAA	GGGAACCTTG	CTCTCTCCCA	1260
	GGCCTTCTCC	AAGGACAGTT	TCCCAAAACT	GAGGATCCCT	GAGGTGCCCT	ATGCCTACCA	1320
	GTGCTGTCCC	TATGGGATGT	GTGCCAGCTT	CTTCAAGGCC	TCTGGGCACT	GGGAGGCTGA	1380
50	AGACCTTCAC	CTTGATGATG	AGGAGTCTTC	AAAAAGGCCC	CTGGGCTTCC	TTGCCAGACA	1440
	AGCAGAGAAC	CACATATGAC	AGGACCTGGA	TGAGCTCCAG	CTGGAGATGG	AGGACTCAAA	1500
	GCCACACCCC	AGTGTCAGT	GTAGCCCTAC	TCCAGGCCCC	TTCAAGCCCT	GTGAGTACCT	1560
	CTTTGAAAGC	TGGGGCATCC	GCCTGGCCGT	TGGGGCCATC	GTGTTGCTCT	CCGTGCTCTG	1620
	CAATGGACTG	GTGCTGTGTA	CCGTGTTCGC	TGGGGGCCCT	GTCCCTCTGC	CCCCGGTCAA	1680
55	GTTTGTGGTA	GGTGGGATTT	CAGGCGCCAA	CACCTTGACT	GGCATTCTCT	TGGGCTTCTT	1740
	AGCCTCAGTC	GATGCCCTGA	CTTTTGTGTA	GTTCTCTGAG	TACGGAGCCC	GCTGGGAGAC	1800
	GGGGCTAGGC	TGGCGGGCCA	CTGGCTTCTT	GGCAGTACTT	GGGTGGAGGG	CATCGGTGCT	1860
	GCTGCTCACT	TGGGCGGAG	TGCAGTGCAG	CGTCTCCGTC	TCTGTGTCTC	GGGCTATGG	1920
60	GAAGTCCCCC	TCCCTGGGCA	GCGTTCCAGC	AGGGGTCTTA	GGCTGCCTGG	CATGGGAGG	1980
	GCTGGCGGCC	GGGCTGCCCT	TGGGCTCAGT	GGGAGAAATAC	GGGGCTTCCC	CATCTGCTCT	2040
	GCCCTACGCG	CCACTGTAGG	GTGAGCCAGC	AGCCCTGGGC	TTCAACGTTG	CCCTGGTGAT	2100
	GATGAATCTC	TTCTGTTTCC	TGGTCTGTGC	CGGTGCTTAC	ATCAAACTGT	ACTGTGACCT	2160
	GCGCGGGGGC	GACTTTGAGG	CGGTGTGGGA	CTGGGCAATG	GTGAGGCAGC	TGGGCTGGCT	2220
65	CATCTTCGCA	CAGGGGCTCC	TCTACTGTCC	CGTGGCCTTC	CTCAGCTTTG	CCTCCATGCT	2280
	GGGCTCTTTC	CCTGTCAOGC	CCGAGGCGGT	CAAGTCTGTC	CTGCTGGTGG	TGCTGCCCTT	2340
	GCCCTGCCTG	CTCAACCCAC	TGCTGTACCT	GCTCTTCAAC	CCCCACTTCC	GGGATGACCT	2400
	TGGGCGGCTT	CGGCCCCGCG	CAGGGGACTC	AGGGCCCTTA	GCCTATGCTG	GGGCGGGGA	2460
	GCTGGAGAAG	AGCTCCTGTG	ATTCTACCCA	GGCCCTGGTA	GCCTTCTCTG	ATGTGGATCT	2520
70	CATTCTGAAA	GCTTCTGAAG	CTGGGCGGCC	CCCTGGGCTG	GAGACCTATG	GCTTCCCTCT	2580
	AGTGACCTTC	ATCTCTGTTC	AGCAGCCAGG	GGCCCCCAGG	CTGGAGGGCA	GCCATTGTGT	2640
	AGAGCCAGAG	GGGAACCACT	TTGGGAACCC	CCAACCTCTC	ATGGATGGAG	AATGCTGCTG	2700
	GAGGGCAGAG	GGATCTACGC	CAGCAGTGG	AGGCTTGTCA	GGGGGTGGCG	GCTTTCAGCC	2760
	CTCTGGCTTG	GCTTTTGTCT	CACACGTGTA	AATATCCCTC	CCCATCTCTC	TCTTCCCTCT	2820
75	TCTTCCCTTT	CCTCTCTCCC	CCTCGGTGAA	TGATGGCTGC	TTCTAAAACA	AATACAACCA	2880
	AAACTCAGCA	GTGTGATCTA	TAGCAGGATG	GCCCACTCCC	TGGCTCCACT	GATCACCTCT	2940
	CTCCTGTGAC	CATCAACCAAC	GGGTGCTCTT	TGGCCTGGCT	TTCCCTTGGC	CTTCTCAGC	3000
	TTCACTTGA	TACTGGGCTT	CTTCTTGTTC	ATGTCTGAAG	CTGTGGACCA	GAGACCTGGA	3060
	CTTTGTCTG	CTTAAGGGAA	ATGAGGGAAG	TAAAGACAGT	GAAGGGGTGG	AGGGTTGATC	3120
	AGGGCAGCT	GGACAGGGAG	ACCTCACAGA	GAAAGGCTTG	GAAGGTGATT	TCCGCTGTGA	3180
80	CTCATGGATA	GGATACAAAA	TGTGTTCCAT	GTACCATTA	TCTTGACATA	TGCCATGCAT	3240
	AAAGACTTCC	TATTAATAA	AGCTTTGGAA	GAG			3273

Seq ID NO: C174 DNA Sequence  
Nucleic Acid Accession #: NM\_130849

Coding sequence: 101..2044

```
1      11      21      31      41      51
5  AGTCTGGCCC TGGACAACCC CAGCAAAGCC GCCCTCAGCC AGCCCAAGAAG CACTGGGCCT 60
   TGGCCACAGC AACACCCACT GAGCACGCTG GGAGCTGAGT ATGGGCTCCC TGGTCTCGCT 120
   GGAGCTGGGG CTGCTTCTGG CTGTGCTGGT GGTGACGGCG ACGGCTCCC CGCTGCTGG 180
   TCTGCTGAGC CTGCTCACCT CTGGCCAGGG CGCTCTGGAT CAAGAGGCTC TGGGCGGCCT 240
   GTTAAATAGC CTGCGGAGCC GTGTGCACTG CACCAACGGG CGGTGTGGAA AGTGCTGTCT 300
10  TGTGGAGGAC GCCCTGGGCC TGGGCGAGCC TGAGGGGTCA GGGCTGCCCC CGGGCCCGGT 360
   CCTGGAGGCC AGGTACGTCG CCGGCTCAG TGCCGCGGCC GTCTGTACC TCAGCAACCC 420
   CGAGGGGACC TGTGAGGACA CTGCGGCTGG CCTCTGGGCC TCTCATGCAG ACCACTCTCT 480
   GGCCTGTCTC GAGAGCCCCA AGGCCCTGAC CCGGGGCTG AGCTGGCTGC TGCAGAGGAT 540
   GCAGGCGCGG GCTCGCGGCC AGACCCCAAA GAOGGCTGC GTAGATATCC CTCAGCTGCT 600
15  GGAGGAGGGG GTGGGGGCGG GGGCTCCGGG CAGTGTGGC GGCCTCTGG CTGCGCTGCT 660
   GGACCATGTC AGGAGCGGGT CTGTCTTCCA CGCTTGCGG AGCCCTCAGT ACTCGTGGGA 720
   CTTTGTGTTT CAGCAGCACA GCAGCGAGGT CCCTATGACG CTGGCCGAGC TGTGAGCCTT 780
   GATGACAGGC CTGGGGGTGG GCAGGGAGGC CCACAGTGAC CACAGTCATC GGCACAGGGG 840
   AGCCAGCAGC CGGACCCCTG TGCCCTCAT CAGCTCCAGC AACAGCTCCA GTGTGTGGGA 900
20  CAOGTATGC CTGAGTGCCA GGGACGTGAT GGCTGCATAT GGACTGTGCG AACAGGCTGG 960
   GGTGACCCCG GAGGCTGGGG CCAACTGAG CCCTGCCCTG CTCCAACAGC AGCTGAGTGG 1020
   AGCCTGCACC TCCAGTGCCA GGGCCCCCGT CCAGGACCAG CTCAGCCAGT CAGAGAGGTA 1080
   TCTGTAGCGC TCCCTGGCCA CGCTGCTCAT CTGCTCTGCG GCGGTCTTTG GCCTCTGCT 1140
   GCTGACCTGC ACTGGGTGCA GGGGGGTGCG CCACTACATC CTGCAGACCT TCCTGAGCCT 1200
25  GGCACTGGGT GCACTCACTG GGGACGCTGT CCGTGCATCT ACGCCCAAGG TGTGGGGCT 1260
   GCATACACAC AGCGAAGAGG GCCTCAGCCC ACAGCCCAAC TGGCGCTCC TGGTATGCT 1320
   GGCGGGGCTC TACGCTTCTT TCCTGTTTGA GAACCTCTTC AATCTCTGCG TGCCAGGGA 1380
   CCGGAGGAGC CTGGAGGAGC GGCCTTGCGG CCACAGCAGC CATAGCCACG GGGGCCACAG 1440
   CCAGGCTGTG TCCTTGACGC TGGCACCAG CGAGCTCCGG CAGCCCAAGC CCCCCACGA 1500
30  GGGCTCCCGC GCAGACCTGG TGGCGGAGGA GAGCCCGGAG CTGCTGAACC CTGAGCCAG 1560
   GAGACTGAGC CCAGAGTTGA GGCTACTGCC CTATATGATC ACTCTGGGCG ACGCGGTGCA 1620
   CAACTTCGCC GACGGGCTGG CCGTGGGCGC CGCCTTCGCG TCCTCTGGA AGACCGGGCT 1680
   GGCCACCTCG CTGGCCGTGT TCTGCCACGA GTTGCCACAC GAGCTGGGG ACTTCGCCGC 1740
   CTTGCTGCAC GCGGGGCTGT CCGTGCGCCA AGCACTGTCT GTGAACCTGG CCTCCGCGCT 1800
35  CACGGCTTTC GCTGCTCTCT ACGTGGCACT CGCGGTTGGA GTCAGCGAGG AGAGCGAGGC 1860
   CTGGATCTCT GCACTGGCCA CCGGCTGTGT CCTCTACGTA GCACTCTGCG ACATGCTCCC 1920
   GCGCATGTTG AAAGTACGGG ACCCGCGGCC CTGGCTCTCT TTCTGCTGCG ACACGTTGG 1980
   CCTGCTGGGC GGTGGAGCCG TCCTGCTGCT GCTGTCCCTG TACGAGGATG ACATCACCTT 2040
   CTGATACCTT GGCCTAGTCC CCACTCTTTC ACTTAAGATC CCACCTCA CAAACCTACA 2100
40  CCCCAGAAC CAGAAGCCCC TATAGAGGCC CCAGTCCCAA CTCCAGTAAA GACACTCTTG 2160
   TCCTTGGAAA AAAAAAAAAA AAAAAAAAAA AA 2192
```

Seq ID NO: C175 DNA Sequence

Nucleic Acid Accession #: NM\_018971

Coding sequence: 1..1128

```
1      11      21      31      41      51
50  ATGGCGAAGC GAGCGAGGCC GGGTGGCAGC GGGCGCGCGG AGGCGGCGCG CCTGGGCCTC 60
   AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CCGGCAACGT GCTGTTGCG 120
   CTGCTGATGC TGCGGGAGCG CAGCTTGACG CGCGCCCGGT ACTACCTGCT GCTCGACCTG 180
   TGCTGCGCGG ACGGGCTGCG CGCGCTCGCC TGCCCTCCCG CCGTCATGCT GCGCGCGCG 240
   CGTGGCGCGG CGCGCGCGGG GCGCGCTGCG GCGCGCTGCG GCTGCAAGCT GCTGCGCTTC 300
   CTGGCGCGCG TCTTCTGCTT CCAAGCGGCC TTCTGTGTCG TGGCGGTGGG CGTCAACCGC 360
55  TACCTGGCCA TCGCGCACCA CCGCTTCTAT GCAGAGCGCC TGGCGGCTG GCGCTGCGCC 420
   GGCATGCTGG TGTGCGCCCG CTGGGCGCTG GCGCTGCGCG CGGCTTCCC GCCAGTCTG 480
   GACGGCGGTG GCGACGACGA GGAACGCGCG TGCGCCCTGG AGCAGCGGCG GAGCGCGCG 540
   CCGGCGCGCG TGGGCTTCTT GCTGCTGCTG GCGGTGGTGG TGGGCGCCAC GCACCTGCTC 600
   TACCTCCGCG TGCTCTTCTT CATCCAGCAG CGCGCAAGA TCGGCGCCCG GCGCTGCTG 660
60  CCGCGCTGCA GCCACGACTG GACCTTCCAC GCGCGCGGCG CCACCGGCCA GCGCGCGCG 720
   AACTGACGCG CGGCTTCTCG CCGCGCGGCC ACGCGCGCGG CGCTTGTGGG CATCGGCGCC 780
   GCAGGGCGCG GCCCGCGCGC GCGCGCGCTC CTGCTGCTGG AAGAATTCAA GACGGAGAAG 840
   AGGCTGTGCA AGATGTTCTA CGCGCTCAGC CTGCTCTTCC TGCTCTCTG GGGGCCCTAC 900
   GTGCTGGCCA GCTACCTGCG GGTCTCTGCT CCGCGCGCGG CGGTCCCGCA GCGCTACCTG 960
65  ACGGCTTCCG TGTGGCTGAC CTTCGCGCAG GCGCGCATCA ACCCGTCTGT GTGCTTCTCT 1020
   TTCAACAGGG AGCTGAGGGA CTGCTCAGG GCCCAGTTCC CTGCTGCCA GAGCCCCCGG 1080
   ACCACCCAGG GACCCATCC CTGCGACCTG AAGGCATTG GTTTATGA 1128
```

Seq ID NO: C176 DNA Sequence

Nucleic Acid Accession #: NM\_005631

Coding sequence: 290..2653

```
1      11      21      31      41      51
75  GGCACGAGGG GGCTGAAGAC AACTTGGATT GCGAGGCTAG GGCTTGGGGA GTCTGTCATC 60
   CCGTTCGCGG CCTCGCAGC CCAACATGGG CCGCGGGTTC CAAAGTTTGC GAAGTTGGGC 120
   GCGAGGGGCG CGGGCGCGCG GGAGCGTCCG GGGGGGCGCG GGCCCGGATT CTCTGGGCGC 180
   ACAGGTGCGC TGAGCGCGCT CCGCGGCGCG CGAGGTGCTG CTGTGCGCG GGGGCGTCCG 240
   AGGAGCAGGG GGGGCGCGCG GGGCTTTTGC TGAGTTGGCG GGTGTGGCCA TGGCCGCTGC 300
   CCGCCAGCGG CGGGGCGCGG AGCTCCCGCT CCTGGGGCTG CTGCTGCTGC TGTGCTGGG 360
   GGACCCGGGG CGGGGCGCGG CCTCGAGCGG GAACGCGACC GGGCTTGGG CTGAGAGCGC 420
   GGGCGGAGC GCGAGGAGGA GCGCGCGGT GACTGGCCCT CCGCGCGCG TGAAGCACTG 480
   CGGCGGGGCT GCGCCCTGCG AGCGCGTCCG CTACCAACGT TGCTTGGGCT CGGTGCTGCC 540
   CTACGGGGCC ACCTCCACAC TGCTGGCGCG AGACTGGGAC TCCAGGAGG AAGCGCACGG 600
```

5	CAAGCTCGTG	CTCTGGTCGG	GCCTCCGGAA	TGCCCCCGCG	TGCTGGGCAG	TGATCCAGCC	660
	CCTGCTGTGT	GCCGTATACA	TGCCCAAGTG	TGAGAATGAC	CGGGTGGAGC	TGCCCAGCCG	720
	TACCCCTCTGC	CAGGCCACCC	GAGGCCCTTG	TGCCATOGTG	GAGAGGGAGC	GGGGCTGGCC	780
	TGACTTCTCT	CGCTGCACTC	CTGACCGCTT	CCCTGAAGGC	TGCACGAATG	AGGTGCAGAA	840
	CATCAAGTTC	AACAGTTCAG	GCCAGTGGGA	AGTGCCCTTG	GTTCGGACAG	ACAAACCCAA	900
	GAGCTGGTAC	GAGGACGTGG	AGGGCTGGCG	CATCCAGTGC	CAGAACCCGC	TCTTCACAGA	960
	GGCTGAGCAC	CAGGACATGC	ACAGCTACAT	CGCGGCCTTC	GGGGCCGTCA	CGGGCCTCTG	1020
	CACGCTCTTC	ACCTGGCCCA	CATTCTGGGC	TGACTGGCGG	AATCTGAATC	GCTACCCCTGC	1080
	TGTTATTCTC	TTCTAGCTCA	ATGCGTGCTT	CTTTGTGGGC	AGCATTGGCT	GGCTGGCCCA	1140
10	GTTCATGAT	GGTGCCCGCC	GAGAGATCGT	CTGCCGTGCA	GATGGCACCA	TGAGGCTTGG	1200
	GGAGCCCAAC	TCCAATGAGA	CTCTGTCTTG	CGTCATCATC	TTTGTCTATG	TGTACTACGC	1260
	CCTGATGGCT	GGTGTGGTTT	GGTTGTGGGT	CCTCACCTAT	GCCTGGCACA	CTTCCTTCAA	1320
	AGCCCTGGGC	ACCACCTACC	AGCCTCTCTC	GGCAAGACCC	TCCTACTTCC	ACCTGCTCAC	1380
15	CTGGTCACTC	CCCTTTGTCC	TCAGTCTGGC	AATCCTTGCT	GTGGCCGAGG	TGGATGGGGA	1440
	CTCTGTGAT	GGCATTTGTT	TTGTGGGCTA	CAAGAACTAC	CGATACCGTG	CGGGCTTCGT	1500
	GCTGGCCCCA	ATCGGCCTGG	TGCTCATCGT	GGGAGGCTAC	TTCTCTATCC	GAGGAGTCAT	1560
	GACTCTGTTC	TCCATCAAGA	GCAACCACCC	CGGGCTGCTG	AGTGAGAAGG	CTGGCAGCAA	1620
	GATCAACGAG	ACCATGCTGC	GCTTGGGCAT	TTTGTGGCTT	CTGGCCCTTG	GCTTTGTGCT	1680
20	CATTACCTTC	AGCTGCCACT	TCTACGACTT	CTTCAACCA	GCTGAGTGGG	AGCGCAGCTT	1740
	CGGGACTATC	TGCTATGTG	AGGCCAATGT	GACCATCGGG	CTGCCACCA	AGCAGCCCAT	1800
	CCCTGACTGT	GAGATCAAGA	ATCGCCCGAG	CCTTCTGGTG	GAGAAGATCA	ACCTGTTTGC	1860
	CATGTTTGA	ACTGGCATCG	CCATGAGCAC	CTGGGTCTGG	ACCAAGGCCA	CGCTGCTCAT	1920
	CTGGAGGGCT	ACCTGTGCA	GGTTGACTGG	GCAGAGTGAC	GATGAGCCAA	AGCGGATCAA	1980
25	GAAGAGCAAG	ATGATTGCCA	AGGCCTTCTC	TAAGCCGGAC	GAGCTCTCTG	AGAACCCAGG	2040
	CCAGGAGCTG	CTCTTACAG	TGCACACTGT	GTCCCAAGAC	GGGCCCGTGG	CGGGCTTGGC	2100
	CTTTGACCTC	AATGAGCCCT	CAGCTGATGT	CTCCTCTGCC	TGGGCCCCAG	ATGTACCCAA	2160
	GATGGTGGCT	CGGAGAGGAG	CCATCTGCTC	CCAGGATATT	TCTGTACCC	CTGTGGCAAC	2220
	TCCAGTGCCC	CCAGAGGAAC	AAGCCAACTT	GTGGCTGGTT	GAGGCAGAGA	TCTCCCCAGA	2280
	GCTGCAGAA	CGCCTGGGCC	GGAGAGAGAA	GAGGAGGAAG	AGGAAGAAGG	AGGTGTGCCC	2340
30	GCTGGGCGCG	CCCCCTGAGC	TTCACCCGCC	TGCCCTGGCC	CCAGTACCA	TTCCTGACT	2400
	GCCTCAGCTG	CCCCCGCAGA	AATGCCCTGG	GGCTGCAGGT	GCCTGGGGAG	CTGGGACTC	2460
	TTGCCGACAG	GGAGCGTGGA	CCCTGGTCTC	CAACCCATTC	TGCCCAGAGC	CCAGTCCCCC	2520
	TCAGGATCCA	TTTCTGCCCA	GTGCACCGGC	CCCGCTGGCA	TGGGCTCATG	GCCGCCGACA	2580
	GGGCCTGGGG	CCATTACTCT	CCGCAACCAA	CCTGATGGAC	ACAGAACTCA	TGGATGCAGA	2640
35	CTCGGACTTC	TGAGCCTGCA	GAGCAGGACC	TGGGACAGGA	AAGAGAGGAA	CCAATACCTT	2700
	CAAGGCTCTT	CTTCTCTACC	GAGCATGCTT	CCCTAGGATC	CCGCTCTCCA	GAGAACCTGT	2760
	GGGCTGACTG	CCCTTCGGA	AGAGTTCTGG	ATGTCTGGCT	CAAGCAGCA	GGAGCTGTGG	2820
	AAAGAGCTCA	ACTCTCTCA	GGGGAGGCTT	CACCCAGGG	ACAGGGCCCT	GGAGCTCAGG	2880
40	GTCTCTGTTT	CTGCCCTGCC	AGCTGCAGCC	TGGTTGGCAG	CATCTGCTCC	ATCGGGGCGG	2940
	GGGGATAGTG	GAGCTTGTGG	TGGGGCAGGA	ACGGTGGAGG	CAGAGGTGAC	AGTTCCACGA	3000
	GTGGGCTTTG	GTGGCCAGGG	AGGCAGCCTA	GCCTATGTCT	GGCAGATGAG	GGCTGGCTGC	3060
	CGTTTCTGGG	GCTGATGGGT	GCCCTTTCCT	GGCAGTCTCA	GTCCAAAAGT	GTGACTGTG	3120
	TCATTAGTGT	TTTGTCTAAG	TAGGGCCAGG	GCACCGTATT	CCTCTCCGAG	GTGTTTGTGG	3180
45	GGCTGGAAGG	ACCTGTCTCC	ACAGGGGCCA	TGTCTCTCT	TAATAGGTGG	CACTACCCCA	3240
	AACCCATCTT	TTGTTCTCTC	ATATCTCTCT	TCTCTGTTC	CATTTCAGTT	CAGTTTCAGC	3300
	GGTGCCAACC	TCTTTTGGTT	TCCTTTTGT	TGATGAGGAC	CCAGAGCTGC	TGCACACACT	3360
	CACCTCTAAC	CCCCCTCCCT	CGCTGCTGGG	CCCCATCTCC	ACAGGAGAGA	CTGGTTCGGC	3420
	TCTAGGGCTC	CTGTGGAGCT	TGGGATAGGA	GCAGTGAGTG	ACAAAGCTTC	TGAAAGATGC	3480
50	ATCATCTCTT	CCTCACACCC	ATTTAGTGGG	GGATGGGTCC	TCTAGACTTG	AGGGGCTACC	3540
	CTGGGAAGCT	TGAGCTAGCTT	CAGCCAGGCA	AGAAAGCTTC	CTTCAACCTG	CATAGCCGGT	3600
	GGGTGAGGAG	ATTCCCACTT	TCCATAGCCT	CCAAACATGT	TCCCAAGGCC	CCACTTTCAA	3660
	GAATCAGACA	GCAGGAAGCC	ATAGATGCTG	GCTGGGTTC	AGGTTATGGG	GAGAAGAAAT	3720
55	ACAGTCAATA	AAAGGTTT	GTATAAAAA	AAAAA	AAAAA	AAAAA	3780
	A						3781

Seq ID NO: C177 DNA Sequence  
Nucleic Acid Accession #: AK094595  
Coding sequence: 1..2853

60	1	11	21	31	41	51	
	ATGGGGGCCC	GGAGCGGAGC	TGGGGGCGCG	CTGCTGCTGG	CACTGCTGCT	CTGCTGGGAC	60
	CGAGGGCTGA	GCCAAAGCAGG	TAGGAAGCGA	TGGGTGAGG	TGCTCCCTGA	CTCCTTCCCG	120
	TCAGCGCCAG	CAGAGCCGCT	GCCCTACTTC	CTGCAGGAGC	CACAGGACGC	CTACATTGTG	180
65	AAGAACAGC	CTGTGGAGCT	CCGCTGCCGC	GCCTTCCCG	CCACACAGAT	CTACTTCAAG	240
	TGCAACGCGC	AGTGGGTGAG	CCAGAACGAC	CACGTACAC	AGGAAGGCCT	GGATGAGGCC	300
	ACCTTGGGGG	CGCGGGGCGG	CCTGCGGGTG	CGCGAGGTGC	AGATCGAGGT	GTGCGGGCAG	360
	CAGGTGGAGG	AGCTCTTTGG	GCTGGAGGAT	TACTGCTGCC	AGTGCGTGGC	CTGGAGCTCC	420
	GCGGGCACCA	CCAAGAGTGG	CCGAGCCTAC	GTCCGATCG	CCTACCTGCG	CAAGAACTTC	480
70	GATCAGGAGC	CTCTGGGCAA	GGAGGTGCC	CTGGACCATG	AGGTCTCTCT	GCAGTGGCGG	540
	CCGCGGAGG	GGGTGCTGCT	GGCCGAGGTG	GAATGGCTCA	AGAAAGGAGA	TGTATCGAC	600
	CCACCCAGG	ACACCAACTT	CCTGCTCACC	ATGACACCA	ACCTCATCAT	CCGCCAGGCC	660
	CGCCTGTGG	ACACTGCCAA	CTATACCTGC	GTGGCCAAGA	ACATCGTGGC	CAACCGCCGG	720
	AGCACCACTG	CCACCGTCT	CGTCTACGTC	AATGGCGGCT	GCTCCAGCTG	GGCAGAGTGG	780
75	TCACCTGCT	CTCAACGCTG	TGGCCGAGGC	TGGCAGAGC	GCACCGGAC	CTGCACCAAC	840
	CCGCTCCAC	TCAACGGAGG	GGCTTCTGC	GAGGGCCAGG	CATTCCAGAA	GACCGCTG	900
	ACCACCACT	GGCCAGTGA	TGGGGCGTGG	ACGGAGTGA	GCAAGTGGTC	AGCCTGCAGC	960
	ACTGAGTGG	CCACTGTGG	TAGCCGCGAG	TGCATGGCGC	CCCCACCCA	GACCGGAGG	1020
	CGTGAAGTGA	GCGGGACGCT	GCTGACTCT	AAGAACTGCA	CAGATGGGCT	GTGCATGCAA	1080
80	AATAAGAAA	CTCTAAGGCA	CCCCAACAGC	CACCTGCTGG	AGGCCTCAGG	GGATGCGGGG	1140
	CTGTATGCGG	GGCTCGTGGT	GGCCATCTTC	GTGGTCTGG	CAATCTCTAT	GGCGGTGGGG	1200
	GTGGTGGTGT	ACCGCCGCAA	CTGCCGTGAC	TTGACACAG	ACATCACTGA	CTCATCTGCT	1260
	GCCCTGACTG	TGTGTTTCCA	CCCCGTCAAC	TTTAAGACGG	CAAGGCCGAC	CAACCGGAG	1320
	CTCTACAC	CCTCTGTGCC	TCTGTACCTG	ACAGCCAGCG	CCGGCATCTA	CCGCGGACCC	1380

5  
10  
15  
20  
25  
30  
35

```

GTGTATGCC TGCAGGACT CACGACAAA ATCCCCATGA CCAACTCTCC TCTGCTGGAC 1440
CCCTTACCCA GCCTTAAGCT CAAGGTCTAC AGCTCCAGCA CCACGGGCTC TGGGCCAGGC 1500
CTGGCAGATG GGGCTGACCT GCTGGGGGTC TTGCCGCGTG GCACATACCC TAGCGATTTC 1560
GCCCGGAGCA CCCACTTCTC GCACCTGCGC AGCGCCAGCC TCGGTTCCCA GCAGCTCTTG 1620
GGCCTGCCCC GAGACCCAGG GAGCAGCGTC AGCGGCACCT TTGGCTGCCT GGGTGGGAGG 1680
CTCAGCATCC CCGGCACAGG GGTGAGCTTG CTGGTGCCCA ATGGAGCCAT TCCCCAGGGC 1740
AAGTTCTACG AGATGTATCT ACTCATCAAC AAGGCAGAAA GTACCCCTCC GCTTTCAGAA 1800
GGGACCCAGA CAGTATTGAG CCCCTCGGTG ACCTGTGGAC CCACAGGCCT CTGCTGTGTC 1860
CGCCCGGTCA TCCTCACCAT GCCCACTGTG GCCGAAGTCA GTGCCCGTGA CTGGATCTTT 1920
CAGCTCAAGA CCCAGGCCCA CCAGGGCCAC TGGGAGGAGG TGGTGACCTT GGATGAGGAG 1980
ACCCTGAACA CACCTGCTA CTGCCAGCTG GAGCCAGGGC CTTGTACAT CTGCTGGGAC 2040
CAGCTGGGCA CCTACGTGTT CACGGGGGAG TCCTATTCCC GCTCAGCAGT CAAGCGGCTC 2100
CAGCTGGCCG TCTTCGCCCC CGCCCTCTGC ACCTCCCTGG AGTACAGCCT CCGGCTCTAC 2160
TGCTTGGAG ACACGCTCTG AGCACTGAAG GAGGTGCTGG AGCTGGAGCG GACTCTGGGC 2220
GGATACTGG TGGCCAGCGG GAAACCGCTA ATGTTCAAGG ACAGTTACCA CAACCTGCGC 2280
CTCTCCCTCC ATGACCTCCC CCATGCCCAT TGGAGGAGCA AGCTGCTGGC CAAATACCGA 2340
GAGATCCCTC TCTATCAGT TTGAGTGGC AGCCAGAGG CCCTCCACTG CACTTTCACC 2400
CTGGAGAGGC ACAGCTTGGC CTCCACAGAG CTCACCTGCA AGATCTGGCT GCGGCAAGTG 2460
GAAGGGGAGG GCCAGATATT CCAGCTGCAT ACCACTCTGG CAGAGACACC TGCTGGCTCC 2520
CTGGACACT CTGCTCTGCG CCCTGGCAGC ACTGTACCA CCCAGCTGGG ACCTTATGCC 2580
TTCAAGATCC CACTGTCCAT CCGCCAGAAG ATATGCAACA GCCTAGATGC CCCCACCTCA 2640
CGGGCAATC ACTGCGCGAT GTAGCACAG AAGCTCTCTA TGGACCGGTA CTTGAATTAC 2700
TTGCCACCA AAGCGAGCCC CACGGGTGTG ATCCTGGACC TCTGGGAGC TCTGCAGCAG 2760
GACGATGGGG ACCTCAACAG CTTGGCGAGT GCCTTGGAGG AGATGGGCAA GAGTGAGATG 2820
CTGGTGGCTG TGGCCACCGA CGGGGACTGC TGAGCTCTCT GGGACAGCGG GCTGGCAGGG 2880
ACTGGCAGGA GGCAGGTGCA GGGAGGCGTG GGGCAGCCTC CTGATGGGGA TGTTTGGCCT 2940
CTGCTTCTCT CAGTTCTACA GCCAGAGTTG CCTCTCTCC TCCTCTTCCC CAACCCCCAG 3000
ACCATGACCA GCTTATGAAA ATCCATGTAC TCTGTTGTTA GAGGGCCAG AGTTCCTTCT 3060
CCACCCCGCG TCTCTCTCTC TTGGCTGAG ATCTCTGTGC AGGAACCAAG ATGGGGCTGA 3120
AGCCTCTGGA TCGGATTTGG TGGGGCGGG CAGGCAAGAG GCCCTCCCTC CACCCCCCA 3180
CCCTCAGCCC GGCACCTTCT GGGTTCATG GGTTTTATG CCGTTCTCGT TTTCTCTCTC 3240
CGTTATTGAT TTCTCTTTTC TCCCTAAGCC CCCTTCTGCT TCCAGCCCTT TTTCTCTTT 3300
GAAGAGTCAA GTACAATTCA GACAACTGC TTTCTCTGT CCAAAAGCAA AAAGGCAAG 3360
GAAAGAAAGA AAGCTTCAGA CCGCTAGTAA GGTCAAGA AGAAGAAAAA CACCAAAACC 3420
ACAAGGAAAG AGAAAAACCC AGTTTCTTAG GAAACGCAAA CGATTATTA TCCAGATTAT 3480
TTGGATAAGT CCTTTTAA A 3501

```

Seq ID NO: C178 DNA Sequence  
Nucleic Acid Accession #: NM\_004625  
Coding sequence: 310..1359

40  
45  
50  
55  
60  
65  
70  
75

```

1 11 21 31 41 51
| | | | |
GAGGGAGGGG CGGGGGCTGG AGGCAGCAGC GCCCGGCGAC TCCCGCGCTC TCGCACACTT 60
GCACCGGTCTG CTGCGCGCGA GCCCGGCGTC GCCCGCGCTC GCGCTCGCTC CTCCCTCCCT 120
CTCTCCGCTC CGTGGCTCCC GTGCTCTCTG CGAGGCTCAG GCGCGGAGCG CGCGGACGGG 180
CGCACCGACA GACGGCCCGG GGAAGCCTC GGTCTGCGCC TCCCGGCGGG GCTATGTTGA 240
TTGCCCGGCC GGGGCGGGCC CGCGGGATCA GCACAGCCCG GCCCGCGGCC CCGGCGGCCA 300
ATCGGGACTA TGAACCGGAA AGCGCGGCGC TGCTTGGGCC ACCTCTTTCT CAGCCTGGGC 360
ATGGTCTACG TCGGATCTGG TGGCTTCTCC TCACTGGTAG CTCTGGGCGC AAGCATCATC 420
TGTAACAAGA TCCAGGCCTT GGCTCCGAGA CAGCGGCGGA TCTGCCAGAG CCGGCCCGAC 480
GCCATCATCG TCATAGGAGA AGGCTCACAA ATGGGCTGG ACGAGTGTCA GTTTCAGTTC 540
CGCAATGGCC GCTGGAAGCT CTCTGCACTG GGAGAGCGCA CCGTCTTGGG GAAGGAGCTC 600
AAAGTGGGGA GCCGGGAGGC TGGCTTCACC TACGCCATCA TTGCCGCGCG CGTGGCCCGC 660
GCCATCACAG CTCGCTGTAT CCAGGGCAAC CTGAGCGACT GTGGCTGCGA CAAAGAGAAG 720
CAAGGCCAGT ACCACCGGGA CGAGGGCTGG AAGTGGGGTG GCTGCTCTGC CGACATCCGC 780
TACGGCATCG GCTTCGCCAA GGTCTTTGTC GATGCCCGGG AGATCAAGCA GAATGCCCGG 840
ACTCTCATGA ACTTGCAAA CAACGAGGCA GGCAGAAAGA TCCTGGAGGA GAACATGAAG 900
CTGGAATGTA AGTGCCACGG CGTGTCAAGC TCGTGACCA CCAAGACGTG CTGGACCCAC 960
CTGCCACAGT TTCGGGAGCT GGGCTACGTG CTCAGGACA AGTACAACGA GSCCGTTTAC 1020
GTGGAGCCTG TGCGTGCCAG CCGCAACAAG CGGCCACCT TCCTGAAGAT CAAGAAGCCA 1080
CTGTCTGACC GCAAGCCCAT GGACACGGAC CTGGTGTA CAAGAAAGTC GCCCAACTAC 1140
TGCGAGGAGG ACCCGGTGAC CGGCACTGTG GGCAACGAGG GCGCGCGCTG CAACAAGACG 1200
GCTCCCGAGG CCAGCGGCTG TGACCTCATG TGCTGTGGGC GTGGCTACAA CACCCACCAG 1260
TACGCCCGCG TGTGGCAGTG CAACTGTAAG TTCCACTGGT GCTGCTATGT CAAGTGCAAC 1320
ACGTGCAAGC AGCGCACGGA GATGTACAG TGCAAGTGA CCGCGTGTGC ACACCACTCT 1380
CCCGCTGCAA GTCAAGATTG TGGAGGACT GGACCGTTTC CAAGCTGCGG GCTCCCTGGC 1440
AGGATGCTGA GCTTGTCTTT TCTGCTGAGG AGGTACTTT TCCTGGGTTT CTGCGAGGCA 1500
TCCGTGGGGG AAAAAAATC TCTCAGAGCC CTCAACTATT CTGTTCCACA CCCAATGCTG 1560
CTCCACCTCT CCCACAGAC AGCCCAAGTC CCTCGGCGGC TGGAGCGAAG CCTTCTGCAG 1620
CAGGAATCTT GGACCCCTGG GCCTCATCAC AGCAATATTT AACAAATTAT TCTGATAAAA 1680
ATAATATTAA TTTATTAAAT TAAAAAGAA TCTTCCACA AAAAAA 1736

```

Seq ID NO: C179 DNA Sequence OBR3  
Nucleic Acid Accession #: NM\_003786  
Coding sequence: 71..4654

80

```

1 11 21 31 41 51
| | | | |
CTCCGGCGCC CGCTCTGCCC GCCGCTGGGT CCGACCGCGC TCGCCTTCTT TGCAGCGCGG 60
CCTCGGCCCC ATGGAACGCC TGTGCGGTTT CGGGGAGCTC GGCTCCAAGT TCTGGGACTC 120
CAACTGTCT GTGCACACAG AAAACCGGGA CCTCACTCCC TGCTTCCAGA ACTCCCTGCT 180
GGCCTGGGTG CCTGCATCT ACCTGTGGGT CGCCCTGCCC TGCTACTTGC TCTACCTGCG 240
GCACCATGTT CGTGGCTACA TCATCTCTC CCACCTGTCC AAGCTCAAGA TGGTCTGGG 300

```

	TGTCCTGCTG	TGGTGCGTCT	CCTGGGCGGA	CCTTTTTTAC	TCCTTCCATG	GCCTGGTCCA	360
	TGGCGGGGCC	CCTGCCCTTG	TTTTCTTTGT	CACCCCTTGG	GTGGTGGGGG	TCACCATGCT	420
	GCTGGCCACC	CTGCTGATAC	AGTATGAGCG	GCTGCAGGGC	GTACAGTCTT	CGGGGGTCTT	480
5	CATTATCTTC	TGGTTCCTGT	GTGTGGTCTG	CGCCATCGTC	CCATTCCGCT	CCAAGATCCT	540
	TTTAGCCAAAG	GCAGAGGGTG	AGATCTCAGA	CCCTTCCGCG	TTCAACCACT	TCTACATCCA	600
	CTTTGCCCTG	GTACTCTCTG	CCCTCATCTT	GGCCTGCTTC	AGGAGAGAAC	CTCCATTTTT	660
	CTCCGCAAAAG	AATGTGACCC	CTAACCCCTA	CCCTGAGACC	AGCGCTGGCT	TTCTCTCCCG	720
	CCTGTTTTTC	TGGTGGTTCA	CAAAGATGGC	CATCTATGGC	TACCGGCATC	CCCTGGAGGA	780
10	GAAGGACCTC	TGGTCCCTAA	AGGAAGAGGA	CAGATCCAG	ATGGTGGTGC	AGCAGCTGCT	840
	GGAGGCATGG	AGGAAGCAGG	AAAAGCAGAC	GGCAOGACAC	AAGGCTTCAG	CAGCACCTGG	900
	GAAAAATGCC	TCCGGCGAGG	ACGAGGTGCT	GCTGGGTGCC	CGGCCAGGC	CCCGGAAGCC	960
	CTCCTTCTGT	AAGGCCCTGC	TGGCCACCTT	CGGCTCCAGC	TTCTCATCA	GTGCTTGTCT	1020
	CAAGCTTATC	CAGGACCTGC	TCTCTTCAT	CAATCCACAG	CTGCTCAGCA	TCCTGATCAG	1080
	GTATTATCTC	AACCCATGG	CCCTCTCTG	GTGGGGCTTC	CTGGTGGCTG	GGCTGATGTT	1140
15	CTGTGCTGCT	ATGTGTCAGT	CGCTGATCTT	ACAACACTAT	TACCACTACA	TCTTTGTGAC	1200
	TGGGGTGAAG	TTTCGTACTG	GGATCATGGG	TGTCATCTAC	AGGAAGGCTC	TGGTTATCAC	1260
	CAACTCAGTC	AAACGTGCGT	CCACTGTGGG	GGAAATGTGC	AACCTCATGT	CAGTGGATGC	1320
	CCAGCGCTTC	ATGGACCTTG	CCCTTCTCT	CAATCTGCTG	TGGTCAGCAC	CCCTGCAGAT	1380
	CATCTGGGCG	ATCTACTTCC	TCTGGCAGAA	CCTAGGTCCC	TCTGTCTGGG	CTGGAGTGGC	1440
20	TTTCATGGTC	TGCTGATTTC	CACTCAACGG	AGCTGTGGCC	GTGAAGATGC	GGCCTTCCA	1500
	GGTAAAGCAA	ATGAAATGGA	AGGACTCGCG	CATCAAGCTG	ATGAGTGAGA	TCCTGAACGG	1560
	CATCAAGGTG	CTGAAGCTGT	ACGCCCTGGG	GGCCAGCTTC	CTGAAGCAGG	TGGAGGGCAT	1620
	CAGGCAGGGT	ATGCTCCAGC	TGCTGCGCAC	GGCGCCCTAC	CTCCACACCA	CAACCACTT	1680
	CACCTGGATG	TGCAGCCCTC	TCTCTGTGAC	CCTGATCACC	CTCTGGGTGT	ACGTGTACGT	1740
25	GGACCCAAAC	ATGTGCTGG	ACGCCGAGAA	GGCCTTTGTG	TCTGTGCTCT	TGTTTAATAT	1800
	CTTAAGACTT	CCCCCTCAAC	TGCTGCCCCA	GTTAATCAGC	AACCTGACTC	AGGCCAGTGT	1860
	GTCTCTGAAA	CGGATCCAGC	AATTCTCTGAG	CCAAGAGGAA	CTTGACCCCT	AGAGTGTGGA	1920
	AAGAAAGACT	ATCTCCCAAG	GCTATGCCAT	CACCATACAC	AGTGGCACCT	TCACCTGGGC	1980
	CCAGGACCTG	CCCCCCTCT	TGCACAGCCT	AGACATCCAG	GTCCCGAAGG	GGGCACTGGT	2040
30	GGCGGTGGTG	GGGCTGTGG	GCTGTGGGAA	GTCTCCCTGT	GTGTCTGCC	TGCTGGGAGA	2100
	GATGAGAGAAG	CTAGAAGSCA	AAGTGCACAT	GAAGGCTCCC	GTGGCTATG	TGCCCCAGCA	2160
	GGCATGGATC	CAGAACTGCA	CTCTTCAGGA	AAACGTGCTT	TTCCGCAAGG	CCCTGAACCC	2220
	CAAGCGCTAC	CAGCAGACTC	TGGAGGCTTG	TGCCCTTGCTA	GCTGACCTGG	AGATGCTGCC	2280
	TGGTGGGGAT	CAGACAGAGA	TGGAGAGGAA	GGGCATTAA	CTGTCTGGGG	GGCAGCGGCA	2340
35	GGCGGTCACT	TGGCTCGAG	CTGTTTACAG	TGATGCCGAT	ATTTCTTGTC	TGGATGACCC	2400
	ACTGTCCGCG	GTGGACTCTC	ATGTGGCCAA	GCACATCTTT	GACCACGTCA	TGGGCCAGA	2460
	AGGCGTGCTG	CGCAGCAAGA	CGCGAGTGCT	GGTGAAGCAC	GGCATTAGCT	TCCTGCCCA	2520
	GACACACTTC	ATCATTTGTC	TAGCTGATGG	ACAGGTGTCT	GAGATGGGCC	CGTACCCAGC	2580
	CTGTCTGAG	CGCAACGCTC	CCTTTGCCAA	CTTTCTCTGC	AACATATGCC	CCGATGAGGA	2640
40	CCAAGGSCAC	CTGGAGGACA	GCTGGACCGC	GTTGGAAAGT	GCAGAGGATA	AGGAGGCATC	2700
	GCTGATTGAA	GACACACTCA	GCAACACAC	GGATCTGACA	GACAATGATC	CAGTCACTTA	2760
	TGTTGTCCAG	AAGCAGTTTA	TGAGACAGCT	GAGTGGCTTG	TCCTCAGATG	GGGAGGGACA	2820
	GGGTCCGCTC	GTACCCCGGA	GGCACCTGGG	TCCATCAGAG	AAGGTGCAGG	TGACAGAGGC	2880
	GAAGGCAGAT	GGGGCACTGA	CCCAAGGAGGA	GAAGCAGGCC	ATTGGCACTG	TGGAGCTCAG	2940
45	TGTTGTCTGG	GATTATGCCA	AGGCGTGGG	GCTCTGTACC	ACGCTGGCCA	TCTGTCTCCT	3000
	GTATGTGGGT	CAAAGTGGCG	CTGCCATTGG	AGCCAATGTG	TGGCTCAGTG	CCTGGACAAA	3060
	TGATGCCATG	GCAGACAGTA	GACAGAACAA	CACCTCCCTG	AGGCTGGGCG	TCTATGCTGC	3120
	TTTAGGAATT	GCTCAAGGGT	TCTTGGTGAT	GCTGGCAGCC	ATGGCCATGG	CAGCGGGTGG	3180
	CATCCAGCTG	GGCCGTGTGT	TGCACACAGC	ACTGCTGCAC	AACAAGATAC	GCTCGCCACA	3240
50	GTCTTCTCTT	GACACACAC	CATCAGGCGG	CATCCTGAAC	TGCTTCTCCA	AGGACATCTA	3300
	TGTGTGTGAT	GAGGTCTCTG	CCCTGTCTAT	CCTCATGCTG	CTCAATTCCT	TCTTCAACGC	3360
	CATCTCCACT	CTTGTGGTCA	TCATGGCCAG	CACGCCGCTC	TTCACTGTGG	TCATCCTGCC	3420
	CCTGGCTGTG	CTCTACACCT	TAGTGCAGCG	CTTCTATGCA	GCCACATCAC	GGCAACTGAA	3480
	GGGGCTGGAA	TCAGTCAAGC	GCTCACTTAT	CTACTCCAC	TTTTCGGAGA	CAGTGAAGTG	3540
55	TGCCAGTGTG	ATCCGGGCTC	ACAACGSCAG	CCGGGATTTT	GAGATCATCA	GTGATACTAA	3600
	GGTGGATGCC	AACAGAGAG	GCTGCTACCC	CTACATCATC	TCCAACCGGT	GGCTGAGCAT	3660
	CGGAGTGGAG	TTGCTGGGGA	ACTGGGTGGT	GCTCTTTGCT	GCATATTGTC	CGCTCATCGG	3720
	GAGGAGCAGC	CTGAACCCGG	GGCTGGTGGG	CCTTTCTGTG	TCCTACTCTC	TGCAGGTGAC	3780
60	ATTGTGCTGT	AACCTGATGA	TACGAATGAT	GTGAGATTG	GAATCTAACA	TGCTGGCTGT	3840
	GGAGAGGGTC	AAGGAGTACT	CCAAGACAGA	GACAGAGGCG	CCCTGGGTGG	TGGAAGGCAG	3900
	CCGCCCTCCC	GAAGTTGGC	CCCCACGTGG	GGAGGTGGAG	TTCCGGAATT	ATTCTGTGCG	3960
	CTACCCGCGG	GGCCTAGACC	TGGTGTCTGAG	AGACCTGAGT	CTGCATGTGC	ACGGTGGCGA	4020
	GAAGGTGGGG	ATCGTGGGCC	GCACCTGGGC	TGGCAAGTCT	TCCATGACCC	TTTGGCTGTT	4080
65	CCGCATCCTG	GAGGCGGCAA	AGGGTGAAAT	CCGCATTGAT	GGCCTCAATG	TGGCAGACAT	4140
	CGGCTCCCAT	GACCTGCGCT	CTCAGCTGAC	CATCATCCCG	CAGGACCCCA	TCCTGTTCTC	4200
	GGGGACCCCT	CGCATGAACC	TGGACCCCTT	CGGCAGCTAC	TCAGAGGAGG	ACATTTGGTG	4260
	GGCTTTGGAG	CTGTCCCAAC	TGCACAGGTT	TGTGAGCTCC	CAGCCGGCAG	GCCTGACTTT	4320
	CCAGTGTCTA	GAGGGCGGGG	AGAATCTCAG	CGTGGGCCAG	AGGCAGCTCG	TGTGCTGGC	4380
70	CCGAGCCCTG	CTCCGCAAGA	GCCGCATCCT	GGTTTTAGAC	GAGGCCACAG	CTGCCATCGA	4440
	CCTGGAGACT	GACAACTCA	TCCAGGCTAC	CATCCGCAAC	CAGTTTGATA	CCTGCACTGT	4500
	CCTGACCATC	GCACACCGGC	TTAACACTAT	CATGGACTAC	ACCAGGGTCC	TGGTCTCGGA	4560
	CAAGAGGAGTA	GTAGCTGAAT	TTGATTCTCC	AGCCAACTTC	ATTGCACTGA	GAGGCATCTT	4620
	CTACGGGATG	GCCAGAGATG	CTGGACTTGC	CTAAAATATA	TTCTGAGAT	TTCTCTCTGG	4680
75	CTTTCTCTCG	TTTTCATCAG	GAAGGAAATG	ACACCAATA	TGTCGCGAGA	ATGGACTTGA	4740
	TAGCAAAAC	TGGGGGCACC	TTAAGATTTT	GCACTGTAA	AGTGCCCTAC	AGGGTAACTG	4800
	TGCTGAATGC	TTTAGATGAG	GAAATGATCC	CCAAGTGGTG	AATGACACGC	CTAAGGTGAC	4860
	AGCTAGTTTG	AGCCAGTTAG	ACTAGTCCCC	CGGTCTCCCG	ATTCCCAACT	GAGTGTATT	4920
	TGCACACTGC	ACTGTTTTCA	AATAACGATT	TTATGAATG	ACCTCTGTCC	TCCTCTGAT	4980
80	TTTTCATATT	TTCTTAAAGT	TTGCTTTCTG	TTTTTAAATA	AAAAGCTTTT	TCCTCTCTGA	5040
	ACAGAAACAC	GCTCTGGGT	CAGGCCACCC	CTAGGAACTC	AGTCTGTAC	TCTGGGGTGC	5100
	TGCTGTAATC	CATTAAAAAT	GGGAGTACTG	ATGAATATAA	ACTACATGGT	CAACAGTAAA	5160
	AAAAAAAAAA	AAAAAA					5176

Seq ID NO: C180 DNA Sequence

	1	11	21	31	41	51	
45	ACAGCATGGA	GTGGGGTTAC	CTGTTGGAAG	TGACCTCGCT	GCTGGCCGCG	TTGGCGCTGC	60
	TGCGACGCTC	TAGCGCGCGT	CGCGCGCGCT	CGCGCAAGGA	GCTGGCATGC	CAGAGATACA	120
	CGTGGCGGCT	GTGTAAGGCG	ATGGGTCACT	ACTACACTTA	CATGCCCAAT	CAGTCTCAAC	180
	ACGACAAGCA	AGACAGGAGG	GGCCTCGAGG	TGCACCAAGT	CTGGCGCGTC	GTGGAGATCC	240
50	AGRTGCTGCC	CGATCTCAAG	TTCTTCTGTT	CGAGCATGTA	CACGCCCATC	TGCCTAGAGG	300
	ACTACAAGAA	CGCGCTGCGC	CCCTGCGCGT	GCGGTGTGCA	GCGCGCCAAAG	CGCGGCTGCG	360
	CGCGCTCACT	CGCCCAAGTA	GGCTTGGCGT	CGCGCCAGCG	CATCGCTCTG	GACCGCTGTC	420
	CCGAGCAAGG	CACCCCTGAC	AGCCTGTGCA	TGGAATACAA	CGCGCCAGCA	CTAACCAAGC	480
	CGCGGCCAAG	CCGCGCGCGC	CGCTGCGCGC	CGCGCCGCGC	CGCGAGACAG	CCGCTTTCGG	540
55	CGAGCGGCGA	CGCGCGCCCG	CGCGGGGCGA	GGCCCCGCGA	CGCGAGAGGC	CAGAGGGGCG	600
	GTGGCGGCGG	GGACGCGGCG	GCGCCCCCAG	CTCGCGGCGG	CGCGCGTGGC	GGGAAGCGCG	660
	GGCCCCCTGG	CGCGCGGCGG	GCTCCCTGCG	AGCCCGGGTG	CCAGTGTCCG	CGCGCTATGG	720
	TGAGCGTGTC	CAGCAGAGCG	CAGCCGCTCT	ACAACCGCGT	CAAGACAGCG	CAGATCGCTA	780
60	ACTGCGGCGT	CGCCTCGCAC	AACCCCTTGT	TCAGCAGAGA	CGAGCGCGCC	TTCAACGCTT	840
	TCGTGATCGG	CTGTGGTGTC	GTGCTCTGCT	TGCTGTCCAC	CTTGCCACAC	GTCTCCACTC	900
	TCTTATTCGA	CATGGAGCGC	TTCAAGTACC	CGGAGCGGCC	CATTATCTTC	CTTCTGCGCT	960
	GCTACTCTTT	CGTGTGCGTG	GGCTACCTAG	TGGCGCTTGT	GCGCGGCCAC	GAGAAGGTGG	1020
	CGTGCAGCGG	TGGCGCGCGG	GCGCGCGGGG	CGCGCTTGGG	CGCGGGCGGG	CGCGCGCGGG	1080
	GCGCGCGCGC	CGCGCGGCGG	GCGCGCGGGG	CGCGCGGGCG	CGCGCGGAGT	TACGAGAGAG	1140
65	TGGCGCGGCT	GGAGCAGCAC	GTGCGCTACG	AGACACAACG	CGCGCGCTCG	TGCACAGTGG	1200
	TCCTCTTCTG	GGTCTACTTC	TTTGGCATGG	CCAGCTCCAT	CTGGTGGGTG	ATCTTGTCCG	1260
	TCACATGGTT	CTGGCGGCCG	GGTATGAAGT	GGGGACAAGA	AGCCATGCGC	GGTACTATCG	1320
	AGTACTTTCA	CCTGGCCGCG	TGGCTTGTGC	CCAGCGTCAA	GTCATGCGG	GTGCTGGCGC	1380
	TCAGCTCGGT	GGAGCGGCAG	CGGCTGGGCG	GCATCTGTGA	CGTGGGCATC	CAGAGCTCGG	1440
70	ACAACTCGTG	CGGCTCTGTC	TGGCGCGCG	TGGTCACTTA	CTCTTTCATC	GGCACCATAT	1500
	TCTGTCTGAG	CGGCTCTGTC	TCCCTGTTAC	GCATCGCGCT	GGTCACTAAG	ACAACGAGAG	1560
	GCCCCACCA	GACGCAACA	GTGAGTAAGC	TGATGATTCG	CTCGGGCTGC	TTCACTGTGC	1620
	TCTACACGTT	GCCCGCGCGG	GTGGTGTGCG	CGTGGCTCTT	CTACAGCAGC	CACAAACGCC	1680
	CGCGCTGGGA	GGCCACGCAC	AATGCTCCGT	CGCTGCGGGA	CTCGAGGCCG	GACCAAGGCAC	1740
75	CGAGGCGCGA	CTACGCGGTC	TTATGCTCTA	AGTACTTCAT	GTGCCTAGTG	GTGGGCACTA	1800
	CCTCGGCGCT	GTGGGTCTGG	TCGGCAAGA	CGCTGGAGTC	CTGGCGCTCC	CTGTGCAACC	1860
	CTGTGCTGTC	GGCGCAGCA	GGCGCGCGCG	TGGGCGGGGG	CGCGCGCTCC	ACGGCGCGGG	1920
	GGGCTGCGGG	GGCGCGGGGG	GGCGCGCGCG	CGCGGGACAG	CGGCGCGCGG	CGGGCGCGGG	1980
	GGGCGCGCGG	GGGCTCCCTC	TACAGCAAGC	TCAGCACTGC	CTGACGTGGG	GGGTGGGGCA	2040
80	CGCGAGAGTC	CGTGTCTTAT	CCAAAGCAGA	TGCCATTGTC	CCAGTCTCTA	GGGAGAGGCA	2100
	GGGGGGCGCC	AGGAGGGGTG	GGGAGGGGGG	CGAGGAGAGC	CAAGTGGCAG	GAAAGGGAC	2160
	TGATGGGCTC	GAGGTTCCTA	CGCCTTCACT	GTGTTGATTG	CTATTAGCAT	GAAATGAAC	2220
	TCCTTAATGGT	ATCCATTAGC	TGGGACTTAA	ATGACTCACT	TAGAACAAGG	TACCTGGGAT	2280
	TGAAGCCTCC	CAGGCTCCAGC	CGCTTTTCTC	CATTGATGTG	CGCGGGAGCT	CCTCCGCGCA	2340

CGCGTTAATT TCTGTTGGCT GAGGAGGGTG GACTCTGCGG CGTTTCCAGA ACCCGAGATT 2400  
 TGGAGCCCTC CCTGGCTGCA CTGGGCTGGG TTTGCAGTCA GATACACAGA TTTCACCTGG 2460  
 GAGAACCTCT TTTTCTCCCT CGACTCTTCC TACGTAAACT CCCACCCCTG ACTTACCCTG 2520  
 GAGGAGGGGT GACCGCCACC TGATGGGATT GCACGGTTTG GGTATTCTTA ATGACCAGGC 2580  
 5 AAATGCCCTA AGTAAACAAA CAAGAAATGT CTTAATTATA CACCCACGT AAATACGGGT 2640  
 TTCTTACATT AGAGGATGTA TTTATATAAT TATTTGTAA ATTGTAAAAA AAAAAGTGT 2700  
 AAAATATGTA TATATCCAAA GATATAGTGT GTACATTTT TTGTAAAAAG TTTAGAGGCT 2760  
 TACCCCTGTA AGAACAGATA TAAGTATTCT ATTTTGTCAA TAAATGACT TTTGATAAAT 2820  
 GATTTAACCA TTGCCCTCTC CCCCCTCTCT TCTGAGCTGT CACCTTTAAA GTGCTTGTCTA 2880  
 10 AGGACGCTG GGGAAAATGG ACATTTTCTG GCTTGTCAAT CTGTACACTG ACCTTAGGCA 2940  
 TGGAGAAAT TACTTGTAA ACTCTAGTTC TTAAGTTGTT AGCCAAGTAA ATATCATTGT 3000  
 TGAACAGAA TCAAAATTGA GTTTTGCAC CTTCCCAAA GACGGTGT TTCTAGGGAG 3060  
 CTCCTTCTG ATCCATGGAT AACAACTCTC ACTTTAGTGG ATGTAAATGG AACTTCTGCA 3120  
 15 AGSCAGTAAT TCCCTTAGG CCTTGTATT TATCTCGCAT GGTATCACTA AAGGTTTCAA 3180  
 AACCTGAAA AAAAA 3195

Seq ID NO: C182 DNA Sequence  
 Nucleic Acid Accession #: XM\_050625  
 Coding sequence: 222..1109

20  
 1 11 21 31 41 51  
 CGGGTGGGA GCCCCCGGA GCTGCGCGG GGCTTGCGAG GCCTCGCCCG CGCTGTCTCT 60  
 25 CGGTTGTCCT GCTTCTCCG GCCCCAGCG CGGGCTGCCA GCTTTTCGGG GCCCCGAGTC 120  
 GCACCCAGCG AAGAGAGCGG GCCCGGACA AGCTCGAAT CGGCGCGCCT CGCCCTTCCC 180  
 CGGCTCGGCT CCCTCTGCC CTCTGGGGTC GCGCGCCAC GATGTGTCAG GGCCTTGGCT 240  
 CGCTGTGCT GCTCTTCTCT GCTCTGCACT GCTGCTGGG CTGCGCGCGC GGGCTCTTCC 300  
 TCTTTGGCCA GCGCGACTTC TCCTACAAGC GCAGCAATTG CAAGCCCATC CTGGCAACC 360  
 30 TGCAGCTGTG CCACGGCATC GAATACCAGA ACATGCGGCT GCCCAACCTG CTGGGCCACG 420  
 AGACCATGAA GAGAGTGCTG GAGCAGGCG CGCTTGGAT CCGCTGGTC ATGAAGCAGT 480  
 GCCACCCGGA CACCAAGAG TTCTGTGCT CGCTCTTGC CCGCTGTGC CTGATGACC 540  
 TAGACGATAC CATCCAGCCA TGCCACTGCT TCTGCTGCA GGTGAAGGAC CGCTGCGCCC 600  
 CGGTATGTC CGCTTGGC TTCCCTGGC CCGACATGCT TGAGTGGAC CGTTTCCCCC 660  
 35 AGGACAACGA CCTTTGCATC CCCCCTGCTA GCAGCGACCA CCTCTGCCA GCCACCGAGG 720  
 AAGCTCCAAA GGTATGTGAA GCCTGCAAAA ATAAAAATGA TGATGACAAC GACATAATGG 780  
 AAACGCTTTG TAAAAATGAT TTGCACTGA AATAAAAGT GAAGGAGATA ACCTACATCA 840  
 ACCGAGATAC CAAATCATC CTGGAGACCA AGAGCAAGAC CATTACAAG CTGAACGGTG 900  
 TGTCCGAAG GGAACCTGAG AAATCGGTGC TGTGGCTCAA AGACAGCTTG CAGTGACCT 960  
 40 GTGAGGAGAT GAACGATC AACCGGCCCT ATCTGGTCT GGGACAGAAA CAGGGTGGGG 1020  
 AGCTGGTGAT CACCTCGGTG AAGCGGTGGC AGAAGGGGCA GAGAGAGTTC AAGCGCATCT 1080  
 CCGCGAGCAT CCGCAAGCTG CAGTGTAGT CCGGCAATCC TGATGGCTCC GACAGGCTG 1140  
 CTCAGAGAC CGCTGACCA TTCTGCTCC GGGATCTCAG CTCGGTTC CCAAGCACAC 1200  
 45 TCCTAGCTGC TCAGTCTCA GCCTGGGCG CTTCCCCCTG CTTTGTGCAC GTTGTGATCC 1260  
 CCAGCATTTT CTGAGTTATA AGGCCACAGG AGTGATAGC TGTTTTCACC TAAAGGAAAA 1320  
 GCCCACCCGA ATCTGTAGA AATATTCAA CTAATAAAAT CATGAATATT TTTATGAAGT 1380  
 TT 1382

Seq ID NO: C183 DNA Sequence  
 Nucleic Acid Accession #: NM\_001306.1  
 Coding sequence: 199..861

50  
 1 11 21 31 41 51  
 AATTGCGCAC GAGGGCAGGT GCAGGCGCAC GCGGCGAGAG CGTATGGAGC OGAGCCGTTA 60  
 55 GCGCGCGCGG TGGTGGAGTC AGTCCGTCCG TCGTCCGTC CGTGGGGGCG CGCGAGCTCC 120  
 CGCCAGCGCC AGCGGCCCGG GCCCTCGTC TCCCGCACCC CGGAGCCACG CGGTGGAGCG 180  
 GGCCTTGGCG CGGCGCCCAT GTCCATGGGC CTGGAGATCA CGGCGACCGC GCTGGCGGTG 240  
 CTGGGCTGGC TGGGCACCAT CGTGTGCTGC GCGTGGCCA TGTGGCGCGT GTGCGCTTC 300  
 60 ATCGGCAGCA ACATCATCAC GTGCGAGAAC ATCTGGGAGG GCCTGTGGAT GAAGTGGGTG 360  
 GTGCAGAGCA CCGGCCAGAT GCAGTGCAAG GTGTACGACT CGTGTCTGGC ACTGCCACAG 420  
 GACCTTCAGG CGGCGCGCGC CCTCATGCTG GTGGCCATCC TGCTGGCGCG CTTGCGGCTG 480  
 CTAGTGGGCG TGGTGGGCGC CCAAGTGCACC AACTGGGTGC AGGACGACAC GGCCAAGGCC 540  
 AAGATCACCA TCGTGGCAGG CGTGTCTTTC CTCTCGCGCG CCTGTCTCAC CCTCGTGGCG 600  
 65 GTGTCTCGGT CGGCCAACAC CATTATCCGG GACTTCTACA ACCCCGTGGT GCCCGAGGCG 660  
 CAGAAGCGCG AGATGGGCGG GGGCTGTAC GTGGGCTGGG CGGCGCGGCG GCTGCAGCTG 720  
 CTGGGGGGCG CGCTGCTCTG CTGCTCGTGT CCCCACGCG AGAAGAAGTA CAAGGCCACC 780  
 AAGGTCTCT ACTCGGCGCC GCGCTCCACC GGCCCGGAG CAGCCTGGG CACAGGCTAC 840  
 GACCGCAAG ACTACGTCTA AGGACAGAC GCAGGAGAC CCAACCAACA CCACCAACAC 900  
 70 CAACACCAAC ACCACCAACG CGAGCTGGAG CGGCGACAG GCCATCCAGC GTGCAGCCTT 960  
 GCCTCGAGG CAGCCCAACC CCCAGAAAGC AGGAAGCCCC CGGCTGGGAC TGGGGCAGCT 1020  
 TCCCAGCAG CCAAGCTTTT GCGGCGCGGG CAGTGCAGTT CGGGGCGCAG GGACCAACCT 1080  
 GCATGAGCTG TGAACCTCTA CCCTTCTGGA GCACGGGGCC TGGGTGACCG CCAATACTTG 1140  
 ACCACCCCGT CGAGCCCAT CCGGCGCGCT CCCCATGTC GCGCTGGGCA GGGACCGGCA 1200  
 75 GCCCTGGAAG GGGCACTTGA TATTTTCAA TAAAAGCCTC TCGTTTATGC 1250

Seq ID NO: C184 DNA Sequence  
 Nucleic Acid Accession #: NM\_012449.1  
 Coding sequence: 66..1085

80  
 1 11 21 31 41 51  
 CGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60  
 AATTAAATGA AAGCAGAAAA GACATCAACA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120  
 GGAGAAATTT AGAAGAAGAC GATTATTGTC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180



5  
10  
15

```

AAAGACCTGT GCTTTTGCAT TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
CAGAACCTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTGCCCAATT AAAATAGCTG 300
CTATTATAGC ATCTCTGACT TTCTTTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG 360
CAACTTCCCA TCACCAATAT TTTTATAAAA TTCCAATCCT GGTTCATCAAC AAAGTCTTGC 420
CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
TCCAACTTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTTTGC TGTACTGCAT GCAATTTATA 600
GTCTGTCTTA CCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660
AGGTCCAACA AAATAAAGAA GATGCCCTGA TTGAGCATGA TGTTTGGAGA ATGGAGATT 720
ATGTGTCTCT GGAATTTGTG GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATT 780
CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACCT TATTGAGAGC AAGCTAGGAA 840
TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCTGGAAT AAGTGGATAG 900
ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCTTCCAA 960
TTGTTGTCTT GATATTTAAA AGCATACTAT TCCTGCCATG CTGAGGAAG AAGATACTGA 1020
AGATTAGACA TGTGTTGGAA GAGTCAACA AAATAACAA AACTGAGATA TGTTCACAGT 1080
TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAATA AAAAA 1195

```

20  
Seq ID NO: C185 DNA Sequence  
Nucleic Acid Accession #: NM\_001775.1  
Coding sequence: 70..972

25  
30  
35  
40  
45

```

1 11 21 31 41 51
CTAAAGCTCT CTGCTGCTCT AGCCTCCTGC CGGCTCATC TTGCCCCAGC CAACCCCGCC 60
TGGAGCCCTA TGGCCCAACT CGAGTTCAGC CCGGTGTCCG GGGACAAACC CTGCTGCCGG 120
CTCTCTAGGA GAGCCCAACT CTGTCTTGGC GTCAATATCC TGGTCTGAT CCTGTGTG 180
GTGCTCGCGG TGGTCTGCTC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG 240
CGCTTTCCCG AGACCGTCTC GGCCTGATGC GTCAAGTACA CTGAAATTCA TCCTGAGATG 300
AGACATGTAG ACTGCGAAAG TGTATGGGAT GCTTCAAGG GTGCATTAT TCAAAAACAT 360
CCTTGCAACA TTAATGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
CCTTGCAACA AGATTCTCTT TTGGAGCAGA ATAAAGATC TGGCCCATCA GTTCACACAG 480
GTCCAGCGGG ACATGTTTAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC 540
ACATGTTGTG GTGAATTCAA CACTTCCAAA ATAAACTATC AATCTTGCCC AGACTGGAGA 600
AAGGACTGCA GCACCAACCC TGTTTCAGTA TTCTGGAAAA CGGTTTCCCG CAGGTTTGCA 660
GAAGCTGCCT GTGATGTGGT CCAATGTGAT CTCAATGGAT CCGCAGTAA AATCTTTGAC 720
AAAAACACA CTTTTGGGAG TGTGGAAGTC CATAATTGTC AACAGAGAA GGTTCAGACA 780
CTAGAGGCCT GGTGTGATACA TGGTGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC 840
ACCATAAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT 900
ATCTACAGAC CTGACAAAGT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGACAC 960
TCTGAGATCT GAGCCAGTGG CTGTGTTTGT TTTAGCTCCT TGACTCTCTG TGGTTTATGT 1020
CATCATACAT GACTCAGCAT ACCTGCTGGT GCAGAGCTGA AGATTTTGGA GGTCTCTCCA 1080
CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCAAA AGTCTTAAAA TAACTTATAT 1140
CATCAGCATA CCTTTATTGT GATCTATCAA TAGTCAAGAA AAATTATTGT ATAAGATTAG 1200
AATGAAAAAT GTATGTTAAG TTACTTCTCT TAG 1233

```

50  
Seq ID NO: C186 DNA Sequence  
Nucleic Acid Accession #: XM\_120513.2  
Coding sequence: 1..2208

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
ATGGTGTCTAT GCACGTTTCTC GGGGCCCCCTA CGGGAACAA ATGAAAAAGT GAAAAAGTTC 60
TAGGCTTTCG GAGCTTTTAT GTTCCGATG AGCTCAGAGG CCGCGATGCT CGGGGAAAGC 120
AGGACCCCAA AGCCCCGTA AACAACGCGG ACCACCCGGG CCAAGATCTT CAAGAGGTTT 180
TTTTCAGAGG GATCGGAGAG CAATTCCCGA TTGGTAGAAG AACTTGCTGT AATACACAG 240
TACTCTGAGC ACCCCGCCCC AACGACTAGC CCCTCTCTCT TGCACCCCG AGAGTTTGGG 300
GTCATGACAG GGGGCCACAG AGCTCGTTTC GGAAGCCGGA CCCCCCCCGC AGCCGCAGAA 360
GCCTCGAGTC CACATCTGGG CATTGGGAGG GCAGCCTGTC AATCAGGAGC TGGGGCGGCA 420
GCCCCCGCGC CGGGGGCTCG GCGATGCCAG CCTCAGCGAC AGGCGCGCGC GCGCGCGGCC 480
ACGGCACAAG CACACACCCCT CCCACAGCGC CGCACCAGGG CAGACCCGGC GGGCAGGCGG 540
CGGAGGCACC CTGGGAGCCC GCGGCCCGGC GGGGAGGGGA CGTGCTCCGA GGGACCGGCC 600
CCGAGGCGCC GATGAGAGGA AGAGATGCAG CCGCAGAGG AGGGGCCAG CGTCCCAAAA 660
ATCTACAAGC AGCGCAGCCC CTACAGGCTC CTCAAGAGCT TCCCAGCAA GAGACCGGG 720
CTGGCCAAAG GCTACGAGCG ACCCACCTG GTGGAGCTGC CGCACGGCCA CTGAGGACT 780
CCGGCGCAGC CGCCGCCCGC GTCCCCCGCC GCTCTCTGTT CGCCGCTGTC 840
GTCAGACTCG GGGCTCTCTC GCGTCCGCCA CGCGTGGAT TTGCGGCGCG GGAACCATC 900
CGGCCCTCTC TTCTGCCCCC GGGAGTCGCA GGCCTCTGCT TCCCACGCC CACGTCGTG 960
TCCCAGCAT CCCCTCTGTC CGTCTGCTG CACGCTGCG CGCCGCGGG AGGACCTCA 1020
CATACACATA TGTGGAGGTC CCAGTCCACA CTTCAGGAT CTGACACCAT GGTCTCTGTC 1080
TTTGGATTGA TGGCTCAGAG AAGATGGCAG CATAGATCTT TAAAGCAGTT TGAGTGGGGA 1140
ATTCTTGGAT TGTGGGTATC TTGGCCATGT GGACAGGATT GGCTGGAGAA GGAGGCTCAG 1200
GTGGCGGTCC TGCTGCCAAG GTCTGAGGCT AATCTGCTCT CTAAGAAGAG TCGAATGATC 1260
TTGGATGCCT TTGCCAGCA GTGCAGTGA GTTCTTAGCC TCTTAAATTG TGGAGGAAAA 1320
CTCCTGGACT CCAACCATTC TCAGTCCATG ATTTCTGCG TAAAGCAGGA AGGCTCAAGT 1380
TACACGAAA GACAGGAGCA CTGTCACTT GGGAAAGGGG TCACAGTCA GACCTCAGAC 1440
AATGTAGACA TAGAGTACCA GTATATGCAA AGGAAACAA AACTTCTGCT CTTTGTGAGG 1500
GTTTCTACTG ACTCTCTACA AAATACCTG CTCTCGGAA GCTTCCAAAC TCCAAACCCC 1560
TGTCAGCCA GTGAATATGG CCATCTGGCC GAGCTGGATC CTCTGTCAAC CTCTCTGTG 1620
CATACATTAG AAAATATTTT ACTTGATTCC ACAGCTTCCC TGTGTAAATC TAGGCACTCA 1680
TCCAGAGAGC CCCCAGTCAA GAGTGATTTT CCAATCTCT TGCAGCAGGC CTGGCTGGG 1740
GGTGCTTCAA GACCATTTTC AGGGGCACAG CAAAGCATCG CTTACAGGCT GAACTCTGAA 1800
CTTGAGGATG GCATCCGAG CCCGTCCTT TTGAGTTGTG AGGCCTTGA AATGGATTG 1860
ACCTCCTTGG GAAGCAAGCA GCTGTTGAAC AACTATCCTG TCTACATAAC GAGCAACAG 1920

```

5 TGGGATGAGG CTGTAAATTC TTCAAAGAAA GATGGGAGAC GGCTCCTTCG ATACCTCATC 1980  
 AGATTGTGTT TCACAACCGA TGAGCTTAAAG TACTCATGCG GCCTTGGGAA AAGGAAAAGG 2040  
 TCAGTGCAGT CAGGAGAGAC AGGTCCCGAA AGACGCCCTC TGGATCCAGT TAAAGTAACA 2100  
 TGCTCCGAG GTACTGCATC CTTCGGCTCA GTGTACCAT CTGTGATCTC ATTTACCCG 2160  
 ATTGGCTGTG GCTCTCCCCG TACAAGTGT T CAGCCTTCG TATTTTGA 2208

Seq ID NO: C187 DNA Sequence  
 Nucleic Acid Accession #: AB037745.1  
 Coding sequence: 26..1744

10 1 11 21 31 41 51  
 15 ATGGTGAAC ACCTGCCCCA CAAACATGGA AACGACCGTT CTCAGTGGGA TCAACTTCGA 60  
 GTACAAGGGC ATGACAGGCT GGGAGGTGGC TGGTGATCAC ATTTACACAG CTGCTGGAGC 120  
 CTCAGACAAT GACTTACATGA TTCTCACTCT GGTGTGCCA GGATTAGAC CTCGCGAGTC 180  
 GGTGATGGCA GACACAGAGA ATAAAGAGGT GGCCAGAAATC ACATTTGTCT TTGAGACCTT 240  
 CTGTTCTGTG AACTGTGAGC TCTACTTCAT GGTGGGTGTG AATTCTAGGA CCAACACTCC 300  
 TGTGGAGAGC TGGAAAGGTT CCAAAGGCAA ACAGTCCCTAT ACCTACATCA TTGAGGAGAA 360  
 CACTACCAGC AGCTTCACTT GGGCCTTCCA GAGGACCACT TTTTATGAGG CAAGCAGGAA 420  
 GTACACCAAT GACGTTGCCA AGATCTACTC CATCAATGTC ACCAATGTGA TGAATGGCGT 480  
 GGCTCTCTAC TGCCGTCCCT GTGCCCTAGA AGCCTCTGAT GTGGGCTCCT CTGCACTCTC 540  
 TTGTCCTGCT GGTACTTATA TTGACCGAGA TTCAGGAACC TGCCACTCCT GCCCCCCATA 600  
 CACAATTCTG AAAGCCCCAC AGCCTTATGG TGTCCAGGCC TGTGTGCCCT GTGGTCCAGG 660  
 GACCAAGAAC AACAAAGATCC ACTCTCTGTG CTACAATGAT TGCACTTCTT CACGCAACAC 720  
 TCCAACCAAG ACTTCAACT ACAACTTCTC CGCTTTGGCA AACACCGTCA CTCTGTCTGG 780  
 AGGGCCAGC TTCACTTCCA AAGGGTTGAA ATACTTCCAT CACTTTACCC TCAGTCTCTG 840  
 TGGAAACCGG GGTAGGAAAA TGTCTGTGTG CACCGACAAT GTCAGTACC TCCGGATTCC 900  
 TGAGGGTGGG TCAGGGTTCT CCAAACTAT CCACAGCTAC GTCTGCCAGG CAGTCATCAT 960  
 CCCCCAGAG GTGACAGGCT ACAAGGCCGG GGTTCCTCCA CAGCCTGTCA GCCTTGCTGA 1020  
 TCGACTTATG GGGGTGACAA CAGATATGAC TCTGGATGGA ATCACTCCOC CAGCTGAACT 1080  
 TTTCCACCTG GAGTCTCTGG GAATACCGGA CGTGATCTTC TTTTATAGGT CCAATGATGT 1140  
 GACCCAGTCC TGCAGTCTCT GGAGATCAAC CACCATCCGC GTCAGGTGCA GTCCACAGAA 1200  
 AACTGTCCCT GGAAGTTTGC TGTGCCAGG AACGTGCTCA GATGGGACCT GTGATGGCTG 1260  
 CAACCTCCAC TTCCTGTGGG AGAGCGCGGC TGCTTGCCCG CTCTGCTCAG TGGCTGACTA 1320  
 CCATGCTATC GTGACAGCT GTGTGGCTGG GATCCAGAAG ACTACTTACG TGTGGCGAGA 1380  
 ACCCAAGCTA TGCTCTGGTG GCATTTCTCT GCCTGAGCAG AGAGTACCA TCTGCAAAAC 1440  
 CATAGATTTC TGGCTGAAGG TGGGCATCTC TGCAGGCACC TGTACTGCCA TCTCTCTCAC 1500  
 CGTCTTGACC TGCTACTTTT GGAAAAAGAA TCAAAAACCTA GAGTACAAGT ACTCCAAGCT 1560  
 GGTGATGAAT GCTACTCTCA AGGACTGTGA CCGTCCAGCA GCTGACAGCT GCGCCATCAT 1620  
 GGAAGGGGAG GGTGTAGAGG ACGACCTCAT CTTTACCAGC AAGAAGTCAC TCTTTGGGAA 1680  
 GATCAATCA TTTACTTCCA AGCAGCCAGC TCCTGTCAAC ATCTCTCTTT CAGAGGACTC 1740  
 CTGATGGATT TGACTCAGTG CGCTGAAGA CATCTCAGG AGGCCAGAC ATGACCTGT 1800  
 GAGAGGCCACT CTGCTCCTC CCGCTCCTC CACTTTCAT AGCACCTTTG CAAGCCTCGG 1860  
 GCGATTGGG TGCCAGCACT CTGCAACACC CACTGCTGGA AATCTCTTCA TGTGSCCTT 1920  
 ATCAGATGTT TGAATTTTCA ATCTTTTTT ATAGAGTACC CAAACCTCTC TTTCTGCTG 1980  
 CCTCAAACT GCCAAATATA CCCACACTTT GTTTGTAAT TATGCCCTTG CTGTATCTT 2040  
 GTTTCCCAA ATGGCCCATC CGCCAGAGCC ATAGCTTCGT CTGCTCATAA TTTCTATAGC 2100  
 TTTGAATGA AATATTTTCT ATCTTCTTAA GTATAGAAAC TATTTCTCT CTGCTCTAAC 2160  
 TTAAGGGCAG AAACAGCTGG GAGTTCCTT CGCATGCCCT CAGCTCATGA TCTCTTCAGG 2220  
 AGAGAGGGAG GGTGTAGAGG GTGTGGGGT TCCCTGGTGG ATAATCTTCA TAGCAGCCTG 2280  
 GATCCATTTC CCTCGGATAA CCAGCTCAAA GGGAGTGAAA ATGTAGTCT GAGGGCAAGG 2340  
 GGAGCAAGGC CTGGGTGAAG AAAGCCTTGA AAAGCATAAA AAGAGGCCGG GCGCGTGGC 2400  
 TCACGCCCTG AATCCACGCA CTTTGGGAGG CCGAGGCGGG CAGATCATGA GGTGGGAGA 2460  
 TTGAGACCAT CTGCTCAAC ACGGTGAAGC CCGCTCTCTA CTGGAATAG AAAAATTAG 2520  
 CCGGGCGTGG TGGCGGTGTC CTGTGGTCCC AGCTACTCGG GAGGCTGAGG CGGAGAGATA 2580  
 GCGTGGGCTT GGAAGCGGGA GCTTGCACTG AGCGAGATC GCGCCACTGC ACTCCATCCA 2640  
 GCCTGGGTGA CAGAGTGAGA CTCTGCCTCA AAAAAAAGAA AAGCAAAAG 2700  
 AGAGGCAACA AGGAATGTTT TTGTTTTTGA GACAGGCTCT CACTCTGTCA CCTAGGCTGG 2760  
 AGTGCAGTGG CGTAATCACT GTTCAGTGCA GCCTCAAGCT CTGCGGCTCA GGCTATCCTC 2820  
 CCATCTCAGC CTCTCAAGTA GCTGGGACTA CGAGTGTGCA CCACCAGGCT CACTAATTTT 2880  
 TGTGTTTTTT GTAGACACGG GGTTCACCG TGTGCCAG GCTGGTCTCC AACTCCTGGG 2940  
 CTCAGTGAT CTGTCCGCTT CGGCCCTCCA AACTGCTGGG ATTACAGGCA TAAGCCACTG 3000  
 CACTCAGCTT TTTATTTGTT TTTTAAACCA CGTAGCTCAT TGCTCTCTCT TAAGTAAATG 3060  
 ATAGATATTC TCACTGAAGC CAAAGGAATA AGTTCAATCA GAAAATGCC AAAGCCCTGG 3120  
 TGGATACATC CTCCCTATCT TTTTTTAA CTTTCACTA TCACTCTATG ACCTGAAAAA 3180  
 GAACCAAGTA AGCCCCAAC CCAGATGTTT CAGCCTTATC CTCTATTGGG TTTACCCACA 3240  
 GACATAGCAA ACCCTGTGAG TGAGGAAAAA TCCCATCCTT TGAGTGCCCC GGTCTAGAA 3300  
 GTTTGGGCCA TATTATGGAA CAGGGGTCTC TTATTTGAAA AGAGCACAAG GAGGCCAAGA 3360  
 TTTTATGGG GCATTTTAGG GGATACAGCC CACAATGGCA TGGGCTTAG GTGGCGTGA 3420  
 TGTCTGCTTC TAAGCTTAA GCATCTGCTC AGGCACAGAA TAAAGCTCTA GGTGGGCCAA 3480  
 AAAAGGAAC GAATCCAGG CCCATAGCC AGCACCAGAA TCAACACAGT CTTCAAGGAA 3540  
 GGAAGGCTAG GAGAGTTTAA CAAGATTTTC ACTGGGCCCA GCATGGTGGC TCACACTGT 3600  
 AATCCCAAGG CAGAATGGTG GCTTGAAGCT AGGAGTTCAA GACCAGCCTG GGCAACACAG 3660  
 TGAGACCTTG TCTCTAAAAA ATTTAAAAAT AAACAAGGTG TTCACCAAGC TGGGATACTT 3720  
 CTCACTAATT AGCCCCATTC TTTCTCTTT TTTCTATCT AATTGCTTTG TGTGATAAAA 3780  
 AACTAAGAG ACTTCTGGTC CAATTTCTGG CAACATCCCT TCTGAAAGGT GAGTAGAGTG 3840  
 GGTGCTTCT ATGCCCATTT TCCCAATTT TACACAACT ATTATCAATG AACTTTAAG 3900  
 TACCTAGAAAT GGGTAAACCC AGAGCAAGAC TTTAAATTAC CTCTCTCTTT CTCTACTGG 3960  
 CAGTCTGCCC TCCATCACTA TCAGGCTAGG GTGACCTTCC CTGTGTCAG CCCCATTG 4020  
 CCAATGTTTG TGCTGTGCCC CTTTCTCCAG TGACCAATTG GTGACCAAGT GGTAGATATA 4080  
 GAAAGGGGAT GGCATTGCA AGTGACTAGT CTGCCACAAA ATGCTCATCT GATTAGCCAC 4140  
 TGCTGCCCTG GCAATGGCTT TGTAAAGTCT AATGAGAACT AGAGCCAGGC TGTGGTCCCT 4200  
 GGCCATCAAC AGTGTGGTG ACGGCAGGGA GTCCCTTTGG TTTAATAAAT CCAGTTTTTC 4260  
 TTTGGGTATC CAAATCTCC CTCTCTTTG TAGGAGTCAG GCTCTCAGAA CCTGTGTC 4320

5  
10  
15  
20

TGTTGGAAC TCCCCAGTG TGGATGCAGA TACGCAGCTC CTGAGCTCCA GCCTAAAGTC 4380  
TTCTGTAGCC TCAGCAATAC TTGGGCACCT GCTGTCTCAC TGAATAGCTT TCTTTTGTGA 4440  
CAAAGGCCAC AGACAGCCCT TAGACTATT CCGAAACAGT AGGAAAAATT ACATATGTCT 4500  
TTGACTTCTT TATTCTGACT CCACTGATT TAGCCATAAT ACTTTAAGGA GCTACTTTTT 4560  
ACTACCCCTT ACCGTGCTGA CTCTGCAGG TCTGCCCTGT GACCTGTCAG GAACTCCTGA 4620  
GTTACGCTAC TGGGGTCACC TGTGTCTCCC CTAGCAAGTT AGGCATGTCA TATATTTTAA 4680  
ACAGCTTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAC ATACGATTCA 4740  
ATGGTTTTCA GCAAACTCAC AGAGTTGTCC GCCCACTTGA GAGCAACAC ATGTTCAATT 4800  
TTCTTTTCTT TTTTTTTTTT GAGACAGAGT CAGCTTTGTC GCCCAGGCTG GAGTGCAGTG 4860  
CCATGATCTT GGCTCACTGC AGCCTCCCA TCCCTGGGTC AAGTGATCCT TCTGCTTCAG 4920  
CCTCCCCAGT AGCTGGGATT ACAGGCATGC GCCACCAAGC CTAGCTAATT TTTGTGTTTT 4980  
TAGTAGAGAT GGGGTTTCAC CGTGTGGGCC AGGCTGGTCT CAAACTCCTG GACTCAAGTG 5040  
ATCCACCCAC CTCGGCCTCC CAAAGTGCTG GGATTGCAGG TGTGAGCCAC CGTGCCTGGC 5100  
CTACGTGTTT AATTTTCTAT GAACAAAGGC TTTAGTCCTT GACCCAGGGC TAAAGTGGTC 5160  
TGTCCAAGCT GTTGTGGTA GAGGAGTAT GATAAATGT TTAATCTCA TTTGTTTACC 5220  
TTGAGTCTCG GAACACGCAG TAACGTGCTG GCTATAGTCA TCATCTGTAT TTGCTGGGA 5280  
ATACAAATGA AGATTGTGGT GTATTCAAGC AGTAGGGTTT TGTCTTTGT TTTTGTTTTA 5340  
GTGCCAACAA AACTTTTTTT TGTCTGACTA CATTAAAGAT AAGACTGACT ATATTATAC 5400  
AACGAAACT TTGTAATAGA TTTTTCAGC TTTGTGAAT CGAATTTTTT TTCATCAGGG 5460  
CTGGTGGAT TTCTTTTATA CCCTGTAATC CAAGCGTTAA TAGTTTGTTA GAAAGTGGT 5520  
TATTGCATGT CACTTTTTTT TTTTGTGAAA ATAAAAACAT ACCTTAC 5567

Seq ID NO: C188 DNA Sequence  
Nucleic Acid Accession #: NM\_014324.1  
Coding sequence: 89..1237

25  
30  
35  
40  
45  
50  
55  
60  
65

1 11 21 31 41 51  
GGCGCGGGA TTGGGAGGGC TTCTTGCAGG CTGCTGGGCT GGGGCTAAGG GCTGCTCAGT 60  
TTCTTTCAGC GGGGCACTGG GAAGCGCCAT GGCATCTCGG GGCATCTCGG TCGTGAGGCT 120  
GTCGCGGCTG GCCCGGGGCC GTNCTGTGTC TATGCTCTCG GCTGACTTCG GGGCGCGTGT 180  
GGTACGCGTG GACCGGGCCG GCTCCCGCTA CGACGTGAGC CGCTTGGGCC GGGGCAAGCG 240  
CTCGCTAGTG CTGGAACCTGA AGCAGCCGCG GAGAGCCGCT GCTGCGGCGT CTGTGCAAGC 300  
GGTCGAGTGT GCTGCTGGAG CCCTTCCGCC GCGGTGTGCT GGAGAAATCT CAGCTGGGCC 360  
CAGAGATCTT GCAGCGGGAA AATCCAAGGC TTATTATGTC CAGGCTGAGT GGATTGGGCC 420  
AGTTCAGGAA AGCTTCTGCC GGTAGCTGG CCACGATATC AACTATTGG CTTTGTGAGG 480  
TGTCTCTCA AAAATTGGCA GAAGTGGTGA GAATCCGTAT GCCCGCTGA ATCTCGTGGC 540  
TGACTTTGCT GGTGTGGGCC TTATGTGTGC ACTGGGCATT ATAATGGCTC TTTTGAACCG 600  
CACAGCGACT GACAAGGGTC AGGTCAATGA TGCAAAATATG GTGGAAGGAA CAGCATATTT 660  
AAGTCTTTTT CTGTGGAAAA CTCAGAAATC GAGTCTGTGG GAAGCACCTC GAGGACAGAA 720  
CATGTTGGAT GGTGGAGCAC CTTTCTATAC GACTTACAGG ACAGCAGATG GGGAAATTCAT 780  
GGCTGTTGGA GCAATAGAAC CCCAGTCTCA CGAGCTGCTG ATCAAAGGAC TTGGACTAAA 840  
GTCTGATGAA CTTCCTCAATC AGATGAGCAC GGATGATTGG CCAGAAATGA AGAAGAAGTT 900  
TGCAGATGTA TTTGCAAGA AGACGAAGGC AGAGTGGTGT CAAATCTTTG ACGGCACAGA 960  
TGCTGTGTG ACTCGGGTTC TGACTTTGA GGAGGTTGTT CATCATGATC ACAACAAGGA 1020  
ACGGGGCTCG TTTATCACCA GTGAGGAGCA GGACGTGAGC CCCCGCTTG CACCTCTGCT 1080  
GTTAAACACC CCAGCCATCC CTCTTCCAA AGGGGATCCT TTCATAGGAG AACACACTGA 1140  
GGAGATACCT GAAGAATTGG GATTGAGCCG AGAAGAGATT TATCAGCTTA ACTCAGATAA 1200  
AATCATTGAA AGTAATAAGG TAAAGAGTAG TCTCTAACTT CCAGGCCAC GGTCAAGTG 1260  
AATTGAAAT CTGCTTTTAC AGTGTAGAGT AACACATAAC ATTGTATGCA TGGAAACATG 1320  
GAGGAACAGT ATTACAGTGT CCTACCACTC TAATCAAGAA AAGAATTACA GACTCTGATT 1380  
CTACAGTGAT GATTGAATTC TAAAAATGGT TATCATTAGG GCTTTTGATT TATAAACTT 1440  
TGGGTACTTA TACTAAATTA TGGTAGTTAT TCTGCCCTCC AGTTTGCTTG ATATATTGT 1500  
TGATATTAG ATTCTGACT TATATTTTGA ATGGGTTCTA GTGAAAAGG AATGATATAT 1560  
TCTTGAAGAC ATCGATATAC ATTATTTTAC ACTCTTGATT CTACAATGTA GAAAATGAGG 1620  
AAATGCCACA AATTGTATGG TGATAAAAGT CAGTGAAC AGAGTGATTG GTTGATCCA 1680  
GGCCTTTTGT CTGGGTGTTT ATGATCTCCC TCTAAGCACA TTCCAACTT TAGCAACAGT 1740  
TATCACACTT TGTAATTTGC AAGAAAAAGT TTCACCTGTA TTGAATCAGA ATGCCTTCAA 1800  
CTGAAAAAAA CATATCCAAA ATAATGAGGA AATGTGTTGG CTCACTACGT AGAGTCCAGA 1860  
GGGACAGTCA GTTTTAGGGT TGCTGTATC CAGTAACCTG GGGCCTGTTT CCCCGTGGT 1920  
CTCTGGGCTG TCAGCTTTCC TTTCTCCATG TGTGTTGATT CTCCTCAGGC TGGTAGCAAG 1980  
TTCTGGATCT TATACCAAC ACACAGCAAC ATCCAGAAAT AAGATCTCA GGAACCCCA 2040  
AAAAAAAAA AAAAAAAAAA AAAAAA 2068

Seq ID NO: C189 DNA Sequence  
Nucleic Acid Accession #: XM\_091332.1  
Coding sequence: 1..1401

70  
75  
80

1 11 21 31 41 51  
ATGCAAAAGT GGACACTGTG GGCTGCAGCC TTCTGACCC TCCACTCTGC ACAGGCCCTT 60  
CCACAAACAG ACATCAGTAT CAGTCCAGCC CTGCCAGAGC TGCCCTGTGC TTCCCTGTGC 120  
CCCTGTCTT GGATGGAGTT CAAAGGCCAC TGCTATOGAT TCTTCCCTCT CAATAAGACC 180  
TGGGCTGAGG CCGACCTCTA CTGTTCTGAG TTCTCTGTGG GCAGGAAGTC CGCCAAAGTG 240  
GCCTCCATCC ACAGCTGGGA GGAGAATGTC TTTGTATATG ACCTCTGAA CAGCTGTGTT 300  
CCCGGATCC CAGCTGAGCT CTGGACAGGC CTTTATGATC ACAGACAGGA AGGGCAGTTT 360  
GAATGGACTG ATGGCTCATC CTATGACTAC AGCTACTGGG ATGGCAGCCA GACTGATGAT 420  
GGCGTCCAGC CGGACCCAGA AGAAGAGGAC TGCGTGAGCA TATGTTACAG GCCTACCAAGT 480  
GAGCAGCTAC AGGCCCCAGA GCCCCAGTTA CTTTATCAA TCTCAGAGGC CACAGATGTC 540  
TATCTCCCTG AGGATTTCCC AGCTGAGCCC AAGCTCATGG ACCAGTCCCT GGTGTCCAGG 600  
AAGAGCCTGA AACCATCCAA GAGTCATCTT ATGGAGCCAC CCACTCCAGT GGCCAAGCAC 660  
CAAAAGGCAA AGACCCGACA TAGGAGCCTG CGCGGCTCT GGTGGCCATC AGGTAAGGCT 720  
GGGTGATGGA AAGAAAGAAAT GAATGCAGAC TACGGGCGAA GAAAGCGATC GGGCCCGAGG 780  
CAGGAAGGCC GGCTCCGGTG CAGGGAGGCG CGCTGCGGG CTGCTTCGGG CCAAGGTGCA 840

	CCCCAGGGGCC	AGCGCAAGCA	GCGGCAACAG	GAGCGCCAGG	AGAGAGGCTG	GGAAGAACTG	900
	GGAGGGGGTGT	CCCCAATGCG	GGGCGCCCAA	GCCTGGCAGC	ACGGGCTGGG	AGCGGGGAGC	960
	CAGCGGGGTG	CGGCGCCGGA	GTGCGGGGAG	AACCAACAGG	CGCGGAATT	GGGGAGCAGC	1020
	TGGAGGGGGC	AGCGGCTCCA	GCCCCAGACC	GCCGCGCTCT	GTCACCTTGC	ATTAAGAAAG	1080
5	CTTCGGGGGA	ATGCACAACG	CCTGGCGGCC	GCCTTCGTGC	AGCCCGCCCT	GCAGGTGCAG	1140
	GAAGAAAAGA	ATAATCGCAC	CCGTTTCTCA	GGTGCTTACT	TCACCATGTC	CGATCCGACG	1200
	TGTGACCAAG	ATAGCAAGGA	GCAGTCTTTA	AGGCGACACG	GCAGAGAGGC	AGAAAAAGAT	1260
	GGGCGTTACC	GGTAGTTAA	GAATAAAGA	GGACCTGTTG	CCTGTCCTTC	TAGCTTTGAA	1320
10	CTACAAAGTG	GAGGGGAAGT	TTGTCTGGAT	TTTCTGTAG	AACTGAGGGC	AGGGACCTGG	1380
	ATTGCTCGAG	AACCTCCATA	A				1401
Seq ID NO: C190 DNA Sequence							
Nucleic Acid Accession #: XM_054869.2							
Coding sequence: 26..2902							
15	1	11	21	31	41	51	
	TAGACGCGGA	GCCCAAGGAG	GTAAATGCA	CACCTGCTGC	CCCCAGTAA	CTTTGGAACA	60
	GGACCTTCAC	AGAAAAATGC	ATAGCTGGAT	GCTGCAGACT	CTAGCGTTTG	CTGTAACATC	120
20	TCTCGTCTTT	TGCTGTGCAG	AAACCATCGA	TTATTATGGG	GAAATCTGTG	ACAATGCATG	180
	TCCTTGTGAG	GAAGAAGGACG	GCATTTTAAC	TGTGAGCTGT	GAAGACCGGG	GGATCATCAG	240
	TCTCTCTGAA	ATTAGCCCTC	CCCGTTTCCC	AATCTACAC	CTCTTGTGTG	CCGGAACCTT	300
	TTTGAACCTG	CTCTATCCCA	ATGAGTTTGT	CAATTACACT	GGGGCTTCAA	TTTTGCATCT	360
	AGGTAGCAAT	GTTATCCAGG	ACATTGAGAC	CGGGGCTTTC	CATGGGCTAC	GGGGTTTGAG	420
25	GAGATTGCAT	CTAAACAATA	ATAAACTGGA	ACTTCTGCGA	GATGATACCT	TCCTTGGCTT	480
	GGAGAACCTG	GAGTACCTAC	AGGTCGATTA	CAACTACATC	AGCGTCATTG	AACCCAATGC	540
	TTTTGGGAAA	CTGCATTTGT	TGCAGGTGCT	TATCCTCAAT	GACAATCTTT	TGTCAGATTT	600
	ACCCAACAAT	CTTTTCGGTT	TTGTGCCCTT	AACGCACCTG	GACCTCCGGG	GGAACCGGCT	660
	GAAACTTCTG	CCCTACGTGG	GGCTCTTGCA	GCACATGGAT	AAAGTTGTGG	AGCTACAGCT	720
30	GGAGGAAAC	CCTTGGAAAT	GTTCTTGTGA	GCTGATCTCT	CTAAGAGATT	GTTTGGACAG	780
	CATCTCCTAT	TCAGCCCTGG	TGGGGGATGT	AGTTTGTGAG	ACCCCTTCC	GCTTACACGG	840
	AAGGGACTTG	GACGAGGTAT	CCAAGCAGGA	ACTTTGCCCA	AGGAGACTTA	TTTCTGACTA	900
	CGAGATGAGG	CCGAGAGCGC	CTTTGAGCAC	CACGGGGTAT	TTACACACCA	CCCGGGGCTC	960
	AGTGAATTC	GTGGCCACTT	CTTCTCTGTC	TGTTTACAAA	CCCCCTTTGA	AGCCCCCTAA	1020
35	GGGACTCTGC	CAACCCAACA	AGCCCAAGGT	GCGCCCCACC	TCTGGGAGC	CCTCTAAGGA	1080
	CTTGGGCTAC	AGCAACTATG	GCCCCAGCAT	CGCCTATCAG	ACCAATCCCT	CGGTGCCTTT	1140
	GGAGTGTCCC	ACCGCGTGCT	CTTGCAACCT	GCAGATCTCT	GATCTGGGCC	TCAAGTAAAA	1200
	CTGCCAGGAG	CGAAGATCG	AGAGCATCGC	TGAACCTGCA	CCCAAGCCCT	ACAATCCCAA	1260
	GAATATGTAT	CTGACAGAGA	ACTACATCGC	TGTGTGCGCG	AGGACAGACT	TCCTGGAGGC	1320
40	CACGGGCTG	GACCTCTGTC	ACCTGGGGAA	TAACCGCATC	TCGATGATCC	AGGACCGGCG	1380
	TTTCGGGGAT	CTCACCAACC	TGAGGCGCCT	CTACCTGAAT	GGCAACAGGA	TCGAGAGGCT	1440
	GAGCCCGGAG	TTATTCTATG	GCGTCGAGAG	CCTGCAGTAT	CTCTTCCCTC	AGTACAATCT	1500
	CATCCGCGAG	ATTCACTCTG	GAACTTTGA	CCCGGTCCCA	AACCTCCAGT	TGCTATTCTT	1560
	GAATAACAAC	CTCCTGAGG	CCATGCCCTC	AGGCGTCTTC	TCTGGCTTGA	CCCTCCTCAG	1620
45	GCTAAACCTG	CAGGCTAACC	ACTTCACTC	CTTGCCAGTG	AGTGGAGTTT	TGGACAGCTG	1680
	GAAGTCACTC	ATCCAAATCG	ACCTGCATGA	CAATCCTTGG	GATTGTACCT	GTGACATTGT	1740
	GGGATATGAG	CTGTGGGTGG	AGCAGCTCAA	AGTGGGCGTC	CTAGTGGAGC	AGGTGATCTG	1800
	TAAGGCGCGG	AAAAAATTGG	CTGAGACCGA	CATGCGCTCC	ATTAAGTCGG	AGCTCTGTGT	1860
	CCCTGACTAT	TCAGATGTAG	TAGTTTCCAC	GCCCCACCCC	TCTCTATCC	AGGTCCCTGC	1920
50	GAGGACCAAG	CGCGGCTGTC	CTGCGGTCCG	GTTGAATAGC	ACCGGGGGCC	CGCGAGGCTT	1980
	GGGCGCAGGC	GGAGGGGGGT	CGTGGGTGCC	CTTGTCTGTG	TTAATCTTCA	GCCTCCTGCT	2040
	GGTTTTCATC	ATGTCCGTCT	TCGTGGCCGC	CGGGCTCTTC	GTGCTGTGTA	TGAAGCGCAG	2100
	GAAGAAGAAC	CAGAGCGACC	ACACCAGCAC	CAACAACCTC	GACGTGAGCT	CCTTTAATAT	2160
	CGAGTACAGC	GTGTAGCGCG	GCGGCGGCGG	CACGGGCGGC	CACCCACAGC	CGCACGTGCA	2220
55	TCACGCGGGG	CCCGGCTGTC	CCAAGGTGAA	GACGCGCGCG	GGCCACGTGT	ATGAATACAT	2280
	CCCCCACCCA	CTGGGCCACA	TGTGCAAAAA	CCCCATCTAC	CGCTCCCGAG	AGGGCAACTC	2340
	CGTAGAGGAT	TACAAGAGCC	TGCACGAGCT	CAAGGTCAAC	TACAGCAGCA	ACCAACCACT	2400
	CGAGACGAGC	CAGAGCGCGC	CGCCGCCACC	GCAGCAGCCA	CAGCAGCAGC	CCCCCGCGCA	2460
	GCTGACGCTG	CAGCCCGGGG	AGGAGGAGAG	GCGGGAAGGC	CACCACTTGC	GGAGCCCGGC	2520
60	CTACAGCGTG	AGCACCATCG	AGCCCGGGGA	GGACCTGCTG	TGCGCGGTGC	AGGACGCGGA	2580
	CCGCTTTTAC	AGGGGCATT	TAGAACCAGA	CAAACTCTGC	TCCACCACCC	CCGCGGCGAA	2640
	TAGCCTTCCG	GAATATCCCA	AATTCCCGTG	CAGCCCGGCT	GCTTACACTT	TCTCCCCCAA	2700
	CTATGACCTG	AGACGCCCCC	ATCAGTATTT	GCACCGGGGG	GCAGGGGACA	GCAGGCTACG	2760
65	GGAACCGGTG	CTCTACAGCC	CCCCGAGTGC	TGTCTTTGTA	GAACCCAACC	GGAAACGAATA	2820
	TCTGGAGTTA	AAAGCAAAAC	TAAACGTTGA	GCCGACTAC	CTCGAAGTGC	TGGAAAAACA	2880
	GACCACGTTT	AGCCAGTCTT	AAAAGCAAAG	AAACTCTCTT	GGAGCTTTTG	CATTAAAAAC	2940
	AAACAAGCAA	GCAGACACAC	ACAGTGAACA	CAITTTGATTA	ATTGTGTTGT	TTCAAGCTTT	3000
	AGGGTGAAGT	GCCTTGGCAC	GGGATTTCTC	AGCTTCGGTG	GAAGATACGA	AAAGGGTGTG	3060
70	CAATTTCTCT	TAAATTTTAC	ACGTGGGAAA	CATTTGTGTA	AACCTGGGAC	ATCACTTTCT	3120
	CTTCTTGCGT	GTGGGGCAGG	TGTGGAGAAG	GGCTTTAAGG	AGGCCAATTT	GCTGCGCGGG	3180
	TGACCTGTGA	AAGGTCAACG	TCATTTTGTG	AGTGGTTGGA	AGTGCTAAGA	ATGGTGGATG	3240
	ATGGCAGAGC	ATAGATTCTA	CTCTTCTCTT	TTTGCTTCTT	CCCCCTCCCC	CGCCCCGCCC	3300
	CCACCTCTCT	TTCTCCCTTT	TTAAGCCATG	GGTGGGTCTA	ACTGGCTTTT	GTGGAGAAAT	3360
	TAGCACACCC	CAACTTTAAT	AGGAAATTTG	TTCTCTTTT	CCGCCCCCTC	CCTTCTCTCC	3420
75	TCCCTTCCCC	TCCCTTCTCA	TTCTTTTCT	TGTTTTTTAA	AGGATGTGTT	TGATGCAATT	3480
	CTGACATTTT	GAATTAATAA	AAAAGTATTT	TGATCCTGTA	AGGATCAACC	ATAGATGTGG	3540
	ACAAATCATT	AAAATTACAG	AGCTATATGA	TCCATAATTG	ATTAGTCAAA	ATAACTTATT	3600
	GATGAATAT	ACAAATATTT	TATTGTAGCA	CCTATTTTTA	TATGCACATT	TAGCATTCCT	3660
	CTTTCCTTCA	CTATTTAGCC	TATGATTTTG	CAGAGGTGTC	ACACTGTATT	AGGATCTGCA	3720
80	TTTCTAAAC	TGCGGTGGTA	TCAGGAAGGC	ATTTTCAACT	ATTCAAAATG	TGGAGAATTT	3780
	AATGGCTAAA	TCTTTAAAG	CCAATGCAAC	CCACCCAATT	GAATCTGCAT	TTTCTTTTAA	3840
	GAACAACAGG	CTGATTGTAT	CCCAATGTAT	TTTAAAAAAT	AGGGCAATTG	ATTGGGCCAT	3900
	TCCGAGAGAA	TGTTTGCATA	GTTTGGGTTT	TTATTAGAAA	ATATTTGAAA	GTATTTTAT	3960
	TAATGAACCA	AAATGACATG	TTCAATTTGAC	TACTATTGTA	GCCGATTTC	GATTGTTTAA	4020

5 CCAAACCCAG TTGCATTGT ACAGATCCAC GTGTACTGGC ACCTCAGAAG ACCAAATCAT 4080  
 GGACTGTACA AGTCTCTATA CAATGTCTTT ATCCCTGTGG GCAGCAAGCA ATGATGATAA 4140  
 TGACAAACAG GATATCTGTA AGATGGGGCT ACTGTTGTTA CAGTCTCATA TGTATCCACG 4200  
 CACATGTAAT TTTTAAATA GTTTCCTGAAT AAACACTTGA TAACTATGTC 4250

Seq ID NO: C191 DNA Sequence  
 Nucleic Acid Accession #: NM\_000793.2  
 Coding sequence: 401..1222

10 1 11 21 31 41 51  
 | | | | |  
 GCCTGCAGAG AGAGGCACTT TGCACCACAG ACAGATAGCA AGAAGGGAAA GACAGAGAGT 60  
 GAGAAAAAAG AGGAGTCACT CGCTCCTGGG GAAGGGAGAG AGTGAGACTG GGAGAAAGAG 120  
 AAGCACAGAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAATAC TACCCTTAAA 180  
 15 GCACATTATA AAAAAAATA CTCTGCCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG 240  
 CATAGAGACA ATGAAAGGCT AAAGAAAATT TTAATATCTC TGCCACAGTC TCATAGGTGC 300  
 TTGGAATGTA AAGTAGAAGT GCCTGTCTTT AACGGAATCT GACAGAGAGG GTGAAGGGGA 360  
 ACCAGAGCGC ACAAGGGGAA TGAATCAGGA GGCAGAGAGG ATGGGCTATC TCAGCGTAGA 420  
 CTGTCTGATC ACATGCAAAA TTCTGCCAGT TTTTCTCTCC AACTGCTCTC TCCTGGCTCT 480  
 20 CTATGACTCG GTCACTCTGC TCAAGCAGCT GGTGCTGCTG TTGAGCCGCT CCAAGTCCAC 540  
 TCGCGGAGAG TGGCGGCGCA TGCTGACCTC AGAGGGAGCT CGCTGCGCTC GGAAGAGCTT 600  
 CCTCTCTGAT GCCTACAAAC AGGTGAATTT GGGTGAGGAT GCCCCCAATT CCAGTGTGGT 660  
 GCATGTCTCC AGTACAGAA GAGGTGACAA CAGTGGCAAT GGTACCCAGG AGAAGATAGC 720  
 TGAGGGAGCC ACATGCCACC TTCTTGACTT TGCCAGCCCT GAGCGGCCAC TAGTGGTCAA 780  
 25 CTTTGGCTCA GCCACTGAC TCCTTTTAC GAGCCAGCTG CCAGCCTTCC GCAAACTGGT 840  
 GGAAGAGTTC TCCTCAGTGG CTGACTTCCT GCTGCTCTAC ATTGATGAGG CTCACTCCATC 900  
 AGATGGCTGG GCGATACCGG GGGACTCCTC TTTGCTCTTT GAGGTGAAGA AGCACCAGAA 960  
 CAGAGGAAGC AGATGTGAGC CAGCCAGCA GCTTCTGGAG CGTTCTCTCT TGCGGCCCCA 1020  
 GTGCCGAGTT TGGCTGAGCC GCATGACAAA TAACGCCAAC ATAGCTTACG GGGTAGCCTT 1080  
 30 TGAACGTGTG TGCATTGTGC AGAGACAGAA AATTGCTTAT CTGGGAGGAA AGGGCCCTT 1140  
 CTCCTACAA CTTCAAGAAG TCCGGCATTG GCTGAGAGAG AATTTCAGCA AGAGATGAAA 1200  
 GAAACTAGA TTAGCTGGTT AAGGTATGTA TTATAAGAGA GCTTATTGTT TAAAAAGTT 1260  
 ATATAAAGCC AAGGAAATTA AGAATGAAAT CCATATTCCA ACAGAGCCCT ATTGGCTTAC 1320  
 TGAAGACAGC GAGTTTATCT ATCGGAAGAA CATGAATCTC TAACAGCTCC ATACTCTTT 1380  
 35 CACTACTCAA ATGCATTGG GCTGAGTAAG TAACCATATC ACCTCTCTTC TTAGTAAAAA 1440  
 GCCCTATGTG AAAAGATCCC AAGATGAGAG GGAAGAAACG CTAATTCAGC ATGTGTTTAT 1500  
 TCTGCATTGA GAAGGAACCT ATACATCTGA TGCACTGCTT GAGACCAGAA GAAAAGACTT 1560  
 ACCCTGAATA TTACTACATT AGGGAAGCTA CTGTCTACGT TAAGATAAAG GGTATTGCCT 1620  
 TGCTCTTATT TGGCATGGAT GGAGCCCACT TGGAAAAATC CCAATATTA CAACAAGTCC 1680  
 40 TTGAACCCAG GCCATGTGGT TAGACGTTGG TGTAAAGGTT AGACCTTATG TTAGATCAT 1740  
 TTCTGATGTT CCAGCTTCTA GCCATGTAGT GCTCTCAGTC TTCATACCCC AGAAATTATT 1800  
 GGTATATTTG TAGATACCGA GAATGATCCC TCAGTCTGAG AGGTTAGAAT GATCATCTGT 1860  
 AATCTGAGGG TTAATTTCTA GGCAGGTGGA GAGAGTGGTA AAAAAGAAAT GAAATTGACA 1920  
 AGCTAGGAAA GAGGAGGAGC AAGATTGAG AAAATTCACA GAGTTTACC CTTAAGCTGT 1980  
 45 AGAGAGTGGG GCATCTGTTG TAGCCACGGA AACATAGAAA CATAACAAG GCCAGAAAAA 2040  
 GAAGAAGGAG CTCACATAAA AGTGGCATAG AGAATACACA TATAAAAAA ATATATTTGT 2100  
 CATATGCTCC TAGAGAGGAG AAAGGGGTGA TTGAAGAAA AAAAAATACT TAAATATTTG 2160  
 TAATTGTGAG GGGTTTCTTT TGGAAATAAT TACTTTTGAA CCATGTATGT GGTATGTATA 2220  
 TTTTCAGTGG GTTAATTTA CCCCATGATA CCTATTAAAG GAAAACCACT GGGTCTGGTG 2280  
 50 GTGCTGCTCT ATTCTCCCC ATCTCTACAA TTTCTATGTG GCCCAAGTCA TTCCTAATCT 2340  
 TGGTCTCTAT AGCAGTGTTC TCTCTAATG CTGAGCTGAA GAAATTATAC GTACATACAC 2400  
 ACATACATAC ATACATACAA ATATATGTAT ATATATTCTC AGCTGCTGCG GGAGGTAGGT 2460  
 ACCATGGCCA TTCAGCACAG CCTTGATTTC CTCCCAAGT AGGTGAGCTA TAGTGAAGAA 2520  
 TAGGTGCAAA CAACAAGCTT TACTTCCATT GCAAAATAGA AGAAGAGGAA GTTAGAGATA 2580  
 55 ATTCATGATC ATCATTTTGG AGGCTTGTGT ATAAGGCAAC CCCCAGTATA TCATGGAATT 2640  
 TCCATTGACA TTGAAATTTG GACTTGGATC TTCCCTTGGT CCCATTAGCT GAGGTTTAGT 2700  
 AATCTAAAGT CCCTATAGTA TATGATTATA ATGCTATTTT AAAAAATATA TATATATAAT 2760  
 ATTTTCTTCT TTTTAAATA GACACTATAG TTTTACCCAT AAGTAATATT TAAAGATTAT 2820  
 AGCTCCCAAA AGAATGGACC AACCACTTTC GTATCATAAT TTCTTTTGG TAAATATGAG 2880  
 60 ACTATTAGA AATCATAGTA TATGATTGTA TTTAAGGTA CAATCAAAGG ATCTTTTGTG 2940  
 CATTCATTA ATAACCTGAT AAAAAATAA TAAATGGAT AGAAAAAAC TAAAGTTGAA 3000  
 AATACATTCT TAACTAGTT GTCTGAAATG AGAAAAGAGT GAGAACTAGG TGTGCAAGAA 3060  
 CCAACGATAT TTTATTTTAT TTTTAAATG GGAGCAACAT ATCAGTCTGT TCACCAGCTG 3120  
 GTATATTGAG TAAATATTA AGCTCCATTG GGAATGATT TTCTAGGCAA CATCAGCTTT 3180  
 65 CTAATGTTCT AAATCTATA AAAACCAACC ACAAGAAAC AAAGCAAAAT TCATTATCTA 3240  
 ATGAGTTGCT GGAATATCAT ATTGAGAATA ATTATTTTCA ATTCTCAGT TGTAACTTC 3300  
 TACATTCAAG GGCTTATCTC TGCCCCATT GATTTTAACT CCAAAATGG TGTGAGATT 3360  
 ACTGTGGAAC CCTAAGCAG TAAATATAA AACCTGGTTG CAGCACATTC ACCTGTTGT 3420  
 CCTTAAATTT CCCCCTTTT CTCTATGTAC GATAAAGTAA CAGTATGTCA GATAAGCCGG 3480  
 70 TGGGGGATG AGATTAGGCT GAGGCACTGC TAGTCAACTG GGGGAAAAGG ATGATGGAAA 3540  
 AATCACCAG TTGTGCTATA TTTTAAAGA AGGAGGTCTG TTATGTGTGC AGCAATTCT 3600  
 CCTGAGGTT AGCCCAATGG AGAAATGAAG CAGAGGAAGG AAACATAGAA AGACATGGGC 3660  
 TATCAGGGAG GAAGATGTTT AATAGAACAT CAGAAATTT CTGGAAGAAA GGCTGTGGAA 3720  
 GGGCCAAATG AGAAAATGAA TGGACAAGC TCAGGAATCC CTACGCTATG TAGAATGTTT 3780  
 75 TTGGTCTGAG TCTCTTTTCT TAGTCCCTAA TCTGTTTCT OCCATAGGCT GTGTTTACAT 3840  
 TATGATTCTT TGTGATGTAT TCCTTTATGA AATTAACAAG AACTCATTTT TTTGAGGTAG 3900  
 AGGAAAATCA ATGCTTTATC TGATATGCTG AGAAATTAAT AGATTGCCAA TACTCATGTG 3960  
 CGTTTCATGT GTTTTATAG GTTTGTTCTT TTGAAGAAAT GTAGTCTTA GTCCACAGG 4020  
 80 GAAATGTGTA TCTATTATA TATCATAGTA TAAATCTATG ATATATTAT ATCATATATA 4080  
 AAAGTCTGAG TTTCTTTTCT TAGTCCCTAA TCTGTTTCT OCCATAGGCT GTGTTTACAT 4140  
 GGAGCTATCG GTTTAGCCTT TTAAGCTTCA TTAGCTTGTG TATTATTGAA ATAGTTTCCA 4200  
 AGAAATTTTA GATATTATCA TAACATCTGG GTCTACTCAA ACCTTATG TTTGAAAGAC 4260  
 TTATGCTTGG GACCTATCAA AAACGACTT TATTATTGCT TTAGTGAATA TACTAGTGGG 4320  
 ATCAACAATG ATTTTCTTGA ATGGGATGA ATGGAGATGC CCGCACAGTA ATGTAGAAAT 4380

5	GTTCATACA GCTATTAAAA TGTAAC TGAC CTCCTTAGAG GCAGATTAGT AACTGTTCTT 4440
	ACTTTGTATA GCTAAGTGAC AGTCACTTAA CTTACATGAC TTTCTTTTTT CACATTGGGT 4500
	CTCTGGTCCT GTGCTCTCAC CTCATTATA GCACGTCTCC TTGATTTTTG GTAGATATCAA 4560
	CTTCCCAGTG ATCTGTTCTAG TTAAGTTCTT CTCCCGTTAA CCAGGAAGTG CTTATTCTCT 4620
	CATCAGAGTG GGAAGAATAG CCTATTGTCT TTCATTTTGC CTGAGTGTAT TTTACTATTT 4680
	GGGCTCTGAA ATAAAAATTA TGAATATGG TGAGGTACCA TGTGGTGCT GCCTTGCTGC 4740
	ATAAATTTCT AGGAGGCGAG GTTAGGAGAC AGTTATGTAT GGCCITTCGG GAAAATTCAA 4800
	AGGGTGGGAT TACAAGGGTG TTCCTCAGGC ATGCCCTATG GGGCCCTATG TGGAGCAAG 4860
10	AAGAATTGAC TGATTACAG GACTTCTCTT TATGTCAATC TTAAGAGGAT GGATGAATCT 4920
	GGACATTGTG TCCACCGAC CTCTGACTGA TGGTTTGGAA AATAACTTTA ATTAGGATCA 4980
	TATGACCAAT GAAAAAGGAA AAATGTAGAC TCTGACTTCC GTCCCACTGA AGGATTAAATG 5040
	AAAACTTTA CTAGCATTTA GAGCTTTTCA GAACATCCCC ACTGTCATGT GTCTCAGCAG 5100
	TGGAGACTGC AAGTAAGGCT TTTAAATTTA GGAGGTTTTT TTTTTTTTTT TTTTTTCCCC 5160
	TAAATGGTAT GGCCAAAGT CAGAGTTAAA ATATATATAG TTAGATTCCA ACTTCCTCCT 5220
15	TCACTCTAAA AAGCAATACC AAACCCACTC TTCATATATG CTTCCAGAAAT GGGGCTTAAG 5280
	TACCAATCTC TGCTTTGCAA TGGGCACAAAT CTGTGTCATG TCCTGAGGCT CTCTAAGAAA 5340
	AGAGAGGATC TGGATGGGA GAGCTAGAAA GTTGCTAACT GGGAGAAACA AGGCCCTGAG 5400
	GGGTGGTCT ACCAATCTGG GAAGATTGTA AAACAACTT CTCGCAACTG AAGGAAGGCT 5460
20	GAAGGTGCT GCAAGTCATT GAGTGACTTT AGGATGAGCA AAACATTGGG CCACCTCTCA 5520
	ATGCCCTATG TGTATAGTAC CAGAAGCAAG GTCTCAGACT TAACAGACCC AGCTCTGTTC 5580
	CAAGGTGATG CTGAACCAAT AGAAGCAAAA CATGTGCAGA TATCCAAACA AGACTGTCTCA 5640
	TGCAAGTCGG CGCTGGCTAC CGCTCTAGG CAGCAACAGC AGAGCTCCAG GGAGCTTATT 5700
	CAATATTTAC TGAGACTTCG AAGACCCAGC AGATGTTTAA TGAAGTCACT ATTTTGGCTC 5760
25	AAACCCCTCA CTTCTCCCC TCCCTCATAA AAGCCACAG GTAAACACAT AAATGAAAGA 5820
	AACCCACAGA AGGCGAATGG AAATAAAGAA AATTCTCTCA AGACTTCTCC AGGCCCATGT 5880
	CACTGGTCAG CGTGGTTTTT ATGTGTATTA GGATTGGGGG ATGTGAAGAA ATAAGTATCC 5940
	AGTACTTTAT AACCAAGCA ATTAATGAT ATTGGGGTAG GGAATGTTGG CCACTTTTGT 6000
	TTAGTTTTGC CATCACATTG TCACCCAGAC CTCACCTAGC CCCAAGTAAT CGGGCGCCCC 6060
30	GAAGAGGGAG ACAGAGATGT GCCAGAGTTG ACCCAGTGTG CGGATGATAA CTACTGACGA 6120
	AAGAGTCATC GACCTCAGTT AGTGGTTGGA TGTAGTCACA TTAGTTTGCC TCTCCCCATC 6180
	TTTGTCTCCC TGGCAAGGAG AATATGCGGG ACATGATGCT AAGAGCCCTG GGTAAATGTG 6240
	GTGAGATGAC ACGCTGCAT ATGCTACACA TATGTGCTTC TCAGTTGCAG AAAATGAATC 6300
35	GCTTTGGGAG ATTATCAGTA GAAAGAGTGT TATCATATTG GTGCTGAGTG CTATGTGTGC 6360
	TTATACAATT TGTTCTTGTA TTTTAATAAA CTTTGAATAA AAGAAATAAA AAAAAAATAA 6420
	AAAAAATAA

Seq ID NO: C192 DNA Sequence

Nucleic Acid Accession #: NM\_006549.2

Coding sequence: 824..2590

40	1 11 21 31 41 51
	GAGCCTGGGG AGGTCGAGGG TGCAGCGAGC CGTGATCGTG CTACTGCACT CCAGCCTGGG 60
45	CAACACAGAG AGACCTGTCT TCAAAACAAA CAAACAAACA AACAAACAAA CAAACAAAG 120
	AAAAAAAAT GGGAGTGGGC CGGGCGCGGT GACTCACACC TGTAAATCCA GCACCTTCGG 180
	AGGCCAAGGC GGGTGGATCA CGAGGTCAAG AATTCAAGAT TAGCCTGGAAC AACATGGTGA 240
	AAACCCATCT CTACGAAAAA TACAAAATTT AGCCAAGTAT GGTGGCCGGC GCTGTAAATC 300
50	CCAGCTACTC GGGAGACTGA GGCAGAGAAC TGCTTGAACC TGGGAGGCAG AGGTTGCACT 360
	GATCCGAGAT CGCTGCTACT CACTCCAGCG TGGGCGCAGAG AGCGAGACTC CGTTTCAGAA 420
	AAGAAAAAAA AAAAAAAGAG AAAAAGGGAG TCGGGGTGGA GCTCTCATG GCTCGTTGCA 480
	TGTGAGTGTCT CCTACGGCCT AGAAAATCCA GAGAAGCACA TCGGAACGGG CTGGAATATC 540
	ACCCAGTTAA CTAGAGGGCT TTGAACCTTT TATTAACITG GAGGTTGACT CTCTGTCTCA 600
	CTCGATTCCC TTTTGGCTGT TTGGCAGGGT CAGTGAGACA TCCCTTGGGT CGCTCGACCC 660
55	CGTAGGACGG TTCCAGGAGC CCTCCAGGTC TTGTTTCTC CTCTTCCCG CACAGTGTG 720
	TTATCCAGCT GGGAGTCCCA ACGCACACTT AAGGCTCCAG CAAAGTGGCT CGCTGCGGG 780
	ATGGGAGTGC CCCAGTGTGC TGGATGAAGC TGGCGCATGC ACCATGTCTC CATGTGTCTC 840
	TAGCCAGCCC AGCAGCAACC GGGCCGCCCC CCAGGATGAG CTGGGGGGCA GGGGCGACAG 900
	CAGCAGCGAA AGCCAGAAGC CCTGTGAGGC CCTGCGGGGC CTCTCATCTT TGAGCATCCA 960
60	CCTGGGCATG GAGTCTCTCA TTGTGTCTAC CGAGTGTGAG CCGGGCTGTG CTGTGGACCT 1020
	CGGCTTGGCG CGGGACCGGC CCCTGGAGGC CGATGGCCAA GAGGTCCCCC TTGACTCTCT 1080
	CGGGTCCCAG GCCCGGCCCC ACCTCTCGGG TCGCAAGCTG TCTCTGCAAG AGCGGTCCCA 1140
	GGGTGGGCTG GCAGCGGTG GCAGCCTGGA CATGAACGGA CGCTGCATCT GCCGTCCCT 1200
	GCCCTACTCA CCCGTCAGCT CCCGSCAGTC CTGCGCTCGG CTGCCCCGCG GGGCGACAGT 1260
65	GGAGTCTCAC CAGTCTCCA TCACGGGTAT GCAGGACTGT GTGCAGCTGA ATCAGTATAC 1320
	CCTGAAGGAT GAAATTGGAA AGGGCTCCTA TGGTGTGCTC AAGTTGGCCT ACAATGAAAA 1380
	TGACAATACC TACTATGCAA TGAAGGTGCT GTCCAAAAAG AAGCTGATCC GGCAGGCGGG 1440
	CTTTCCAGST CGCCCTCCAC CCGAGGCAC CCGGCCAGCT CCTGGAGGCT GCATCCAGCC 1500
	CAGGGGCCCC ATTGAGCAGG TGTACCAGGA AATTGCCATC CTCAGAAGC TGGACCAACC 1560
70	CAATGTGGTG AAGCTGGTGG AGGTCTCTGA TGACCCCAAT GAGGACCATC TGTACATGGT 1620
	GTTCCGAAGT GTCAACCAAG GGCCCGTGAT GGAAGTGGCC ACCCTCAAAAC CACTCTCTGA 1680
	AGACCAAGGC CGTTTCTACT TCCAGGATCT GATCAAAGGC ATCGAGTACT TACACTACCA 1740
	GAAGATCATC CACCGTGACA TCAAACTTTC CAACCTCTTG GTGAGGAAAG ATGGGCACAT 1800
	CAAGATCGCT GACTTTGGTG TGAGCAATGA ATTCAAGGGC AGTGACGCGC TCCTCTCCAA 1860
75	CACCGTGGGC ACGCCCGCTT TCATGGCACC CGAGTCTGCT TCTGAGACCC GCAAGATCTT 1920
	CTCTGGGAAG GCCTTGGATG TTTGGGCCAT GGGTGTGACA CTATACTGCT TTGTCTTTGG 1980
	CCAGTGCCCA TTCAATGAGG AGCGGATCAT GTGTTTACAC AGTAAGATCA AGAGTCAGGC 2040
	CTGTGAATTT CCGACATAGC CGACATAGC TGAGGACTTG AAGGACCTGA TCAACCGTAT 2100
	GCTGGACAAG AACCCCGAGT CGAGGATCGT GGTGCCGGAA ATCAAGCTGC ACCCTGGGT 2160
80	CAGGAGGCAT GGGGCGGAGC CGTGTGCGTC GGAGGATGAG AACTGCACGC TGGTGAAGT 2220
	GACTGAAGAG GAGTCTGAGA ACTCAGTCAA ACACATTCCC AGCTTGGCAA CCGTATCTCT 2280
	GGTGAAGACC ATGATACGTA AACGCTCCTT TGGGAACCCA TTGAGGGGCA GCCCGCGGGA 2340
	GGAAACGCTCA CTGTACGCGC CTGGAAACTT GCTCAACAAA AAACCAACCA GGAATGTGA 2400
	GTCCCTGTCT GAGCTCAAGG AAGCAAGGCA GCGAAGCAA CCTCCAGGGC ACGGACCCGC 2460
	CCCCCGTGGG GGAGGAGGAA GTGCTCTTGT GAGAGGCAGT CCCTGCGTGG AAAGTTGCTG 2520

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50

```

GGCCCCCGCC CCGGCTCC CCGCAGCAT GCATCCACTG CGGCGGAGG AGGCCATGGA 2580
GGCCGAGTAG CTGCTGGGAT CGCTCGACCT GGCATGCGCG CCGCGTCGCC TCTGGGGGGC 2640
TGCTGCACCG CGTTTCCATA GCAGCATGTC CTACGGAAAC CCAGCACGTG TGTAGAGCCT 2700
CGATCGTCAT CTCTGGTTAT TTGTTTTTTC CTTTGTGTGT TTAAGGGGGA CAAAAAATA 2760
AAAAAAGGA CTTGACTCCA TGACGTGAC CGTGGCGGCT GGCTGGCTGG ACAGGCGGCT 2820
GTGAGGAGTT GCAGACCCAA ACCCAGTGC ATTTTGGGAA ATTGCTTTT AAAAGATTTT 2880
TATGCCAAAA ATCCTTCATT GTGATTTTCA GAACCACGTC AGATATACCA AGTGACTGTG 2940
TGTGGGGTTT GACAACTGTG GAAAGGCGAG CAGAAAATC CGGGGTCTG AGGCCATGGA 3000
GGTGGTGTCT GCATTGAGA GGGAGTAGGG GGCTAGATGT GGCTCCTAGT GCAAAACCGA 3060
AACCATGGGA CTTTCCAGAG CGTGGTCTC AAGGAGTCAG AGCAGGGCTG GCCCTCAGTA 3120
GCTGCAGGGA GCTTTGATGC AACTTATTTG TAAGAAGGAT TTTTAAATT TTTATGGGTA 3180
GAATTGTAGT CAGGAAACAA GAAAGGGCTT GAAATTTAAT AAGTGCTGCT GGAAGGGGAT 3240
TTTCCAAGCC TGGAGGGTGA TTCAGCAGCT GTGGTGGGGA AACATTTCTC CTGAAAGACT 3300
GAACGTGTTT CTTTCATGAC GCTGCTCAA CAGGTTTCTC GAGATAGCTG ACCGAGCTCT 3360
GGTAAATCTC TTGTCAAAT TACGAAAAT TCAGGGTGAA ATCCTATGCT TTCATGTACA 3420
TTACATGGCT TAAGATTAAA CAAAAACATT TTTCAAGTCT CTAAGTAGAG TGAAGTCTAG 3480
AGCACAGTAG TTACGAAACT ATTTAGAGCT TCCAGGATAT ATTTACAGC TTCAGGCATG 3540
TGATCAGTTA GAGCCGATGA AACCTATGCC CGCCTGTATA TATATTAGCA GCTTAGCTAG 3600
TTCATAACCT GTATATTCTA AAGACTGCTA AGGTTTTGTT TTCATTTTAA ATCTAGCTG 3660
ATTGTTGGTG TCAATGAAAT ACCCAGTTTC TGAAGGGCCA GGTGGGAAAT GCTTTTCTG 3720
GACCAACACA CAAATGATCA TCCAGAGGAT CTGAGCTTCC CTAGACTCCA CACAATAACC 3780
TTGGGGCACC CTTTATAGAG AGACTGTGTA AACCCACAGC ACTCGTTGGG GTATGAGGAA 3840
ACCAAGGCTT GGCACAGGAA GTTCCCTTT GTAGCTAAAA GTCCAGAAAG AAGGGTTTCA 3900
TCTTTTGTAC TTCCAATGTA TATTGGGAAG TTTGGTTGAG GTTCAAGTGT GACTCCTTCC 3960
AGAGCCACAG GTAGGGGAGT GTGAAGTTGA GGGGAGGAA AGCTGGAAGG ACTCTGCCTT 4020
GGGAGATTCC CAGCTCTGCT TTCCAGCGCT TGGTGGAAAT TGGCTGGGG AAGACCGCA 4080
CCGGGAAACT CTGCTTCCCT ATTGTTTCCA TCTGATCAGC TGTGGTGTGA GGACTTCTCA 4140
GACAAAGGGA AGGCTCTGCT GCGCTGCCA GCCCATTCAT GGAGCCCTGG GCCTTCTTGG 4200
CTTCCATAGA TCTTAGCTC TTGACTGTAG TTAGCCAGA CTGTTTGTG TATCTTATAA 4260
GCAGTTCAGA ATTAGGGAAT GCTGGTTTG AAGAGCAAAG GACAGGTAGT CTAGAGAGGG 4320
TCGCTGGGCC TGCTGTCTGG GTCTTTGTAA CCCAGCACTT CCTCTTGCCT TCTGGCTTT 4380
ATGTTTATGG GAGAGGACTC AATAGCTCCA CCCCTCTGG CACCAGATGG GGCTTGGTTA 4440
GTTTGCATAA AGCACCTTGC AGAGGTTAAA GCCAGCGGGT CCCTAGTCTT AGGCCACGCC 4500
TGCTTGTGTG GGCTCTGGCC TGGCCTGGTG GCTGGCCGAG GGGGCGAGC TGCTTAGAGC 4560
TCTGTAGGG CTCTCTTGTG TTACACAGCT GCATCAGACA ATGCCATTT TCCCCACCAC 4620
GGAACCTTCC ATCTAAGATT TCTTCCAGGG AATGCCAGCA ATCAGGCAGC ACCCAGCTGT 4680
GGGGGCGAGT GGGTGGGGGA GACCCACATT GATGACTTTT TTTTTCCTT TTAATGAAGA 4740
AACACAAAG AAGCTGTGG AAGGACCTG CCCCACATGA AAGGATAGG CCAAGATGGC 4800
TGTAAACACA GAGCATTGA GCTGCCACTC TTGAGGACCA TTGATTTTTC AAAAGCCAGC 4860
TCTGTAGAG TCTGTGTGCT GTTATGACA GCTCTTCCAG TGGGCAAGA GGAAGCCCAT 4920
AATTTCTTCC ATTGCTAGCT CATCTGTGG ACCAATTTGG TGAAGCAAC CTGTGGCCTG 4980
CACTTGTGGC CTGGAAGGAA GCACAAACCC TCCATCCACT TCCATTTCC TCTGCCCTTT 5040
TCCACTCCCT CCTTCCATCC CACCAGCTGC CAGTGGCTCC CAGAAAGGCT TATTGAGCCC 5100
CTTGTGACA CTTGGGGCTG CGGAGGCTT TCCCTACTGG TCTGGCTTT CTTGAGAGGC 5160
AGGCTCTCCG TCTCAGAGT CTTCTGGAA CAGGAGAAAT GCCTGTGAG GTGGACACAC 5220
AGGCTTGGCC TGTCGCTCTC ACTTGTCTTC CAGGGGGGAG CTTCAGTTG CCGAGTGGAA 5280
GAACCATGAC CTGCACTTGC TTCCAAGGTG CTAGGGAAGT TTCAGGGTAC GCTGGTTCCC 5340
CTCTCAGCT GCGAGCGGAG TTTCTGGGGA CTGCAGATT TTTCTACTCT TGATCGATTCC 5400
AATGCCGAT GCTTCTGTTT CATTCGCCAC CCTTCTACT ATGCATTTTC CTTTATCAG 5460
GTGTATAAG TTAATATCTG TGTATTATC ACTAAAAAGT ACATGAACCT AAGAGACAAC 5520
TAAGCCTTTC GTGTTTTTCC ACAGGTGTTT AAGCTTCTCT GTACAGTTGA AATAACAGA 5580
CAGCAAAATG GTAAAAAATA AAAAAAATA A 5611
  
```

Seq ID NO: C193 DNA Sequence  
 Nucleic Acid Accession #: NM\_018646  
 Coding sequence: 217..2394

60  
 65  
 70  
 75  
 80

```

1      11      21      31      41      51
|      |      |      |      |      |
GCTCTGCCAA GTGTAACAAA CTCACAGCCC TCTCCAAACT GGCTGGGGCT GCTGGGAGAC 60
TCCCAAGGAA CTGTCAGGA AGGCAGGAGA CAGGAGACGG GACCTCTACA GGGAGACGGT 120
GGGCGCGCCC TTGGGGGGGG TGATGTGGCC CCAAGGCTGA GTCCCGTCAG GGTCTGGCCT 180
CGGCCCTCAG CCCCAAGGA GCGGCGCCTA CACCCATAGG GTTTGTCACT GCCCAAGGAG 240
AAAGGGCTAA TTCTCTGCCT ATGGAGCAAG TTCTGCAGAT GGTTCAGAG ACGGGAGTCC 300
TGGGCCACGA CCGGAGATGA GCAGAACCTG CTGCAGCAGA AGAGGATCTG GAGTCTCCT 360
CTCCTCTTAG CTGCCAAGA TAATGATGTC CAGGCCCTGA ACAAGTTGCT CAAGTATGAG 420
GATTGCAAGG TGCAACAGAG AGGAGCCATG GGGGAAACAG CGCTACACAT AGCAGCCCTC 480
TATGACAACC TGGAGGCCGC CATGGTGTG ATGGAGGCTG CCCCGAGCT GGTCTTTGAG 540
CCCATGACAT CTGAGCTCTA TGAGGGTCAG ACTGCACTGC ACATCGCTGT TGTGAACAG 600
AACATGAACC TGGTGGGAGC CCGTCTTGG CGCAGGGCCA GTGTCTCTGC CAGAGCCACA 660
GGCACTGCGT TCGCGGTAG TCCCTGCAAC CTCATCTACT TTGGGAGCA CCTTTGTCC 720
TTTGCTGCTT GTGTGAACAG TGAGGAGATC GTGCGGCTGC TCATTGAGCA TGGAGCTGAC 780
ATCCGGGCCC AGGACTCCCT GGGAAACACA GTGTTACACA TCTTCATCT CCAGCCCAAC 840
AAAACTTTG CCTGCCAGAT GTACAACCTG TTGCTGTCTT ACGACAGACA TGGGAGCCAC 900
CTGCAGCCCC TGGACCTCGT GCCCAATCAC CAGGGTCTCA CCCCTTCAA GCTGGCTGGA 960
GTGGAGGGTA ACACCTGTGAT GTTTCAGCAC CTGATGCAGA AGCGGAAGCA CACCCAGTGG 1020
ACGTATGGAC CACTGACCTC GACTCTCTAT GACCTCACAG AGATCGACTC CTCAGGGGAT 1080
GAGCAGTCCC TGCTGGAAC TATCATCACC ACCAAGAAGC GGGAGGCTCG CCAGATCCTG 1140
GACCAGACGC CGGTGAAGGA GCTGGTGAGC CTCAGTGGGA AGCGGTACGG GGGGCGGTAC 1200
TTCTGCAATG TGGTGGCCAT ATATCTGCTG TACATCATCT GCTTCACCAT GTGCTGCATC 1260
TACCGCCCCC TCAAGCCAG GACCAATAAC CGCAGAGGCC CCGGGGACAA CACCTCTTA 1320
CAGCAGAAGC TACTTCAGGA AGCCTACATG ACCCTAAGG ACGATATCCG GCTGGTGGGG 1380
GAGCTGGTGA CTGTCAATGG GGCTATCATC ATCCTGCTGG TAGAGGTTC AGACATCTTC 1440
AGAATGGGGG TCACTCGCTT CTTTGGACAG ACCATCCTTG GGGGCCCAT CCATGTCCTC 1500
  
```



5 ATCATCACTT ATGCTTCAT GGTGCTGGT ACCATGGTGA TGGGCTCAT CAGTGCCAGC 1560  
 GGGGAGGTGG TACCATGTGC CTTTGCACTC GTGCTGGGCT GGTGCAACGT CATGTACTTC 1620  
 GCGGAGGATG TCCAGATGCT AGGCCCCCTC ACCATCATGA TTCAGAAGAT GATTTTGGC 1680  
 GACCTGATGC GATTCTGCTG GCTGATGGCT GTGGTCATCC TGGGCTTTGC TTCAGCCTTC 1740  
 10 TATATCATCT TCCAGACAGA GGACCCCGAG GAGCTAGGCC ACTTCTACGA CTACCCCATG 1800  
 GCGCTGTTCG GCACCTTCGA GCTGTTCCTT ACCATCATCG ATGCCCCAGC CAACTACAAC 1860  
 GTGGACCTGC CTTTCATGTA CAGCATCACC TATGCTGCCT TTGCCATCAT CGCCACACTG 1920  
 CTCATGCTCA ACCTCCTCAT TGCCATGATG GCGGACACTC ACTGGCGAGT GGCCCATGAG 1980  
 CGGGATGAGC TGTGAGGGGC CCAGATTGTG GCCACCAACG TGATGCTGGA GCGGAAGCTG 2040  
 CTTGCTGCTC TGTGCTGCTG CTCGGGATC TGGGAGCGGG AGTATGGCCT GGGAGACCGC 2100  
 TGGTTCCTGC GGGTGAAGA CAGGCAAGAT CTCACCCGCG AGCGATCCA ACCTACGCA 2160  
 CAGGCTTCC ACACCCGGGG CTCTGAGGAT TTGGACAAAG ACTCAGTGA AAAACTAGAG 2220  
 CTGGGCTGTC CCTTCAGCCC CCACCTGTCC CTTCTATGC CCTCAGTGC TCGAAGTACC 2280  
 15 TCCCGACGA GTGCCAATTG GGAAGGCTT CGGCAAGGGA CCTGAGGAG AGACCTGCGT 2340  
 GGGATATCA ACAGGGCTCT GGAGGACGGG GAGAGCTGGG AATATCAGAT CTGACTGCGT 2400  
 GTTCTCACTT CGCTTCTGG AACTTGCTCT CATTTTCTTG GGTCCATCA ACACAAACAA 2460  
 AACCAACAC CCAGAGGTCT CATCTCCAG GCCCAGGGG AGAAAGAGGA GTAGCATGAA 2520  
 GCGCAAGGAA TGTACGTTGA GAATCACTGC TCCAGGCTCG CATTACTCTC TCAGCTCTGG 2580  
 20 GGCAGAGGAA GCGGAGCCCA AGCAGCGGGC TGGCAGGGCG TGAGGAACCT TCCTGTGGCC 2640  
 TGCTCATGAC CCTTCCGACA GGAGCACTGC ATGTACAGAG ACTTTAAAA CAGGCCAGCC 2700  
 TGCTTGGGCG CTGCTCTCC ACCCCAGGGT CATAAGTGGG GAGAGAGCCC TTCCCAGGGC 2760  
 ACCCAGGCG GTGCGAGGAA GTGCAGAGCT TGTGGAAGC GTGTGAGTGA GGGAGACAGG 2820  
 AACGGCTCTG GGGGTGGGAA GTGGGCTAG GTCTTGCCAA CTCCATCTTC AATAAGTGC 2880  
 25 TTTTGGGATC CCTGAAAAA AAAAAA AAAAAA 2918

Seq ID NO: C194 DNA Sequence  
 Nucleic Acid Accession #: NM\_021910.1  
 Coding sequence: 260..601

30 1 11 21 31 41 51  
 | | | | |  
 GTTCTCCACA ACTGCCAGCA ATCCTTCCAC CAGGCAAAAC ACATCATCTA AGGAAAAGAA 60  
 GTGAGGTTTG CTTAGGGCGT GGCAGCTTCG GATAAACGCA GGACTCCGCC TGGCAGCCCG 120  
 35 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACACA GGGCCGAGTT TCACCCAGTC 180  
 CCACTCCAC GGTGCGCTG GGCCTTATCT CTCAGCCAG CGAGATGCCA GCCTTCTGT 240  
 CCCGGGCCAG CGCTCTGACA TGCAGAAGGT GACCCTGGGC CTGCTTGTGT TCCTGGCAGG 300  
 CTTTCTGTG CTGAGGCGCA ATGACCTAGA AGATAAAAC AGTCCTTCT ACTATGACTG 360  
 GCACAGCCTC CAGGTTGGCG GGCTCATCTG CGCTGGGGTT CTGTGGGCCA TGGGCATCAT 420  
 40 CATGCTCATG AGTGAGTGA GGAGCTGGG GGAGCAGGCG GGGCGGGGCT GGGGCTCCCC 480  
 TCCCTGACC ACTCAGCTCT CCCCACAGG TGCAAAATGC AAATGCAAGT TTGGCCAGAA 540  
 GTCGGTCCAC CATCCAGGGG AGACTCCACC TCTCATCACC CCCGCTCAG CCCAAAGCTG 600  
 ATGAGGACAG ACCAGCTGAA ATTGGGTGGA GGACCGTTCT CTGTCCCGAG GTCTGTCTCT 660  
 TGCACAGAAA CTTGAATCCC AGGATGGAAT TCTTCTCTCT CTGCTGGGAG TCCTTTGCAT 720  
 45 GGCAGGGCCT CATCTACCT CTGCAAGAG GGTCTCTTTG TTCAATTTT TTTAATCTAA 780  
 AATGATTGAG CTTCTGCCA AGCAGCCTGG AGACTTCCTA TGTGTGCAAT GGGGTGGGCG 840  
 TTGGGGCACC ATGAGAAGGT TGGCGTGCCC TGGAGGCTGA CACAGAGGCT GGCACGTAGC 900  
 CTGCTGTGTT GGAAGAGCCC ACAGGCTGT TCCCTTGTGG CTGGGACAT GGCACAGGCC 960  
 CGCCCTCTGC CTCCTCAGCG ATGGGACCTC ATATGCAATT TGGGATTAC TAGTAGCCAA 1020  
 50 AAGGAATGAA AGAGAGCTCT AACAGATGG AACCTGGAA CATTCCAGTG GACCCCTGGAC 1080  
 CATTCCAGTA AACTTGGGAG ATAGGATCGT CCGCTATGA TGGAGTGT CAGACAGTTT 1140  
 ATAATAGTAA GCCCTGTGA CCCTCTCACT TACCCGAGA CTTCACTTTA TTACAAGATC 1200  
 TTTCCAAATA CCCAAATATC CTGCAAGCC CGTTAAATAA TTCCCTATGC TACCCTTAAT 1260  
 AACATACAT CAGACACATG TGTGAGAACT TCCAACAAGC CTCAAAGTCC CTTGAGACTC 1320  
 55 CCCAATACCT AATAAGGCAT GCGAAATGTT CTCATGAAC ACCCCACAAC ACGCTTAAAA 1380  
 CTCAAAACAC CCAAAATAT CTCTCCAAT GTCTGAGAC ATGAACCCAA AAGAGAGACC 1440  
 ACAATAAAT COTGACTGTG CCCCTC 1466

Seq ID NO: C195 DNA Sequence  
 Nucleic Acid Accession #: NM\_005971.2  
 Coding sequence: 176..439

60 1 11 21 31 41 51  
 | | | | |  
 GTTCTCCACA ACTGCCAGCA ATCCTTCCAC CAGGCAAAAC ACATCATCTA AGGAAAAGAA 60  
 GTGAGGTTTG CTTAGGGCGT GGCAGCTTCG GATAAACGCA GGACTCCGCC TGGCAGCCCG 120  
 65 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACACA GGGCCGAGTT CTGACATGCA 180  
 GAAGGTGACC CTGGGCTGCG TTGTGTTCTT GGCAGGCTTT CTTGTCTGCG ACCCAATGA 240  
 CCTAGAAGAT AAAACAGTCT CTTTCTACTA TGACTGGCAC AGCCTCCAGG TTGGCGGGCT 300  
 70 CATCTGCGCT GGGGTTCTGT GCGCCATGGG CATCATCATC GTCATGAGTG CAAAATGCAA 360  
 ATGCAAGTTT GGCAGAAAGT CCGGTCAACA TCCAGGGGAG ACTCCACCTC TCATCACCCG 420  
 AGGCTCAGCC CAAAGCTGAT GAGGACAGAC CAGCTGAAAT TGGGTGGAGG ACCGTTCTCT 480  
 GTCCCGAGGT CCGTCTCTG CACAGAACT TGAACCTCAG GATGGAATTC TTCTCTCTCT 540  
 GCTGGGACTC CTTTGCATGG CAGGGCTCA TCTCACTCT CGCAAGAGGG TCTCTTGT 600  
 75 CAATTTTTT TAATCTAAAA TGATTGTGCC TCTGCCAAG CAGCCTGGAG ACTTCTATG 660  
 TGTGCAATGG GGTGGGGCTT GGGGCACCAT GAGAAGGTTG GGTGCGCCTG GAGGCTGACA 720  
 CAGAGGCTGG CACTGAGCCT GCTTGTGGG AAAAGCCAC AGGCCTGTTT CTTGTGGCT 780  
 TGGGACATGG CACAGGCCCG CCCTCTGCC CTTCAGCCAT GGGACCTCAT ATGCAATTG 840  
 GGATTTACTA GTAGCCAAA GGAATGAAAG AGAGCTCTAA CCAGATGGAA CACTGGAACA 900  
 80 TTCCAGTGA CCTTGGACCA TTCCAGGAAA ACTGGGACAT AGGATCGTCC CGCTATGATG 960  
 GAAGTGTGA CCGTGTATAT AATAGTAAGC CCCTGTGACC CTCTCACTTA CCCGAGAGCC 1020  
 TCACTTTATT ACAAGATCTT TCCAAATACC CAAATATCCC TGCAAGCCCG TTAATAAAT 1080  
 CCCTATGCTA CCCTTAATAA CATACAATGA CCACATAGTG TGAGAACTTC CAACAAGCCT 1140  
 CAAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTTCT CATGAACACT 1200  
 CCCACAACAC GCCTAAAACT CAAAACACCC AAAAAATATCT CCTCAATGT CTTGAGACAT 1260



GAACCCAAAA AGAGACCCAC AATAAACTCG TGACTTGTCC CCTC

1304

Seq ID NO: C196 DNA Sequence  
Nucleic Acid Accession #: NM\_004961.2  
Coding sequence: 55..1575

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60

1	11	21	31	41	51	
GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTCCGCG	CGGTCTCCGC	GGAAATGTTG	60
TCCAAAGTTC	TTCCAGTCTC	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	GGTCGAGGGA	120
CCTCAGACTG	AATCAAGAA	TGAAGCCTCT	TCCCGTGATG	TTGTCTATGG	CCCCCAGCCC	180
CAGCCTCTGG	AAATCAGCT	CCTCTCTGAG	GAACAAAGT	CAACTGAGAC	TGAGACTGGG	240
AGCAGAGTTG	GCAAACTGCC	AGAAGCCTCT	CGCATCCTGA	ACACTATCCT	GAGTAATTAT	300
GACCACAAAC	TGCGCCCTGG	CATTGGAGAG	AAGCCCACTG	TGGTCACTGT	TGAGATCGCC	360
GTCAACAGCT	TTGGTCTCT	CTCTATCCTA	GACATGGAAT	ACACCATGGA	CATCATCTTC	420
TCCCAGACCT	GGTACGAGCA	ACGCTCTGT	TACAACGACA	CCTTTGAGTC	TCTGTCTCTG	480
AATGGCAATG	TGGTGAGCCA	GCTATGGATC	CCGACACCTT	TTTTTAGGAA	TTCTAAGAGG	540
ACCCACGAGC	ATGAGATCAC	CATGCCCAAC	CAGATGGTCC	GCATCTACAA	GGATGGCAAG	600
GTGTTGTACA	CAATTAGGAT	GACCAATTGAT	GCGCGATGCT	CACCTCCACAT	GCTCAGATTT	660
CCAATGGATT	CTGCTCTTG	CCCTCTATCT	TTCTCTAGCT	TTTCTATCC	TGAGAAATGAG	720
ATGATCTACA	AGTGGGAAAA	TTTCAAGCTT	GAAATCAATG	AGAAGAACTC	CTGGAAGCTC	780
TTCCAGTTTG	ATTTTACAGG	AGTGAGCAAC	AAAACCTGAA	TAATCACAA	CCCAGTTGGT	840
GACTTCATGG	TCATGACGAT	TTTCTTCAAT	GTGAGCAGCG	GGTTTGGCTA	TGTTGCCCTT	900
CAAAACTATG	TCCCTTCTTC	CGTGACCACG	ATGCTCTCCT	GGTTTCTCTT	TTGGATCAAG	960
ACAGAGCTCG	CTCCAGCCCG	GACCTCTCTA	GGGATCACCT	CTGTTCTGAC	CATGACCAAG	1020
TTGGGCACTC	TTTCTGCTAA	GAATTTCCCG	CGTGTCTCCT	ATATCACAGC	CTTGGATTTC	1080
TATATCGCCA	TCGTCTCTGT	CTTCTGCTTC	TGGCTCTGT	TGGAGTTTGC	TGTGCTCAAC	1140
TTCTGTATCT	ACAACCCAGC	AAAAGCCCAT	GCTTCTCTTA	AACTCCGCCA	TCCTCGTATC	1200
AATAGCCGTC	CCCATGCCCC	TACCCGTGCA	CGTTCGCCAG	CCTGTGCCCG	CCAACATCAG	1260
GAAGCTTTTG	TGTAGTCAGT	TGTCAACCAT	GAGGGAAGTG	ATGGAGAGGA	CGCCCGCTCT	1320
TGCTCAGCCC	AGCAGCCCCC	TAGCCCAAGT	AGCCCTGAGG	GTCCCGCAG	CCTCTGCTCC	1380
AAGCTGGCCT	GCTGTGAGTG	GTGCAAGCGT	TTTAAAGAGT	ACTTCTGCAT	GGTCCCGAT	1440
TGTGAGGGCA	GTACCTGGCA	GCAGGGCCGC	CTCTGCATCC	ATGTCTACCG	CCTGGATAAC	1500
TACTCGAGAG	TTGTTTTC	AGTGACTTTC	TTCTTCTTCA	ATGTGCTCTA	CTGGCTTGTT	1560
TGCTTAACCT	TGTAGGTACC	AGCTGGTACC	CTGTGGGGCA	ACCTCTCCAG	TTCCCCAGGA	1620
GGTCCAGGCC	CCTTGCCAA	GGAGTTGGGG	GAAAGCAGCA	GCAGCAGCAG	GAGCGACTAG	1680
AGTTTCTTCT	GCCCATCTCC	CCAAACAGAA	GCTTGCAAG	GGTTTGTCTT	TGCTGCCCT	1740
CTCCCTTACC	TGGCCCATTC	ACTGAGTCTT	CTCAGCAGAC	CATTTCAAAT	TATTAATAAA	1800
TGGGCCACCT	CCCTCTTCTT	CAAGGAGCAT	CGTGATGCT	CAGTGTTCAA	AACCACAGCC	1860
ACTTAGTGAT	CAGCTCCCTA	AAACCATGCC	TAAGTACAGG	CGGATTAGCT	ATCTTCCAAC	1920
AATGCTGACC	ACCAGACAAT	TACTGCAATT	TTCCAGAAGC	CCACTATTGC	CTTTGTAGTG	1980
CTTTGGGCTT	CGCCCTTGCC	TCAGCCTCAA	AGTGCACOGA	CTAGTTGCTT	GCCTATACCT	2040
GGCACCTCAT	TAAGATGCTG	GGCAGCAGTA	TAACAGGAGG	AAGAGATCCC	TCTCCTTGG	2100
TCAGATTATT	ATGTTCTCAG	TTCTCTCTCC	CTGCTACCCC	TTTCTCTGCA	GATAGATAGA	2160
CTAGTGCAAT	ATCCCTTTAG	GAAGAGGGGG	GGGCAGCAAG	AGAGCCTATT	TGGGACAGCA	2220
TTCTCTCTCT	TCGTCTGCTG	TGACATCTCC	CTCTCCTTGC	TGGCTCCATC	TTTGTCTGTC	2280
ACTACCAATT	CMTAGCCCTT	CATCCAATGG	GTATCTATT	TTGTGTGTGA	TTATAGTAAC	2340
TACTCCCTGC	TTTATATGCC	ACCCCTCTTC	TTCTCTTTGA	CCCCTGTGAC	TCTTTCTGTA	2400
ACTTTCOCAG	TGACTTCCCC	TAGCCCTGAC	CCAGGCACTA	GGCCTTGGTG	ACTTCTCTGG	2460
GCCAAGAAAC	TAAGGAAACT	CGGCTTTGCA	ACAGGCATTA	CTCGCCATTG	ATTGGTGCCC	2520
ACCCAGGGCA	CACGTGCGGA	GTTCTATCAC	TTGCTTGACC	CCTGGACCCA	TAAACCAAGT	2580
CACGTGTATA	CCCGGGGCAC	TCTAACCATC	ACAATCAATC	AATCAAAATC	CCTTAAATTT	2640
GTATGGCACT	GGAACTTTGG	CAAAGCACTT	TTGACAAGTT	GTGTCTGATT	GGAGCTTCAT	2700
GATAGCCTTG	TGACATCTTT	AGGGCAGGAT	TCTTATCCCC	ATTTTGCAGA	TGAAAACCTT	2760
GAGTCACAGA	TTTCTGTGGG	ACTGTGGATC	TCATCTGAAG	CTATCCAAGA	GCCCACTGTC	2820
ACCTTCTAGA	CCACATGATA	GGGCTAGACA	GCTCAGTTCA	CCATGATTCT	CTTCTGTAC	2880
CTCTGCTGGC	ACACAGTGG	CAAGGCCAG	AATGGCGACC	TCTCTTTAGC	TCAATTTCTG	2940
GGCCTGAGGT	GCTCAGACTG	CCCCCAAGAT	CAAATCTCTC	CTGGCTGTAG	TAACCCAGTG	3000
GAATGAATTT	GGACATGCCC	CAATGCTTCT	ATATGCTAAG	TGAAATCTGT	GTCTGTAAAT	3060
TGTTGGGGGG	TGGATAGGGT	GGGGTCTCCA	TCTACTTTT	GTACCACTCA	TCTGAAATGG	3120
GGAAATATGT	AAATAATAT	ATCAGCAAAG	CAAAAAGAAA	AAAAAAA		3168

Seq ID NO: C197 DNA Sequence  
Nucleic Acid Accession #: NM\_021984.1  
Coding sequence: 572..1753

65  
70  
75  
80

1	11	21	31	41	51	
GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTCCGCG	CGGTCTCCGC	GGAAATGTTG	60
TCCAAAGTTC	TTCCAGTCTC	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
CAGAGAAGTG	CTCAATCAT	AAGTGACAG	CTGATGAGTT	GTCAAAAAAT	GACCAAGCG	180
GTGTAAGAAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
CACCTGCCCT	CAGCAAGGCG	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGGACC	300
TCAGACTGAA	TCAAGAAATG	AAGCCTCTTC	CGGTGATGTT	GTCTATGGCC	CCAGCCCCA	360
GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAATTATGA	480
CCACAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTG	AGATCTCCGT	540
CAACAGCCTT	GGTCTCTCT	CTATCTAGA	CATGGAATAC	ACCATGACA	TCATCTCTC	600
CCAGACCTGG	TACGACGAAC	GCCTCTGTTA	CAACGACACC	TTTGAAGTCT	TGTTCTGAA	660
TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
CCACAGGATC	GAGATCAACA	TGCCCAACCA	GATGGTCCCG	ATCTACAAGG	ATGGCAAGGT	780
GTGTACACA	ATTAGGATGA	CCATTGATGC	CGGATGCTCA	CTCCACATGC	TCAGATTTC	840
AATGATATCT	CACCTCTGCC	CTCTATCTTT	CTCTAGCTTT	TCCTATCCTG	AGAATGAGAT	900
GATCTACAAG	TGGGAAAATT	TCAAGCTTGA	AATCAATGAG	AAGAACTCCT	GGAGCTCTT	960

5	CCAGTTGGAT	TTTACAGGAG	TGAGCAACAA	AACTGAAATA	ATCACAACCC	CAGTTGGTGA	1020
	CTTCATGGTC	ATGACGATT	TCTTCAATGT	GAGCAGGCGG	TTTGGCTATG	TTGCCCTTCA	1080
	AAACTATGTC	CCTTCTTCGG	TGACCACGAT	GCTCTCTGGG	GTTTCCTTTT	GGATCAAGAC	1140
	AGAGTCTGCT	CCAGCCCGGA	CCTCTCTAGG	GATCACCTCT	GTTCTGACCA	TGACCACGTT	1200
	GGGCACCTTT	TCTCGTAAGA	ATTTCCCGCG	TGTCTCCTAT	ATCACAGCCT	TGGATTCTTA	1260
	TATGCCATC	TGCTTGTCT	TCTGCTTCTG	CGCTCTGTTG	GAGTTTGTG	TGCTCAACTT	1320
	CCTGATCTAC	AACCAGACAA	AAGCCCATGC	TTCTCCTAAA	CTCCGCCATC	CTCGTATCAA	1380
	TAGCCGTGCC	CATGCCGTA	CCOGTGCACG	TTCCCGAGCC	TGTGCCCCGC	AACATCAGGA	1440
10	AGCTTTTGTG	TGCCAGATTG	TCACCACTGA	GGGAAGTGAT	GGAGAGGAGC	GCCCGTCTTG	1500
	CTCAGCCGAG	CAGCCCCCTA	GCCCAGGTAG	CCTGAGGGT	CCCGCAGGCC	TCTGCTCCAA	1560
	GCTGGCCTGC	TGTGAGTGGT	GCAAGCGTTT	TAAGAAGTAC	TTCTGCATGG	TCCCGATTG	1620
	TGAGGGCAGT	ACCTGGCAGC	AGGCCCGCCT	CTGCATCCAT	GTCTACCGCC	TGGATAACTA	1680
	CTCGAGAGTT	GTTTTCOCAG	TGACTTTCTT	CTTCTCAAT	GTGCTTACT	GGCTTGTGTTG	1740
15	CCTTAACTTG	TAGGTACCA	CTGGTACCT	GTGGGGCAAC	CTCTCCAGTT	CCCCAGGAGG	1800
	CTCAGAGCC	TGCTCGCTGG	AGTTGGGGGA	AAGCAGCAGC	AGCAGCAGGA	GCGACTAGAG	1860
	TTTTTCTGTC	CCCATTTCCC	AAACAGAAAG	TTGCAGAGGG	TTTGTCTTTG	CTGCCCTCT	1920
	CCCCTACCTG	GCCCATTCAC	TGAGTTTCT	CAGCAGACCA	TTTCAAAATA	TTAATAAATG	1980
	GGCCACCTCT	CTCTTCTTCA	AGGAGCATCC	GTGATGCTCA	GTGTTCAAAA	CCACAGCCAC	2040
20	TGATGATCA	GCTCCCTAAA	ACCATGCCTA	AGTACAGGCG	GATTAGCTAT	CTTCCAAACAA	2100
	TGCTGACCA	CAGACAATA	CTGCATTTT	CCAGAAGCCC	ACTATTGCCT	TTGCACTGCT	2160
	TTCCGCCAG	TTCTGGCCTC	AGCCTCAAAG	TGCACGACT	AGTTGCTTGC	CTATACCTGG	2220
	CACCTCATT	AGATGCTGGG	CAGCAGTATA	ACAGGAGGAA	GAGATCCCTC	TCCTTTGGTC	2280
	AGATTATTAT	GTTCTCAGTT	CTCTCTCCCT	GCTACCCCTT	TCTCTGAGA	TAGATAGACA	2340
25	CTGGCATTAT	CCCTTTAGGA	AGAGGGGGGG	GCAGCAAGAG	AGCCTATTG	GGACAGCATT	2400
	CTCTCTCTC	TGCTGCTGTG	ACATCTCCCT	CTCCTTGTG	GCTCCATCTT	TGCTCTGCAC	2460
	TACCAATTCA	ATGCCCTTCA	TCCAATGGGT	ATCTATTTT	GTGTGTGATT	ATAGTAACTA	2520
	CTCCCTGCTT	TATATGCCAC	CCTCTTCTT	CTCTTTGACC	CCTGTGACTC	TTTCTGTAAC	2580
	TTTCCAGTG	ACTTCCCTTA	GCCCTGACCC	AGGCCTAGG	CCTTGGTGAC	TTCTGGGGC	2640
30	CAAGAACTA	AGGAACTCG	GCTTTGCAAC	AGGCATTACT	CGCATTGAT	TGGTGCCAC	2700
	CAGGGCACA	CTGTGGAGT	TCTATCACT	GCTTGACCC	TGGACCCATA	AACCACTCCA	2760
	CTGTATACC	CGGGCCTC	TAACCATCAC	AATCAATCAA	TCAAATTCCC	TTAAATTTGT	2820
	ATGGCACTGG	AACTTTGGCA	AAGCACTTTT	GACAAGTTGT	GTCTGATTGG	AGCTTCTATGA	2880
	TAGCCTTGTG	ACATCTTTAG	GCGAGGATTC	TTATCCCAT	TTTGAGATG	AAAACCTGA	2940
35	GTCAAGATT	TCTGTGGGAC	TGTGGATCTC	ACTGGAAGCT	ATCCAAGAGC	CACTGTCTAC	3000
	CTTCTAGACC	ACATGATAGG	GCTAGACAGC	TCAGTTCAAC	ATGATCTCT	TCTGTCACT	3060
	CTGCTGAC	ACCACTGGCA	AGGCCAGAA	TGGCGACCTC	TCCTTAGCTC	AATTTCTGGG	3120
	CCTGAGGTGC	TCAGACTGCC	CCCAAGATCA	AATCTCTCT	GGCTGTAGTA	ACCCAGTGGG	3180
	ATGAATTTGG	ACATGCCCA	ATGCTTCTAT	ATGCTAAGTG	AAATCTGTGT	CTGTAATTTG	3240
40	TTGGGGGGTG	GATAGGGTGG	GGTCTCCATC	TACTTTTGT	CACCATCATC	TGAAATGGGG	3300
	AAATATGTAA	ATAAATATAT	CAGCAAGC				3329

Seq ID NO: C198 DNA Sequence  
Nucleic Acid Accession #: NM\_021987.1  
Coding sequence: 572..1657

45	1	11	21	31	41	51	
	GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTGGGCG	CGGTCTCCGC	GGAAATGTTG	60
50	TCCAAGATTG	TTCCAGTCTT	CCTAGGCATC	TTATTGATCC	TCCAGTCCAG	AACATGTATA	120
	CAGAGAAGTG	CTCAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCACAGCG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCGGAA	TGTGAGCAGG	ACCTCAGAA	CCCCCTTTGT	240
	CATGCTCTCC	CAGCAAGGC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGGACC	300
	TCAGACTGAA	TCAAGAATG	AAGCCTCTTC	COGTGATGTT	GTCTATGGCC	CCGAGCCCCA	360
55	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AACTCTGCCA	AAGCCTCTCG	CATCCTGAAC	ACTACTCTGA	GTAATTATGA	480
	CCACAAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTGT	AGATCTCCGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCCTAGA	CATGGAATAC	ACCATTGACA	TCATCTTCTC	600
	CCAGACCTGG	AATTCTAAGA	GGACCCACGA	GCAATGAGATC	ACCATGCCCA	ACCAGATGGT	660
60	CCGATCTAC	AAGGATGGCA	AGGTGTTGTA	CACAATTAGG	ATGACCATTG	ATGCCGGATG	720
	CTCACTCCAC	ATGCTCAGAT	TTCCAATGGA	TTCTCACTCT	TGCCCTCTAT	CTTTCTCTAG	780
	CTTTTCTCAT	CCTGAGAATG	AGATGATCTA	CAAGTGGGAA	AATTCAAGC	TTGAAATCAA	840
	TGAGAAGAAC	TCTTGAAGC	TCTTCCAGTT	TGATTTTACA	GGAGTGAGCA	ACAAAACCTGA	900
	AATAATCACA	ACCCAGTTG	GTGACTTCAT	GGTCATGACG	ATTTTCTTCA	ATGTGAGCAG	960
65	GCGGTTTGGC	TATGTTGCCT	TTCAAACTA	TGTCCCTTCT	TCCGTGACCA	CGATGCTCTC	1020
	CTGGGTTTCT	TTTTGGATCA	AGACAGAGTC	TGCTCCAGCC	CGGACCTCTC	TAGGGATCAC	1080
	CTCTGTTCTG	ACCATGACCA	CGTTGGGCAC	CTTTTCTCGT	AAGAATTTCC	CGCGTGTCTC	1140
	CTATATCACA	GCCTTGGATT	TCTATATCGC	CATCTGCTTC	GTCTTCTGCT	TCTGCGCTCT	1200
	GTGGAGTTT	GCTGTGCTCA	ACTTCTGAT	CTACAACCAG	ACAAAAGGCC	ATGCTTCTCC	1260
70	TAAACTCCGC	CATCTCGTA	TCAATAGCG	TGCCCATGCC	CGTACCCGTG	CAOGTTCCCG	1320
	AGCCTGTGTC	CGCCAAACAT	AGGAAGCTTT	TGTGTGCCAG	ATTGTCAACA	CTGAGGGAAG	1380
	TGATGGAGAG	GAGCGCCCGT	CTTGCTCAGC	CCAGCAGCCC	CCTAGCCCAT	GTAGCCCTGA	1440
	GGGTCCCGCG	AGCCTCTGCT	CCAAGCTGCG	CTGCTGTGAG	TGGTGCACGC	GTTTAAAGAA	1500
	GTACTTCTGC	ATGGTCCCGG	ATTGTGAGGG	CAGTAOCTGG	CAGCAGGGCC	GCCTCTGCAT	1560
75	CCATGTCTAC	CGCTTGGATA	ACTACTCGAG	AGTTGTTTTC	CCAGTGACTT	TCTTCTTCTT	1620
	CAATGTGCTC	TACTGGCTTG	TTTGCCCTTAA	CTTGTAAGTA	CCAGCTGGTA	CCCTGTGGGG	1680
	CAACCTCTCC	AGTTCCCGAG	GAGGTCCAAG	CCCTTGCCCA	AGGGAGTTGG	GGGAAGCAG	1740
	CAGCAGCAGC	AGGAGCGACT	AGAGTTTCTT	CTGCCCATTT	CCCCAAACAG	AAGCTTGCAG	1800
	AGGGTTTGTG	TTTGCTGCCC	CTCTCCCTTA	CCTGGCCCAT	TCAGTGAGTT	TTCTCAGCAG	1860
80	ACCATTTCAA	ATTATTAATA	AATGGGCCAC	CTCCCTCTTC	TCAAGGAGC	ATCGTGTATG	1920
	CTCAGTGTTG	AAAAACACAG	CCACTTAGTG	ATCAGCTCCC	TAAAAACATG	CCTAAGTACA	1980
	GGCGGATTAG	CTATCTTCCA	ACAAATGCTGA	CCACAGACCA	ATTACTGCAT	TTTTCCAGAA	2040
	GCCCACTATT	GCCTTTGCG	TGCTTTCGCG	CCAGTTCTGG	CCTCAGCCTC	AAAGTGCACC	2100
	GACTAGTTGC	TGCGCTATAC	CTGGCACCTC	ATTAAGATGC	TGGGCAGCAG	TATAACAGGA	2160
	GGAAAGATAC	CCTCTCCTTT	GGTCAGATTA	TTATGTTCTC	AGTTCTCTCT	CCCTGCTACC	2220

5 CCTTCTCTG CAGATAGATA GACACTGGCA TTATCCCTTT AGGAAGAGGG GGGGGCAGCA 2280  
 AGAGAGCCTA TTGGGACAG CATTCCCTCTC TCTCTGCTGC TGTGACATCT CCCTCTCCTT 2340  
 GCTGGCTCCA TCTTTCGTCT GCACTACCAA TTCAATGCCC TTCAATCCAAT GGGTATCTAT 2400  
 TTTTGTGTGT GATTATAGTA ACTACTCCCT GCTTTATATG CCACCCCTTT CTTCTCTCTT 2460  
 GACCCCTGTG ACTCTTCTG TAACCTTCCC AGTGACTTCC CCTAGCCCTG ACCAGGCACT 2520  
 AGGCCTTGGT GACTTCTCTG GGGCAAGAAA CTAAGGAAAC TCGGCTTTGC AACAGGCATT 2580  
 ACTGCGCATT GATTGTGTCC CACCCAGGGC AACTGTGCG AGTTCTATCA CTTGCTTGAC 2640  
 CCCTGGACCC ATAAACCACT CCACTGTTAT ACCCGGGGCA CTCTAACCAT CACAATCAAT 2700  
 CAATCAAAAT CCCTTAAATT TGTATGGCAC TGGAACTTTG GCAAAGCACT TTGACAAAGT 2760  
 10 TGTGTCTGAT TGGAGTCTCA TGATAGCCTT GTGACATCTT TAGGGCAGGA TTCTTATCCC 2820  
 CATTTTCCAG ATGAAACCC TGAGTCAGAG ATTTCTGTGG GACTGTGGAT CTCACTGGAA 2880  
 GCTATCCAG AGCCCACTGT CACCTTCTAG ACCACATGAT AGGGCTAGAC AGCTCAGTTC 2940  
 ACCATGATTC TCTTCTGTCA CCTCTGCTGG CACACCAGTG GCAAGGCCCA GAATGGCGAC 3000  
 CTCTCTTTAG CTCAATTTCT GGGCCTGAGG TGCTCAGACT GCGCCCAAGA TCAATCTCT 3060  
 15 CCTGGCTGTA GTAAACCACT GGAATGAATT TGGACATGCC CCAATGCTTC TATATGCTAA 3120  
 GTGAAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGGTCTCC ATCTACTTTT 3180  
 TGTCAACATC ATCTGAAATG GGGAAATATG TAAATAAATA TATCAGCAAA GC 3232

20 Seq ID NO: C199 DNA Sequence  
 Nucleic Acid Accession #: NM\_021990.1  
 Coding sequence: 1309..2490

25 1 11 21 31 41 51  
 GCCAGAGGTT GAGCCGCGAC CTCGCGCGAG GTGGTGGCGC CGGTCTCCGC GGAAATGTTG 60  
 TCCAAAGTTC TTCCAGTCTC CTAGGCACTC TTATTGATCC TCCAGTCGAG AACATGTATA 120  
 CAGAGAAGTG CTCAATCATC AAGTGTACAG CTGATGAGTT GTCAAAAAT GACCACAGCG 180  
 GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTTGT 240  
 30 CACTGCTCCG CAGCAAAAGC AGCACTATCC GGACTTCTAA CACCATCGGT GAGTTTCATA 300  
 CCTTGGCAGA TGGCCTTTAA CATTTTGTG TAATTCAATT ATTCTTACTA ATCTTCTTCT 360  
 TTTTCTTGGC TGTGTGTGAT GGCTGTGGAG CTCAGGCTGG ACTCCTGTTG GGCAGCCAGT 420  
 TCCGTGGTGG CTGTCTGTGG GTGGAGGACT CCTGCCCTTC CTGTTTAGAC ACCCAACAAG 480  
 GCTGCTCTTT AGCCTCCTTC CCTTCATCCC CTTCCTCTGC CCCAGTGCA ACGAGTATTA 540  
 CACAACCAAC AAAACCGCAA AATATTCCCA CAATTTTCTG GTCCTCTCTG GGAGAGGCCG 600  
 35 CTCTGGCTTT TCTCTCAGC CCTGGCCCTC TGCCCTGCTCC TCACTCCTGG TTGGTGTCTG 660  
 TCAGGCTGAC TAGAGGCCAA GGCAGCCAAC ACTAGGCAAA CGCGGCCAGC GCTCAGACAT 720  
 AATGCCCCCT TCTATTCCAC GTGTAACATT CTTTAAAT CTAGGTCTGT GTTTGTGTA 780  
 TTTTCTCTTA AATAAAGAG TGATCATAAA AGAGGGACAG CATAGAAAGT CCCCAGAGAG 840  
 CAGCAAGGTT TTAAGAAAT TCACAGCCCT AATCTGTAC TGTCTTATAA TTGCTATTA 900  
 40 CCAAGTACAA TTTAACTAGG TTTTGTGTG AAAACTTGTG TTGTTTGTCT TCTGTCCCAA 960  
 GAGGCACTAG CTCGGGCCCC TACAGAGTGC AGGCGCAGAG TTCATTTTTC GTTTGAATGT 1020  
 TCTAGGTGAG AGGGAACCTCA GACTGAATCA AAGATGAAG CCTCTTCCCG TGATGTGTCT 1080  
 TATGGCCCCC AGCCCCAGCC TCTGGAATAT CAGCTCCTCT CTGAGGAAAC AAGTCAACT 1140  
 GAGACTGAGA CTGGGAGCAG AGTTGGCAAA CTGCGCAGAG CCTCTCGCAT CCTGAACACT 1200  
 45 ATCCTGAGTA ATTAGACCA CAAACTGCGC CCTGGCATG GAGAGAAGCC CACTGTGCTC 1260  
 ACTGTGTAGA TCTCCGTCAA CAGCCTTGGT CCTCTCTCTA TCCTAGACAT GGAATACACC 1320  
 ATTGACATCA TCTCTCCCA GACCTGTGAC GACGAACGCC TCTGTTACAA CGACACCTTT 1380  
 GAGTCTCTTG TTTGTAATGG CAATGTGGTG AGCCAGCTAT GGATCCCGGA CACCTTTTTT 1440  
 AGGAATTTCTA AGAGGACCCA CGAGCATGAG ATCACCATGC CCAACAGAT GGTCCGCACT 1500  
 50 TACAAGGATG GCAAGGTGTT GTACACAATT AGGATGACCA TTGATGCCGG ATGCTCACTC 1560  
 CACATGCTCA GATTTCGAAT GGAATCTCAC TCTTGCCCTC TATCTTTCTC TAGCTTTTCC 1620  
 TATCCTGAGA ATGAGATGAT CTACAAGTGG GAAATTTTCA AGCTTGAAAT CAATGAGAAG 1680  
 AACTCCTGGA AGCTCTTCCA GTTTGATTTT ACAGAGTGA GCAACAAAC TGAAATAATC 1740  
 ACAACCCAG TTGGTGACTT CATGGTCATG ACGATTTTCT TCAATGTGAG CAGGCGGTTT 1800  
 55 GGCTATGTTG CCTTCTAATA CTATGTCCTT TCTTCCGTGA CCAAGATGCT CTCTGGGTTT 1860  
 TCCTTTTGGG TCAAGACAGA GTCTGCTCCA GCGCGGACCT CTCTAGGGAT CACCTCTGTT 1920  
 CTGACATGTA CCAAGTTGGG CACCTTTTCT CGTAAGAATT TCCCGCGTGT CTCCTATATC 1980  
 ACAGCCTTGG ATTTCTATAT CGCCATCTGC TTCGTCTTCT GCTTCTGCGC TCTGTGGAG 2040  
 TTTGCTGTGC TCACTTCTCT GATCTACAAC CAGACAAAAG CCCATGCTTC TCCTAAACTC 2100  
 60 CGCCATCTTC GTATCAATAG CCGTGCCCAT GCCCGTACCC GTGCACGTTT CCGAGCCTGT 2160  
 GCGCGCAAC ATCAGGAAGC TTTTGTGTGC CAGATTGTCA CCACTGAGGG AAGTGATGGA 2220  
 GAGGAGCGCC CGTCTTGCTC AGCCAGCAG CCCCCTAGCC CAGGTAGCCC TGAGGGTCCC 2280  
 CGCAGCCTCT GCTCCAAGCT GGCCTGCTGT GAGTGGTGCA AGCGTTTAA GAAGTACTTC 2340  
 TGATGTGTC CCGATTGTGA GGGCAGTACC TGGCAGCAGG GCGGCTCTG CATCCATGTC 2400  
 65 TACCGCCTGG ATAACACTC GAGAGTTGTT TTCCAGTGA CTCTCTCTT CTTCAATGTG 2460  
 CTCTACTGGC TTGTTTGCTT TAACTTGTAG GTACCAAGCT GTACCTGTG GGGCAACCTC 2520  
 TCCAGTTCCC CAGGAGTCCC AAGCCCTTGG CCAAGGGAGT TGGGGGAAAG CAGCAGCAGC 2580  
 AGCAGGAGCG ACTAGAGTTT TTCTGCCCCC ATTCCCCAAA CAGAAGCTTG CAGAGGGTTT 2640  
 GTCTTTGCTG CCCCCTCCC CTACCTGGCC CATCTACTGA GTTTTCTCAG CAGACCATTT 2700  
 70 CAAATTATTA ATAAATGGGC CACCTCCCTC TTCTTCAAGG AGCATCCGTG ATGCTCAGTG 2760  
 TTCAAAACCA CAGCCACTTA GTGATCAGCT CCTTAAATCC ATGCCTAAGT ACAGGCGGAT 2820  
 TAGCTATCTT CCACAATGC TGACCAACAG ACAATTACTG CATTTTCCCA GAAGCCCACT 2880  
 ATTGCTTTTG CAGTGCTTTC GGGCAGTTC TGGCCTCAG CTCAAAGTGC ACCGACTAGT 2940  
 75 TGCTTGCTTA TACCTGGCAG CTCATTAAGA TGCTGGGCG CAGTATAACA GGAGGAAGAG 3000  
 ATCCCTCTCC TTTGGTCAGA TTATTATGTT CTCAGTTCTC TCTCCCTGCT ACCCCTTTCT 3060  
 CTGACAGATG ATAGACACTG GCATTATCCC TTTAGGAAGA GGGGGGGGCA GCAAGAGAGC 3120  
 CTATTTGGGA CAGCAATCCCT CTCTCTGTC TGCTGTGACA TCTCCCTCTC CTGCTGGCT 3180  
 CCATCTTTTG TCTGCACTAC CAATTCAATG CCCTTCATCC AATGGGTATC TATTTTGTG 3240  
 80 TGTGATTATA GTAACACTC CCTGCTTTAT ATGCCACCTT CTTCCTTCTC TTTGACCCCT 3300  
 GTGACTCTTT CTGTAACCTT CCGAGTGACT TCCCTTAGCC CTGACAGGC ACTAGGCCCT 3360  
 GGTGACTTCC TGGGGCCAGG AAATCAAGGA AACTCGGCTT TGCAACAGGC ATTAAGCTGC 3420  
 ATTGATTGGT GCCACCCAG GGCACACTGT CGGAGTTCTA TCACTTGCTT GACCCTGGA 3480  
 CCCATAAACC AGTCACTGT TATACCCGGG GCACTCTAAC CATCAATCA AATCAATCAA 3540  
 ATTCCCTTAA ATTGTATGAG CACTGGAAC TTGGCAAGC ACTTTTGACA AGTTGTGTCT 3600

5 GATTGGAGCT TCATGATAGC CTTGTGACAT CTTTAGGGCA GGATTCTTAT CCCCATTTTG 3660  
CAGATGAAAA CCCTGAGTCA CAGATTTCTG TGGGACTGTG GATCTCACTG GAAGCTATCC 3720  
AAGAGCCACG TGTCACCTTC TAGACCACAT GATAGGGCTA GACAGCTCAG TTCACCATGA 3780  
TTCTCTCTG TCACCTCTGC TGGCACAACA GTGGCAAGGC CCAGAAATGGC GACCTCTCTT 3840  
TAGCTCAATT TCTGGGCTG AGGTGCTCAG ACTGCCCCCA AGATCAAATC TCTCCTGGCT 3900  
GTAGTAACCC AGTGAATGA ATTTGGACAT GCCCAATGC TTCTATATGC TAAGTGAAAT 3960  
CTGTGTCTGT AATTGTGTGG GGGGTGGATA GGGTGGGTC TCCATCTACT TTTTGTACCC 4020  
ATCATCTGAA ATGGGGAAAT ATGTAATAA ATATATCAGC AAAGC 4065

10 Seq ID NO: C200 DNA Sequence  
Nucleic Acid Accession #: NM\_021819.1  
Coding sequence: 39..1619

15 1 11 21 31 41 51  
TAGGGGGGTC GGTAATTGCG GCACGAGGGC GCTCACGTAT GCCGGCGGTC AGTGGTCCAG 60  
GTCCCTTATT CTGCTTCTC CTCTGCTCC TGGACCCCA CAGCCCTGAG ACGGGGTGTC 120  
CTCCTCTACG CAGCTTTGAG TACAAGCTCA GCTTCAAAGG CCCAAGGCTG GCATTGCTG 180  
GGGCTGGAAT ACCTTCTGCG AGCCATCATG GAGACGCCAT CCTGGGCTG GAGGAAGTGC 240  
GGCTGACGCG ATCCGCTGAG AACCGGAGTG GCGCGTGTG GAGCAGGGCC TCTGTCCCT 300  
TCTCTGCTGT GGAAGTAGAG GTGCAATGA GGGTGACGG ACTGGGCGC CGGGAGGCC 360  
ACGGCATGGC CGTGTGGTAC ACCCGGGGCA GGGGCCATGT AGGCTCTGTC CTTGGGGGGC 420  
TGGCTTCTGT CTAGCGCATC GGGATCTTCT TTGACTCTCC GGCAGAGGAT ACTCAGGACA 480  
GTCTGCTCAT CGTGTGCTG GCCAGGACG GGCACATCCC CTCTGAGCAG CCTGGGGATG 540  
GAGCTAGCCA AGGGCTGGGC TCTGTCTATT GGGACTTCCG GAACCGGCCA CACCCCTTCA 600  
GAGCAGGAT CACCTACTGG GGGCAGAGGC TGGCATGTC CTTGAACAGT GGCCTCACTC 660  
CCAGTGATCC AGGTGAGTTC TGTGTGGATG TGGGGCCCTT GCTTTTGGTC CCTGGAGGTT 720  
TCTTTGGGCT CTAGCAGGCC ACCGGCACCC TGGCAGATGA TCATGATGTC CTGTCCCTTC 780  
TGACCTTCAG CCTGAGTGAG CCCAGCCCA AGGTTCCTCC TCAGCCCTTC CTGGAGATGC 840  
AGCAGCTCCG CCTGGCGAGG CAGCTGGAAG GGTGTGGGC AAGGCTGGGC TTGGGCACCA 900  
GGGAGGATGT AACTCCAAA TCAGACTCTG AAGCTCAAGG AGAAGGGGAA AGGCTCTTTG 960  
ACCTGGAGGA GAGCTGGGCG AGACACCGCC GGATCTCTGA GGTCTGCGG GGTCTCTCCA 1020  
AGCAGCTGGC CCAGGCTGAG AGACAATGGA AGAAGCAGCT GGGGCCCCCA GGCCAAGCCA 1080  
GGCCTGACGG AGGCTGGGCC CTGGATGCTT CTGCCCAGAT TCCATCCACC CCAGGGAGGG 1140  
GTGGCCACCT CTCCATGTC TCAATAAGG ACTCTGCCAA GGTGCGTGGC CTGTCCATG 1200  
GACAGTGGAC TCTGTCTCAG GCCCTGCAAG AGATGAGGGA TGCAGCTGTC CGCATGGCTG 1260  
CAGAAGCCCA GGTCTCTTAC CTGCTGTGG GCATTGAGCA TCATTCTTA GAGCTGGACC 1320  
ACATCTGGG CCTCTGCGG GAGGAGCTTC GGGGCCCGGC GAAGGCAGCA GCCAAGGCC 1380  
CCGCCCCACC TGGCCAGCCC CCAAGGGCCT CCTGTGCTCT GCAGCTGGC ATCTTCTCTG 1440  
TCTACCTCT CATTGAGACT GTAGGCTTCT TCGGCTACGT GCATCTCAGG CAGGAGCTGA 1500  
ACAAGAGCCT TCAGGAGTGT CTGTCCACAG GCAGCCTTCC TCTGGGTCTT GCACCAACA 1560  
CCCCAGGGC CCTGGGATT CTGAGGAGGC AGCTCTCTCC TGCCAGCATG CCTGCCTGAC 1620  
CCACCTCAGA CCTGCTTTG CATCACTGGG AAGCAGGCAG TGTCTTGGGT GGGGGCTTGG 1680  
TCAGTATCT CTGCTGTG GTGCCAGCT CCCACGACA CTGAGCTTT CGGCATGCTC 1740  
45 CCACCTGTT AAAGGTGATT TCCTCTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1800  
A 1801

50 Seq ID NO: C201 DNA Sequence  
Nucleic Acid Accession #: XM\_117036.1  
Coding sequence: 25..495

55 1 11 21 31 41 51  
AGCCAAGAGA GGGGGGACAG ACAGATGGAA AGACGGACAC GGGGAGCTCT GGGGAGCAGG 60  
CGGCCCCAC CCCCACTTCC AGCTCTGAGA CATTGTGCA CAGGCTGCA GGGGCTGGG 120  
ATGGCCTGGC CGGGCAGCCT CTGGAGACAC ACATGCCAAG GCAGGCGCNG GGCAGCCGAG 180  
GGCCGCTGGG GGTGTGTCG ACCACACAGG TGCCCGAGGG AGGCAGGCGA GGCCTCGTG 240  
GGACCCAGCG CGAAGACGCA GGTGTGCGC CAGCTTTGCA GCGCGCTGC CGTGTGGTG 300  
GATGAGCGGG AACCGGGGCG CGGCGCTTAC GCATGTCAGG TTACGCGCG GTGGAAGGG 360  
TGTACCGCC ACAGCGGGCG CACCGTGCCT GGTCTGTGTT CTGGAACAG TCCAGAACAG 420  
GCAGCCCGCG AGACAGGGAG GGGCCAGCG GTGCGCAGG GAAGTGGGA TGGGAATGAG 480  
TGCGGATGG GCTGAGGTTT TTCCTGAAG ATGAATGCTC TGAACCTGTG AATAGACACA 540  
CGGAACCTG CACGTTACAC GGTGAACCGT GTGGGAGTGG AATCCATCTC AACAGAGCTG 600  
TTACACAGT AACAAAGACA CGANGGGTGG AGGCNCTTG TCTGCTCCTG CAGATGAGC 660  
65 CGGCTGCTCA GAGCGGGAG ATGGCCACTC AGCTCCTTTA ACTG 704

70 Seq ID NO: C202 DNA Sequence  
Nucleic Acid Accession #: XM\_167803.2  
Coding sequence: 1162..1488

75 1 11 21 31 41 51  
AACATCATAC ATAGTAGGTG AATCGTTTTG TAGAGTGAAG AATGCTAATG TAAAGCAAAT 60  
AGTACCCAC GTTCTTTGTA AATCCAAATG TTTCTATATT GTAGCTTTGC TTAATATGGG 120  
GTGGGCCCA ACTGCATCCT CTTCTTTGGC GGGCTGGGGA GCGGCCCCCA GCCGGGACGG 180  
GAGGGCAGCG ACCCGAGGCG CTGCTGGAGC TGGGAGAGAG TGTGGTGGGA AGTCTTGAGC 240  
GGAGGAGGG ATCTGCCCTT CTCCACTCCT CTCTTGGATC GGCCTCGGTT TCTGTCCCT 300  
CCACCAACC CGTGGCCCGC GGAAGACCG CAGTGAGCC AGCCCCACC TTCCAGGCGC 360  
CTTGGCCCTG GGGATCCAA CACTTTGTAT CGAGTGGCG GGGCAACGCG TCCCATTTT 420  
80 TCCCGAGCCC CGCCACAGA GCTCTTAGCC AATCTATGC AGAGAGCATC TCTGGCAGG 480  
GGTCTCTCC CAACAGACC CCACCCAGGC ACATTAGCGA CCAGCTTGG GCTTCCCCAG 540  
CGCCCCACA CCACCACTG CAGGTGAGC TCTGGATGC TATGTTGGGG CGGCAAGCGG 600  
TGGGCGAGG GCGGGTAGG CTAGCAGGG AGTTAAGGT GGTATGGGAT GGGCGGGGG 660  
CGGTCTAGGG CAATAGGAGA GCAGAGAATG GGGGAACCTG AGGGTGGGG GAGGGCACCG 720

5  
10  
15

```

GAGCCTTGCC ACCATCCCAG GACTTTGGGC AAGTCACCCG CACTCCCTGG GCCTCGGTTT 780
CCCCATCTGT AAAATGATGG TAATAATACT TCACCTACCT CATAGGGGAG GTTGTGAGGC 840
CACCATCACC TGACCTGGGG GTCAAGGCAG GAGGACTCOG AAGGTGCTAC CCGTGAGCAA 900
AGTGTAATTA CGAATCCTG ACTGCAAGGC CCACCTGCCC CTCCCCACA GAGCCTCCAG 960
AGCTAGCTGA GGCACAACGCA GGCCCATCCG TCTCTTCACT CTGTGCGAGG CCCTTTCATG 1020
GGCTTCGTCT GCCATCTTTG TGGGTGCCCT AGACTTAGTC CTATCTTGT CCTGGTTTCC 1080
TTTCTTGTGA CCATCTCCCC ATGAAAGTGC TGTACAAATT CCACCGCCC CAGGACCCCC 1140
GCACCTGCCC TCTGGCACC AATGCCAGG AAGGGACAGA GGAAACAGC CACAAACAAG 1200
CCAGGGGGG TCCCCGAGC CCCAGGGGTG GGGATTGGTG GCCACTGTGT GTATGTTCTT 1260
GAGTGCAAGT GTTTTATAAA AAATAAAACA AAAACCCACC ATCACAACAA AAAAAATTTT 1320
GCAGCGAAGA GAAATGAAGA AAAACTGAAG AAAAAACAAA AACAGGAAAA AAAGAACCAT 1380
ACAAATTTT TCCACCACAC ATACCTCTA AGCCAGCAAG ATTTCTCTT TGCAAAATCA 1440
TATTTTGTG GGAATGGGCC CTGCTTTTGG TGGCAAGGCC TGTTCGTATT AATAAAGGAT 1500
CGTGAATAAG T 1511

```

Seq ID NO: C203 DNA Sequence  
Nucleic Acid Accession #: NM\_024780.1  
Coding sequence: 31..1023

20  
25  
30  
35  
40  
45  
50  
55

```

1      11      21      31      41      51
|      |      |      |      |      |
ATTAATCTGG CCGTGCCATG CATCTACTCC ATGTTCAAGC TTGTGGAGAG GTACGAGATG 60
CCACGGCAGG AAGTCTACGT TCTCTGATC CGAAACATCT TTTTGAATAT ATCAATCATT 120
GGCATTCTTT GTTACTATTG GCTCAACACC GTGGCCCTGT CTGGTGAAGA GTGTGGGAA 180
ACCTTCATTG GCCAGGACAT CTACCGGCTC CTCTGTATGG ATTTTGTGTT CTCTTTAGTC 240
AATTCCTTCC TGGGGGAGIT TCTGAGGAGA ATCATTGGGA TGCAACTGAT CACAAGTCTT 300
GGCCTTCAGG AGTTTGACAT TGCCAGGAAC GTTCTAGAAC TGATCTATGC ACAAACCTCTG 360
GTGTGGATTG GCATCTTCTT CTGCCCCCTG CTGCCCCCTT TCCAAATGAT TATGCTTTTC 420
ATCATGTTCT ACTCCAAAAA TATCAGCCTG ATGATGAATT TCCAGCCTCC GAGCAAGGCC 480
TGGCGGGCCT CACAGATGAT GACTTTCTTC ATCTTCTTGC TCTTTTCCAC ATCCTTCACC 540
GGGGTCTTGT GCACCTGGC CATCACCATC TGGAGATTGA AGCCTTCAGC TGACTGTGGC 600
CCTTTTCGAG GTCTGCTCTT CTTCATTAC TCCATCTACA GCTGGATCGA CACCCTAAGT 660
ACACGGCCTG GCTACCTGTG GGTGTTTGG ATCTATCGGA ACCTCATTGG AAGTGTGCAC 720
TTCTTTTCCA TCCTCACCCCT CATGTGCTTA ATCATCACCT ATCTTTACTG GCAGATCACA 780
GAGGGAAGCA AGATTATGAT AAGGCTGCTC CATGAGCAGA TCATTAATGA GGGCAAGAT 840
AAAATGTTCC TGATAGAAAA ATTGATCAAG CTGCAGGATA TGGAGAAGAA AGCAAAACCC 900
AGCTCACTTG TTCTGGAAGG GAGAGAGGTG GAGCAACAAG GCTTTTGA CA TTTGGGGGAA 960
CATGATGGCA GTCTTGACTT GCGATCTAGA AGATCAGTTC AAGAAGGTAA TCCAAGGGCC 1020
TGATGACTCT TTTGTAAACC AGACACCAAT CAAATAAGGG GAGGAGACGA AAATGGAATG 1080
ATTTCTTCCA GTCACCTCTG GCTTTTAGGA ACTGCCCAGA AGAAAATCCA AGGCTTTAGC 1140
CAGGAGCGGA AACTGACTAC CATGTAATTA TCAAGTAAAT ATTGGGCATT CCATGCTATT 1200
TTTAATACCT GGATTGCTGA TTTTCAAGA CAAATACTT GGGGTTTCC AATAAGATT 1260
GTGTAAATAT TGAAATGAGC CTACAAAAAC CTAGGAAGAG ATAAGTGGG AATAATGTAT 1320
ATTATCTTCA AGAAGTGTGT GCAGGAATGA TTGTTCTTA GAAATCTCTC CTGCCAGACT 1380
TCCACAGACT GGCAGAGGTT TAGAACTGT TGCTAAGAAA AGTGGTCCAT CCTGAATAAA 1440
CATGTAATAC TCCAGCAGGG ATATGAAGCC TCTGAATTGT AGAAGCTGCA TTTATTGTG 1500
ACTTTGAAC AAGACATCC CCCATGTCCC AAAGTGGGAA TACAACCAAG GGTCTCATCT 1560
CTGAACCTTC TTGGGTACTG ATTACATGAG TCTTTGGAGT CGGGATGGA GGAGGTTCTG 1620
CCCCGTGAG GTGTATACAT TGACCATCAA AGTCTCTAGT CAAGCTAGCT TTGAGTGGC 1680
AGTACCGTAG CCAATGAGAT TTATCCGAGA CGCGATTATT GCTAATTGGA AATTTTCCCA 1740
ATACCCACAC GTGATGACTT GAAATATAAT CAGCGCTGGC AATTTTGCAG AGTCTCTACG 1800
GAGACTGAAT AAG 1813

```

Seq ID NO: C204 Protein Sequence  
Protein Accession #: Eos sequence

60  
65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
AGCGGGGTTA GATGCAGGGA GTTATGTTGT GATTGTGTGA GGGGTGGCTT TGGTGAGCTC 60
ATCCTGGCAT TTTAAAAATA ATGTGAATGG TGTATCCCTT TGTGATCATC ATCACTTTT 120
CCCTGCGAGT CCAATCAAT GCGGGTGTGA CTGCTGTATG AAGTCTCAGG AAGCCCAACC 180
CAGTGGAGAA GAAGGCTTGC AGGAGGCAGG AGATGCTGTC CGATGACCAC GTGAATGAAA 240
TCATCATACA GGTGAGAAAT GTTCTCTCTG GGTGCCAAG CCACCATCC TCAATCAGA 300
TTTTCAAGA AAAGGTGCTG CTAGACTCAA GCATCAACAT GGTTTTGTCA ATATCTGACA 360
TTGATGTGAT AGACTCTCAG ACAGTCAGCA AAAGGAATGA CCAAAAGGCT AACCAGGTGC 420
TGGGTTTTC AACATCTTTG AATGAGTCTG TGTCTCAGAC CCTTCATAGC CTAGAATGCA 480
TGGGCATAGA CACTCTCTGT TCTTCACATG AAAGTGTTC AAGACAGAAG TTAATCGCAT 540
CCCTTATACC CATGACATCC AGAGACAGAA TTAAGCCAT CAGGAACCAAG CCAAGGACCA 600
TGAAGAGAA AAGGAACCTT AGGAAAATAG TTGACAAAGA AAAAAGCAAA CAGACCCATC 660
GTATCCITCA GCTCAATTGC TGTATTCACT GTCTGAACCT CATTTCCCGG GCTTATCGGA 720
GATCCAAAGA CAGCCTGTGC GAAATCTGA ATTCCATCAG CCTGTGGCAG AAGACGCTGA 780
AGATCATGGG AGGCAAGTTT GGAACCAAGC TCCTCTCCTA TTTCAACTTT CTGAGATGGC 840
TTTTGAAGTT CAACATTTTC TCATTATCC TGAATCTCAG CTTCATCATA ATCCCTCAGT 900
TTACCGTGGC CAAAGAAAC ACCCTCCAGT TCACTGGGCT GGAGTTTTC ACTGGGGTGG 960
GTATTATTAG GGACACAGTG ATGTACTATG GCITTTACAC CAATTCACAC ATCCAGCACG 1020
GGAACAGCGG GGCATCTTAC AACATGCAGC TGGGCTACAT CTTCACAATC GGAGCATGCT 1080
TGACCACTGT CTCTCTCACT TTGCTGTTCA GCATGGCCAA GTATTTCGGG AACAACITCA 1140
TTAATCCCA CATTTACTCC GGAGGGATCA CCAAGCTGAT CTTTGTCTGG GACTTCACTG 1200
TCACTCATGA AAAGAGCTGT AAGCTAAAC AGAAGAACT TAGCACTGAG ATAAGGGAGA 1260
ACCTGTGAGA GCTCGGTGAG GAGAATTCCA AGTTGAGCT CAATCAGCTG CTGACCCGCT 1320
TCTCTGCTTA CATGGTAGCC TGGGTGTCT CTACAGGAGT GGCCATAGCC TGCTGTGCAG 1380
CGGTGCTATT CTTGGCTGAG TACAACITAG AGTTCTGAA GACACACAGT AACCTGGGG 1440
CGGTGCTGTT ACTGCTTTC GTTGTGCTCT GCATTAATCT GGCCGTGCCA TGCACTTACT 1500
CCATGTTTCA GCTTGTGGAG AGGTACGAGA TGCCACGGCA CGAAGTCTAC GTTCTCTCTGA 1560

```

TCCGAAACAT CTTTTGAAA ATATCAATCA TTGGCATTCT TTGTTACTAT TGGCTCAACA 1620  
 CGTGGCCCT GTCTGGTGAA GAGTGTGGG AAACCCCTCAT TGGCCAGGAC ATCTACCGGC 1680  
 TCCTTCTGAT GGATTTTGTG TTCTCTTTAG TCAATTCCTT CCTGGGGGAG TTTCTGAGGA 1740  
 GAATCATTTG GATGCAACTG ATCACAAGTC TTGGCCCTTCA GGAGTTTGAC ATTGCCAGGA 1800  
 ACGTTCTAGA ACTGATCTAT GCACAAATC TTGGTGTGGAT TGGCATCTTC TTCTGCCCCC 1860  
 TGCTGCCCTT TATCCAAATG ATTATGCTTT TCATCATGTT CTACTCCAAA AATATCAGCC 1920  
 TGATGATGAA TTCCAGCCT CCGAGCAAAG CCTGGCGGGC CTCACAGATG ATGACTTTCT 1980  
 TCATCTTCTT GCTCTTTTTC CCATCCTTCA CCGGGGTCTT GTGCACCTG GCCATCACCA 2040  
 TCTGGAGATT GAAGCCTTCA GCTGACTGTG GCCCTTTTCG AGGTCTGCCT CTCTTCATT 2100  
 ACTCCATCTA CAGCTGGATC GACACCTTAA GTACAOCGCC TGGCTACCTG TGGGTTGTTT 2160  
 GGATCTATCG GAACCTCATT GGAAGTGTGC ACTTCTTTT CATCTCACC CTCATTGTGC 2220  
 TAATCATCAC CTATCTTTAC TGGCAGATCA CAGAGGGAAG GAAGATTATG ATAAGGCTGC 2280  
 TCCATGAGCA GATCATTAAAT GAGGGCAAAG ATAAAAATGTT CCTGATAGAA AAATTGATCA 2340  
 AGCTGCAGGA TATGGAGAAG AAAGCAAACC CCAGCTCATT TGTCTGGAA AGGAGAGAGG 2400  
 TGGAGCAATA AGGCTTTTTC CATTTGGGGG AACATGATGG CAGTCTTGAC TTGGATCTA 2460  
 GAAGATCAGT TCAGAAGGT AATCCAAGGG CCTGATGACT CTTTGTGTAA CCAGACACCA 2520  
 ATCAATAAG GGGAGAGAGY GAAATGGAA TGATTCTTC CATGCCACT GTGCCCTTAG 2580  
 GAACTGCCCA GAAGAAAATC CAAGGCTTTA GCCAGGAGCG GAACTGACT ACCATGTAAT 2640  
 TATCAAGTA AAATTTGGCA TTCCATGCTA TTTTAAATAC CTGGATTGCT GATTTTTCAA 2700  
 GACAAATAC TTGGGGTTT CCAATAAAGA TTGTGTAAAT ATTGAANRA RMMWAMAAA 2760  
 ACCTAGGAAG AGATAACTAG GGAATAATGT ATATTATCTT CAAGAAGTGT GTGCAGGAAT 2820  
 GATTGTTCT TAGAAATCTC TCCTGCCAGA CTCCACAGAC CTGCCAAGG TTTAGAAAT 2880  
 GTTGCTAAGA AAAGTGGTCC ATCCTGAATA AACATGTAAT ACTCCAGCAG GGATATGAAG 2940  
 CCTCTGAATT GTAGAACCTG CATTTATTTC TGACTTTGAA CTAAAGACAT CCCCCATGTC 3000  
 CCAAGGTGG AATACAAACA GAGGTCTCAT CTCTGAACCT TCTTGCCTAC TGATTACATG 3060  
 AGTCTTTGGA GTGCGGGATG GAGGAGGTTT TGCCCTGTG AGGTGTTATA CATGACCATC 3120  
 AAAGTCTTAC GTCAAGCTAG CTTTGCAGTG GCATGACCGT AGCCAATGAG ATTTATCCGA 3180  
 GACGCGATTA TTGCTAATTG GAAATTTTCC CAATACCCCA CCGTGTATGAC TTGAAATATA 3240  
 ATCAGCGCTG GCAATTTTTC ACAGTCTCTA CCGAGACTGA ATAAG 3285

Seq ID NO: C205 DNA Sequence  
 Nucleic Acid Accession #: NM\_002250.1  
 Coding sequence: 397..1680

1 11 21 31 41 51  
 GTCTTGGGT GTCTGGGTGT GGTGAGTAGA GGTGTGTGTC ACAAGTACA GACCATTGTG 60  
 TGTGACAAAG CCCATCTGTG GTCTGTGTGT GTCTTTATCC ACGTGGATGG ACGTCTCTTT 120  
 CTGCTCTGCG CCCAAGACAC ACCCTAGCCC CTCTTTATTC TCAAAGGGG GAGCTGGGGA 180  
 GCTCTCCCCC ACCCTGGGGC CTCCCCTGCC CCTCCCCGCC CTGCGTGCCG GTCAACACTC 240  
 CCCAGAGGGC ACAGGGCTCT GCTGTGCTTC AGAGCAAAG TCCCAGAGCC AGCAGAGCAG 300  
 GCTGACGACC TGCAAGCCAC AGTGGCTGCC CTGTGCTGTC TGCGAGGTGG GGGACCTGG 360  
 GCAGGAAGCT GGCTGAGCCC CAAGACCCCG GGGGCCATGG GCGGGATCT GGTGCTTGGC 420  
 CTGGGGCCCT TGAGACGCCG AAAGCGCTTG CTGAGCAGG AGAAGTCTCT GGCCTGGTGG 480  
 GCACGTGTGC TGGCAGGAAC TGGCATTGGA CTGATGGTGC TGATGACAGA GATGCTGTGG 540  
 TTGCGGGGGT GCTGTGGGGC GCTCTACCTG TTCTGTGTTA AATGACAGAT CAGCATTTC 600  
 ACCCTCTTAC TCCTCTGCTT CATCGTGGCC TTTCATGCCA AAGAGGTCCA GCTGTTCTAG 660  
 ACCGACAACG GGCTGCGGGA CTGGCGGCTG GCGCTGACCG GCGGCGAGCG GCGCGAGATC 720  
 GTGCTGGAGC TGGTGGTGTG TGGGCTGCAC CCGGCGCCCG TGCGGGGCCG GCGTGGCTG 780  
 CAGGATTTAG GGGCGCGGCT GACCTCCCGC CAGCCCTGGC CGGGATTCTT GGGCCAAGGG 840  
 GAAGCGCTGC TGTCCTGGC CATGCTGCTG CGTCTTACC TGGTGCCCCG CGCGGTGCTC 900  
 CTGCGCAGCG GCGTCTGCT CAACGCTTCC TACCGCAGCA TCGCGCTCT CAATCAAGTC 960  
 CGCTTCCGCC ACTGTTTCTG GGCAGGCTT TACATGAACA CGCACCTTGG CCGCTGCTG 1020  
 CTGCGCTTCA CGCTTGGCTT CTGCTGACCC ACCGCTGGG TGCTGTCCGT GGCAGAGAG 1080  
 CAGGCTGTTA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATT 1140  
 CTGACCATCG GCTATGGTGA CGTGGTCCCG GGCACCATGT GGGGCAAGAT CGTCTGCTG 1200  
 TGCATGGAG TCATGGGTGT CTGCTGCACA GCGCTGCTG TGGCGTGGT GGCCTGGAG 1260  
 CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACTTCA TGATGGATAT CCAGTATACC 1320  
 AAAGAGATGA AGGAGTCCCG TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 1380  
 ACTCGCAGGA AGGAGTCTCA TGCTGCCCGC AGGCATCAGC GCAAGCTGCT GGCCTGCCAT 1440  
 AACGGTTTCC GCCAGGTGCG GCTGAACAC CGGAAGCTCC GGAACAAGT GAACTCCATG 1500  
 GTGGACATCT CCAAGATGCA CATGATCTG TATGACCTGC AGCAGATCT GAGCAGCTCA 1560  
 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CCTGACTGAG 1620  
 CTGCTTAGCA CTGCCCTGGG GCGGAGGAGC CTTCAGAAC CCAGCCAGCA GTCCAAAGTAG 1680  
 CTGGAACCCAC GAGGAGGAAC CAGGCTACTT TCCCAGTAC TGAGGTGGTG GACATCGTCT 1740  
 CTGCCACTCC TGACCCAGCC CTGAACAAAG CACCTCAAGT GCAAGGACCA AAGGGGGCCC 1800  
 TGGCTTGAGT TGGGTTGGCT TGCTGATGGC TGCTGGAGGG GACGCTGGCT AAAGTGGGTA 1860  
 GGCCTTGGCC CACCTGAGGC CCCAGGTGGG AACATGGTCA CCCCCTCTCT GCATACCTCT 1920  
 ATCAAAAACA CTCTCACTAT GCTGCTATGG ACGACCTCCA GCTCTCAGTT ACAAGTGCAG 1980  
 GCGACTGGAG GCAGGACTCC TGGGTCCCTG GGAAGAGAGG TACTAGGGGC CCGGATCCAG 2040  
 GATTCTGGGA GGCTTCAGTT ACCGCTGGCC GAGCTGAAGA ACTGGGTATG AGGCTGGGGC 2100  
 GGGCTGGAG GTGGCGCCC CTGGTGGGAC AACAAAGAGG ACACCATTTT TCCAGAGCTG 2160  
 CAGAGAGCAC CTGGTGGGGA GGAAGAAGTG TAACCTACCA GCCTCTGCTC TTATCTTTGT 2220  
 AATAAATGTT AAAGCCAG 2238

Seq ID NO: C206 DNA Sequence  
 Nucleic Acid Accession #: NM\_025257.1  
 Coding sequence: 1..2139

1 11 21 31 41 51  
 ATGGGGGGAA AGCAGCGGGA CGAGGATGAC GAGGCCTACG GGAAGCCAGT CAAATACGAC 60  
 CCTCTCTTTC GAGGCCCAT CAAGAACAGA AGCTGCACAG ATGTCATCTG CTGCGTCTCT 120  
 TTCTGCTCTC TCATTCTAGG TTACATGTGT GTGGGGATTG TGGCCTGGTT GTATGGAGAC 180

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

CCCCGGCAAG TCCTCTACCC CAGGAAGTCT ACTGGGGCCT ACTGTGGCAT GGGGGAGAAC 240  
AAAGATAAGC CGTATCTCCT GTACTTCAAC ATCTTCAGCT GCATCCTGTC CAGCAACATC 300  
ATCTCAGTTG CTGAGAACGG CCTACAGTGC CCCACACCCC AGGTGTGTGT GTCTCTCTGC 360  
COGGAGGACC CATGGACTGT GGGAAAAAAC GAGTTCTCAC AGACTGTGG GGAAGTCTTC 420  
TATACAAAAA ACAGGAACCT TTGTCTGCCA GGGGTACCCCT GGAATATGAC GGTGATCACA 480  
AGCCTGCAAC AGGAAGTCTG CCCCAGTTTC CTCTCCCTCT CTGCTCCAGC TCTGGGACGC 540  
TGCTTTCCAT GGACCAACAT TACTCCACCG GCGCTCCAG GATCACCAC TGACACCACC 600  
ATACAGCAGG GATCAGCGG TCTTATTGAC AGCCTCAATG CCCGAGACAT CAGTGTAAAG 660  
ATCTTTGAAG ATTTTGCCCA GTCTGTGTAT TGGATTCTTG TTGCCCTGGG GGTGCTCTG 720  
GTCTTGAGCC TACTGTTTAT CTGCTTCTG CGCTGTGTGG CTGGGCCCTT GGTGCTGGTG 780  
CTGATCCTGG GAGTGTCTGG CGTGTGGCA TATGGCATCT ACTACTGCTG GGAGGAGTAC 840  
CGAGTGTGTC GGGACAAGGG CGCTCCATC TCCAGCTGG GTTTCACCAC CAACCTCAGT 900  
GCCTACCAGA GGTGACAGGA GACCTGGCTG GCGGCCCTGA TCGTGTGGC GGTGCTGAA 960  
GCCATCTGTC TGCTGGTGT CATCTTCTG CGGCAGCGGA TTGATATTGC CATGCCCTCT 1020  
CTGAAGGAGG CAGTGTGCTT TGTGGGACAG ATGATGTCTA CCATGTTCTA CCCACTGGTC 1080  
ACCTTTGTCC TCCTCTCTAT CTGCATTGCC TACTGGGCCA TGACTGCTCT GTATCTCTG 1140  
CCCACGACG CAGCCACTCT TGGATATGTG CTCTGGGCAT CCAACATCAG CTCGCCCGGC 1200  
TGTGAGAAAG TGCAATATAA TACATCATGC AACCCACCG CCCACCTGT GAACTCTCG 1260  
TGCCAGGGG TGATGTGGT CTTCAGGGG TACTCATCCA AAGCCCTAAT CCAACGTCT 1320  
GTCTTCAATC TCGAATCTA TGGGGTCTG GGGCTCTCT GAGCCCTTAA CTGGGTACTG 1380  
GCCCTGGGCC AATGCGTCTT CGCTGGAGCC TTTGCTCTCT TCTACTGGGC CTTCACCAAG 1440  
CCCAGGACA TCCTTACCTT CCCCTTAATC TCTGCTTCA TCCGCACACT CCGTTACCAC 1500  
ACTGGGTGAT TGGCATTTGG AGCCCTCATC CTGACCTTG TGCAGATAGC CCGGGTCATC 1560  
TTGGAGTATA TTGACACCAA GCTCAGAGGA GTGCAGAAC CTGTAGCCCG CTGCATCATG 1620  
TGCTGTTTCA AGTGTGCTT CTGGTGTCTG GAAAAATTTA TCAAGTTCTT AAACCGCAAT 1680  
GCATACATCA TGATCGCCAT CTACGGGAAG AATTTCTGTG TCTCAGCCAA AATGCGTTC 1740  
ATGCTACTCA TGGCAACATC TGTGAGGGT GTGCTCTGG ACAAGTCAAC AGACCTGCTG 1800  
CTGTTCTTTG GGAAGCTGCT GGTGGTCGGA GCGGTGGGG TCCTGTCTCT CTTTTTTTTC 1860  
TCCGGTCGCA TCCCGGGGCT GGGTAAAGAC TTTAAGAGCC CCCACCTCAA CTATTACTGG 1920  
CTGCCCATCA TGACCTTCAT CTTGGGGGCC TATGTATCG CCAGCGGCTT CTTCAGGCTT 1980  
TTGGCATGT GTGTGGACAC GCTCTTCTC TGCTCTCTG AAGACCTGGA GCGGAACAAC 2040  
GGCTCCTGG ACCGGCCCTA CTACATGTCC AAGAGCCTTC TAAAGATTCT GGGCAGAAG 2100  
AACGAGGCGC CCCGAGACAA CAAGAAGAGG AAGAAGTGAC AGTCCCGGCC CTGATCCAGG 2160  
ACTGACCCCC ACCCCACCG TCCAGCCATC CAACCTCACT TCGCTTACA GGTCTCCATT 2220  
TTGTGTTTAA AAAAGTCTT AGGCCAGCG CCGTGGCTCA GCCTGTAAAT CCAACACTTT 2280  
GAGAGGCTGA GCGGGCGGA TCACCTGAGT CAGGAGTTCG AGACCAGCCT GGCCACACATG 2340  
GTGAAC 2347

Seq ID NO: C207 DNA Sequence  
Nucleic Acid Accession #: NM\_016180.1  
Coding sequence: 26..1618

1 11 21 31 41 51  
45  
50  
55  
60  
65  
70  
75  
80

CAGGAAGGTT CCTCTCCAG TGGCCATGGG TAGCAACAGT GGGCAGGCTG GCCGCCACAT 60  
CTATAAATCC CTAGCTGATG ATGGCCCTT TGACTCTGTG GAGCCGCTTA AAAGACCCAC 120  
CAGCAGACTC ATCATGCACA GCATGGCCAT GTTCGGAAGA GAGTTCTGCT ACGCGGTGGA 180  
GGCAGCGTAT GTGACCCGAG TCCTGCTCAG CGTAGTCTG CCCAGCAGCC TGTACAGCAT 240  
TGTGTGGTTC CTCAGCCCCA TCCTGGGATT CTGCTGCAG CCGTGGTTCG GATCGGCCAG 300  
CGACCACTGC CGGTCCAGGT GGGGCCGCGG GAGACCTTAC ATCTTCACCC TGGGAGTCA 360  
GATGCTCGTG GGCATGGCTC TGTACCTCAA TGGGCTACT GTGTAGCAG CTTTGATTGC 420  
TAACCCAGG AGGAAGCTGG TTTGGGCCAT AAGTGTCAAC ATGATAGGTG TCGTCTCTT 480  
TGATTTGCT GCCGACTTCA TTGATGGGCC CATCAAAGCC TACTTATTTG ATGCTGTCTC 540  
CCATCAGGAC AAGGAAGAAG GCCTCCACTA CCATGCCCTC TTCACAGGTT TTGAGGTTGC 600  
CTGGGTTTAC CTTTGGGTG CTATAGACTG GGCCCATCTG GAGCTGGGAA GACTGTTGGG 660  
TACAGAATTC CAGGTCAATG TCTTCTCTC TGCAITGGTG CTCACCTTGT GTTTTACTGT 720  
TCATCTGTGC AGTATCTCTG AAGCCCCACT TACAGAGGTT GCAAAGGGCA TTCCCCACA 780  
GCAAAACCCCT CAGGACCTC CATTTGTATC AGATGGAATG TACGAGTATG GTTCTATCGA 840  
GAAAGTTTAA AATGTTTACG TAAATCCAGA GCTGGCAATG CAGGGAGCAA AAAACAAAAA 900  
TCATGTGAA CAGACTCGCA GGGCAATGAC ATTAAAGTCA CTGCTGAGAG CACTGTGTAA 960  
CATGCTCCT CACTACCGCT ACCTTTGCAT CAGCCACCTC ATTGATGGA CGGCCTTCT 1020  
GTCCACATG CTGTTCTTCA CAGATTTTAT GGGCCAGATT GTGTACCGG GGGATCCCTA 1080  
TAGTGCACAC AACTCCACAG AGTTTCTCAT CTACGAAAGA GGAGTGGAGG TTGATGTTG 1140  
GGGCTTCTGC ATCAACTCAG TGTTTTCTC ACTTTATCT TACTTTCAGA AAGTTTGGT 1200  
ATCTTACATT GGATTAAGG GTCTTTACTT CACGGGATAT TTGCTGTTTG GCCTGGGAC 1260  
GGGATTATT GGGCTCTTCC CGAATGTCTA CTCACCTGTC GTCTGTGCA GCCTGTTGG 1320  
TGTAATGTCC AGCACCTGT ACCTGTGCC CTTTAACTC ATTACTGAGT ACCACGCGA 1380  
GGAAGAAAG GAGAGGACG AGGCCCCAGG AGGGGACCCA GACACAGCG TGAGAGGGA 1440  
GGGATGGAC TGGGCCACCC TCATATGCAT GGTGAGCTG GCTCAGATCC TGGTGGAGG 1500  
TGGCTGGGC TTTTGTGTCA ACACAGCCGG GACCGTTGTC GTGCTGGTGA TCACAGGTC 1560  
TGCGTGGCA CTGATAGGT GTTGTCTTGT CGCTCTCTT GTTAGATATG TGGATTAGGT 1620  
CAATAAGAG ACAATGACCC TAAAAA 1650

Seq ID NO: C208 DNA Sequence  
Nucleic Acid Accession #: NM\_003273.1  
Coding sequence: 255..2024

1 11 21 31 41 51  
80

CGCCGCGGG CGGATCCTC CGCGCGGCC AGTCCATCTC CTGGAAATG GGGCGACAG 60  
TGTTTCTTGG ACTGACTATT GTGAGCGCCC TCTCTCTCG GCGGAGCGGA GACCATGCCC 120  
CCCACTCAG CCCCAGGGCC CGCTGGAAT TCGAGGGCC CCGGTAAAT GGGCAGAGA 180  
GATGGGACCT GGGCAAAAG CTAAGCGAAG GAGAGCTGA GCGGTGAAC TAAGACGGG 240  
GGGAGATCT GAGGATGGA GGCCTTGGG GTGTGGAGG CAGAGGGACC CCGGGTTTG 300

5  
10  
15  
20  
25  
30

```

CAGCGAAGGG TGTCTGGAGA GGGAGAGCTG AGGAGGGGGC GGTTCCTGGG GCTGCAGAAC 360
GGGGATTAT GGTGTGCACT GGGAGCAGGA GGAGGGTCTT CGAGGGGCGT GGGGGCGGGG 420
GACTAAGATG GACGCTGGG AAGGGAACCT GGAGGCAGCG GGGTGCCTGG GGGCCGAGGG 480
CTGAGGACGG GGTGCGGAGG CGCACTCTGG GAATGCCGAG AGGGTCCCGC AGAGACGTCA 540
GGGCGCGGTG CGGGCCGGCG GGGAGCTGGG GGGCTAGGGG CGGACGCCGA CGTGATGGCC 600
CTTCCGCGAG GCGCGCGGCG TGTGCTACTG CTGCTGCCCG CCACCATGTT CCACCTGCTC 660
CTGGCGGCCC GTTCGGGCCC CGCGCGCTCG CTGGTCCAC CGCGTCCCT GCCCGGGCTG 720
GAGGTGCTGT GGAGCCCAAG GCGCTGCTCG CTGTGGCTCG CCTGGCTCGG CCTGCAGGCG 780
GGGCTCTACC TACTGCCGCG GGCAGAGGTG CGGGCCCCCG TCGCGGACGC TCGGGGGAGG 840
GAAGCGAATG GGTGCGGCGA GGGAAAGGAC GCCCGGGGCC TTATCAGAGC CCCCTTGAC 900
CCGCACTGGC CGAGGGGCGA GAATTGAAGG ACAAGAGTCG CTTGCGCTAT CCTATTAAAG 960
GCTTCCAGGC CCTGTGCTG ACAGCCCTGT TGGTGGGGCT GGGGATGTCA GCGGGGCTGC 1020
CTCTGGGGGG GCTCCCGGAA ATGCTCTCG CTCTGGCGTT TGTGCCACCC CTCACGCTTT 1080
TCATCTTCAG CCTCTTCTC TACATGAAGG CGCAGGTAGC CCCAGTTTCG GCCCTGGCAC 1140
CTGGGGGAA CTGGGTGCCC CGGATTACG ACTTTTCTT GGGACGAGAG CTCACCCCTC 1200
GTATCTGTTT CTTCGACTTC AATATTCTT GTGAAGTGGC ACCCGGCTC ATCGGCTGGG 1260
TCCTCATCAA CTGGCCCTG TTGATGAAGG AGGCAGAGCT TCGAGGCACT CCTCACTGG 1320
CCATGTGGCT GGTCAATGGC TTCCAGTTGC TCTACGTGGG TGATGCCCTC TGGCAGGAGG 1380
AGGCGTCTCT CACCAACATG GATATCACAC ATGACGGGTT TGGCTTCATG CTGGCGTTTG 1440
GGGACATGGC CTGGGTGCCC TTCACTACA GCCTGCAGGC CCAGTTCTCG CTGCACCACC 1500
CGCAGCCCTT GGGGTGCCCC ATGGCTCTG TCATCTGCTT CATCAATGCT ACTGTTACT 1560
ACATCTTCG TGGGCGCAAT TCCAGAAAA ACCTTTCCG AAGAATCTT TCTGACCCCA 1620
GAGTGGCTGG GCTTGAGACC ATCTCTACAG CCACAGGGCG GAAACTGCTG GTGTCTGGGT 1680
GGTGGGGTAT GGTCCGCCAT CCCAACTATC TTGGAGACCT CATCATGGCT CTGGCTTGGT 1740
CCTTCCCTG CGGGGTGTC CACTGCTGC CTTACTTCTA CCTCCTCTAC TTCACCGCGC 1800
TGCTGGTGCA CCGTGAGGCC CGGATGAGC GGAGTGCCTG CAGAAGTACG GCCTGGCCTG 1860
GCAGGAGTAC TGCCGGCGTG TGCCCTTACG CATCATGCCC TACATCTACT GAAGCGGCTC 1920
CACCAACCCG GTGGGGGATC GTGCCCACTC ATCCACCAGC ACACCCAGGA CCAGGAGCCT 1980
CGACACACTT GGGACTCAAG GGTTCGACC CCACCCAGCC CTGAGGATGA ACAACCTCAG 2040
AGAAGAGGTG GTTAGAGCA AGGAAAAAAA TGAAACCACT GACCAAAAAA AAAAAAAA 2100

```

Seq ID NO: C209 DNA Sequence  
Nucleic Acid Accession #: NM\_015720.1  
Coding sequence: 21..1838

35  
40  
45  
50  
55  
60  
65  
70  
75

```

1 11 21 31 41 51
| | | | |
CCAGTTCGGC CACGAGGACC ATGGGCGGCG TGCTGCGGGC CGCCCGGCTG CGCCCGCTGC 60
TTTCGCGCGT GCTGCTTCTG CTGGTTGGGG GAGCGTTCCT GGGTGCCTGT GTGGCTGGGT 120
CTGATGAGCC TGGCCAGAGG GGCCTCACTT CCACCTCCCT GCTAGACCTC CTGCTGCCCA 180
CTGGCTTGA GGCATGAGC TCAGAGGAGC CTAGTGAGAC CATGGGCTG GAGCTGGGCG 240
TGGGAGCCCC TGGCTCAGGC TTCCCAAGCG AAGAGAAATG AGAGTCTCG ATTCTGCAGC 300
CACCAAGTA CTTCTGGGAA GAGGAGGAAG AGCTGAATGA CTCAGTCTG GACCTGGGAC 360
CCACTGCAGA TTATGTTTTT CTTGACTTAA CTGAGAGGCG AGGTTCCTAT GAAGACACTA 420
GCCAGGCTCA AGAGCTGCCA AACCTCCCTT CTCCCTTGCC CAAGATGAAT CTGGTTGAGC 480
CTCCCTGGCA TATGCTCCCG AGAGAGGAGG AAGAGAGGGA AGAGGAAGAG GAGGAGAGGG 540
AGAGAGGAAG GGTAGAGAAA CAAGAGGAGG AGGAAGAGGA GGAGCTGCTC CTTGTGAATG 600
GATCCCAAGA AGAAGCCAGG CCTCAGGTCC GTGACTTTTC TCTCACCAGC AGCAGCCAGA 660
CCCCAGGGCG CACCAAAAGC AGGCATGAAG ACTCCGGGGA CCAGGCTCA TCAGGTGTGG 720
AGGTGGAGAG CAGCATGGGG CCAGCTTGGC TGCTGCTTTC AGTCACCCCA ACTACAGTGA 780
CTCCGGGGGA CCAGGATCC ACCAGCCAAG AGGCAGAGGC CACAGTGTG CCAGCTGCAG 840
GGCTTGGGGT AGAGTTCGAG GCTCCTCAGG AAGCAAGCGA GGAAGCCACT GCAGGAGCAG 900
CTGGTTTGTG TGGCCAGCAC GAGGAGGTGC CGGCTTGCC TTCATTCCCT CAAACCACAG 960
CTCCAGTGG GGGCGAGCAC CCAGATGAAG ATCCCTTGG CTCTAGAACC TCAGCTCTTT 1020
CCCCACTGGC CCTTGAGAG ATGGAACCTGA CACCTTCTCT TGCTACCTTG GGACAGAAG 1080
ATCTCAACCA CGAGCTCCTA GAAGGCGAGG CAGCTGAAGC TCAATCCAGG ATACCTGGG 1140
ATTCTAGCA GGTGATCTGC AAGGACTGGA GCAATCTGGC TGGGAAAAAC TACATCTTC 1200
TGAACATGAC AGAGAACATA GACTGTGAGG TGTTCCGCA CCACCGGGG CCACAGCTCC 1260
TGGCCCTGGT GGAAGAGGTG CTGCCCCGCC ATGGCAGTGG CCACCATGGG GCCTGGCACA 1320
TCTCTCTGAG CAAGCCAGC GAGAAGGAGC AGCACCTTCT CATGACACTG GTGGGGGAGC 1380
AGGGGGTGGT GCCCACTCAA GATGTCTTTT CCAATGCTGG TGACATCCCG AGGAGCCTGG 1440
AGGAGATTGG CATCCAGAAC TATTCACAA CCAGCAGCTG CCAGGCGCG GCGAGCCAGG 1500
TGCGCAGCGA CTACGGCAGC CTCTCGTGG TGCTGGTGGT CATTGGGGCC ATCTGCATCA 1560
TCATCATGCG GCTTGGCCTG CTCTAACAAT GCTGGCAGCG CGGCTGCCCC AAGCTCAAGC 1620
ACGTGTGCGA CGGCGAGGAG CTGCGCTTGG TGGAGAACGG CTGCCACGAC AACCCACGCG 1680
TGGAGTGGC CAGCGACAGC CAGTCGAGA TGCAGGAGAA GCACCCGAGC CTGAACGGCG 1740
GCGGGGCCCT CAAAGCGCGG GGGAGCTGGG GGGCGCTCAT GGGGGGCAAG GGGGACCCCG 1800
AGGACTCGGA CGTGTTCGAG GAGGACAGCG ACCTGTGAGC GCAGCGAGGC GCAGGCGGAG 1860
TGGGCGGCGA GGACCAAGCG AGGTGAGACC CGAAACGGAC GGGCGGAGC CCGCACCCAGC 1920
CCCGCGCTCA CCGGCGCGCC CCGCGGCTG GCGCTGGGG CGGCTCTCTT CCGCTTCTCC 1980
CGCACTTCA CCGGCGGCTT CGGACCAACT CCTCACTCC CGCCCGAGGG GCAGGCTCA 2040
AAGCCCGCT TGGCCCGCTT TTCCCGCCCC TGAACCCCG CCGCGCGGCG GCGGGGCGCG 2100
CTTCTGTGGC CCGGGGATC AATTAAACCC GCGCGGAGAC CAGCGGGGCC CAGCGAAAAA 2160
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2220
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2269

```

Seq ID NO: C210 DNA Sequence  
Nucleic Acid Accession #: NM\_001197.3  
Coding sequence: 61..543

80

```

1 11 21 31 41 51
| | | | |
GACACGAAGC CTCCCGGGTG GCTTACAGAC GCTGCCAGCA TCGCCGCGCG CAGAGGAGAA 60
ATGTCTGAAG TAAGACCCCT CTCCAGAGAC ATCTTGATGG AGACCTCTCT GTATGAGCAG 120

```



5 CTCTGGAAC CCCGACCAT GGAGTTCTT GGCATGACTG ACTCTGAAGA GGACCTGGAC 180  
 CCTATGGAGG ACTTCGATT TTTGGAATGC ATGGAGGGCA GTGACGCATT GGCCCTGCGG 240  
 CTGGCCCTGCA TCGGGACGA GATGGACGTG AGCCTCAGGG CCCCGCGCCT GGCCAGCTC 300  
 TCCGAGGTGG CCATGCACAG CTTGGGTCTG GCTTTCATCT ACGACCAGAC TGAGGACATC 360  
 AGGGATGTTC TTAGAGTTT CATGGACGGT TTCACCACAC TTAAGGAGAA CATAATGAGG 420  
 TTCTGGAGAT CCCGAACCC CGGTCCTGG GTGTCTGCG AACAGGTGCT GCTGGCGCTG 480  
 CTGCTGCTGC TGGCGTCTG GTCGCGCTG CTCAGCGGGG GCCTGCACCT GCTGCTCAAG 540  
 TGAGGCCCGG GCGGCTCAGG GCGGGGCTGG CCCACCCCC ATGACCACTG CCCTGGAGGT 600  
 10 GGCGGCTGCT TGCTGTATAT TTTTAACTG TTTTCTCATG ATGCTTTT ATATTAAAC 660  
 CCGAGATAG TGCTGGAAACA CTGCTGAGGT TTTATACTCA GGTTTTGTG TTTTITTTA 720  
 TTCCAGTTTT CGTTTTTCT AAAAGATGAA TTCTATGTC TCTGCAATTG TCACCGGTTA 780  
 ACTGTGGCT GTGCCAGGA AGAGCCATTC ACTCTGCCC CTGCCACAC GGCAGGTAGC 840  
 AGGGGAGTG CTGGTCACAC CCTGTGTGA TATGTGATGC CCTCGCAA GAATCTACTG 900  
 15 GAATAGATTC CGAGGAGCAG GAGTGCTCAA TAAATGTG GTTCCAGCA AAAAAA 960  
 AAA 963

Seq ID NO: C211 DNA Sequence  
 Nucleic Acid Accession #: AF272357  
 Coding sequence: 83..1060

20 1 11 21 31 41 51  
 25 GCTGCTCCCG ACGCGGAGCC CGGAGCCCGC GCGGAGCCCC TGGCCTCGCG GTGCCATGCT 60  
 GCGCCGCGCG CGGCGCTGAA GGATGGCGAC GCGGCTGCGT CGGCCCTCCC CGCGGCACCT 120  
 GCGGCTGCTG CGGCTGCTGC TCTCCGCGCT GGTCTCTGCG GCGGCGCTGC GTGGAGCCGC 180  
 GCGCGGCCAC CCGGATGTAG CCGCTGTGCC CGGAGGCTGG GACTGTGCCC TGAAGAGGCG 240  
 GGCAAGGTGT CTTCTGTGTG CACATGCTGT TGGGCGCTGC CTTGAGCCCT TCCAGGAGGA 300  
 CCAGCAAGGG CTCGTGTGTC CCAGGATGCG CCGGCTTCCA GCGGGGGGCC GGCCCCAGCC 360  
 30 CAGACTGGAA GATGAGATTG ACTTCCTGGC CCAGGAGCTT GCGCGGAAGG AGTCTGGACA 420  
 ATCAACTCCG CCGCTACCCA AGGACCGACA GCGGCTCCCG GAGCCTGCCA CCTGGGCTT 480  
 CTGGCACCGG GGGCAGGGGG TGGAGCTGGG CCTCCCTTCC ACTCCAGGAA CCCCCACGCC 540  
 CACGCCCCAC ACCTCCCTGG GCTCCCTGTG GTCATCCGAC CCGGTGCACA TGTGCGCCCT 600  
 GGAGCCCGCG GGAGGGCAAG GCGACGGCCT CGCCCTTGTG CTGATCCTGG CGTCTGTGT 660  
 GGCCGCTGCA GCGCCCTCTT CCGTAGCCTC CCTCTGTGG TGCAGGCTGC AGCGTGAGAT 720  
 35 CCGCCTGACT CAGAAGGCGG ACTACGCCAC TCGGAAGGCC CCTGGCTCAC CTGAGCTCC 780  
 CCGGATCTCG CTTGGGAGCC AGCGGCTGGC ACAGAGCGCG GAGATGTACC ACTACCAGCA 840  
 CCAACGCAAA CAGATGCTGT GCTGGAGCG GCATAAGAG CACCCCAAGG AGCTGGACAC 900  
 GGCCTCTCTG GATGAGGAGA ATGAGGACGG AGACTTTCAG GTGTACGAGT GCGCGGCGCT 960  
 40 GGCCCGGACC GGGGAAATGG AGGTGCGCAA CCTCTGTTC GACCCAGCGG CACTGTCCGC 1020  
 GCGCCCTGCC CCGCCAGCTC CACCGCCTGC ACTGCCATGA CCTGGAGGCA GACAGACGCG 1080  
 CACCTGTCTC CCGACCTCGA GCGCCCGCGG GAGGGGCGAG GCCTGGAGCT TCCCACTAAA 1140  
 AACATGTTTT GATGCTGTGT GCTTTTGGCT GCGCCTCGGG CTCAGGCGCC TGGGACCCCT 1200  
 TGCCAGGGAG ACCCCCGAAC CTTTGTGCCA GGACACCTCC TGGTCCCTCG CACTCTCCT 1260  
 45 GTTCGGTTTA GACCCCAAAA CTGGAGGGGG CATGGAGAAC CGTAGAGCGC AGGAACGGGT 1320  
 GGGTAATTCT AGAGACAAAA GCCAATTAAA GTCCATTCA GAAAAA 1371

Seq ID NO: C212 DNA Sequence  
 Nucleic Acid Accession #: NM\_004445.1  
 Coding sequence: 799..3819

50 1 11 21 31 41 51  
 55 CGGAGGGGGG GGGCCGGGCT GCGTTGCTCT CAGCCGCGGC TCTACAGCAG CGGGCGGCGG 60  
 GACCCGGGAC CCAGCTTGGC GACGGCGATT CTGACGCGG GCGCCAGGAA TTCTCCCGGC 120  
 GCGCCACCTC TGGAGCAGCC CCGCGCGCCA GCGTCAGGTC CACCCCGGAA TCCAGGGAC 180  
 TCTCGGCGCC GAACGACCCC GGGCGGCTGC AACGGGGTCC CCGGACTGGA GAAGACGCGG 240  
 GTGGCACCGT GCGAGCTCCA GGAGCCCGCG GTCCACTGCG AGGCTCTGGG GGGCGCAGAC 300  
 CTGCAGAGAC TGGCGCCAAC GGAAGAAAT AAAGGGATTA TAGTCCACCC AATTCACAGA 360  
 60 CTCTGAGAC TCAGACAGCA GGAGAGATAG AGAACCGCCA ATCTCTAGAT CAACAAGCAA 420  
 AGGAGGTGCC AAGCCTGTTT GTCTTCATTG TGACACTGGA GTCTAGATGC TGGGAAGTCC 480  
 AAGATCAGGG TGCCGGCATG GTCACTTCTT GCGGAAGCCT CTCTCTAGG TTTCAGACTG 540  
 CCCTCTTCTT TGTGTGTGCC TCGAATGGCA GAAAAAGGGG TGGCTGTGG AGGAAGGGAG 600  
 GAGAGTAART GAAGAGAAAG AACTGGAATA ACCCCTTGCA GAAAAA 660  
 65 CTAGCTGTA CACCCTGAGT CTTGCAAAAG CTGCAGCCCC ACCCAGGAGC AGGCTGTGTG 720  
 CTGGGGCGAT GGTGGACGCC CTGAAGATGT CCCATGGCTA CTGAAGGGGC TGCCAGTTA 780  
 GGGAACAGAG TGGCGGCAT GGTGTGTAGC CTATGGGTGC TGCTCCTGCT GTCTTCAGTT 840  
 CTGGCTTGG AAGAGGTATT GCTGGACACC ACGGAGAGA CATCTAGAT TGGCTGGCTC 900  
 ACCTACCCAC CAGGGGGGTG GGCAGAGGTG AGTGTCTGG ACGACAGCG ACGCTGACT 960  
 70 CGGACCTTGG AGGCATGTCA TGTGGCAGGG GCGCCCTCCAG GCACCGGGCA GGACAAATGG 1020  
 TTGCAGACAC ACTTTGTGGA GCGGCGCGGG GCGCAGAGGG CGCACATTGG ACTCCACTTC 1080  
 TCTGTGCGGG CATGCTCCAG CTTGGGTGTG AGCGGCGGCA CCGTCCGGGA GACCTTCACC 1140  
 CTTTACTACC GTACGGCTGA GGAGCCCGAC AGCCCTGACA GCGTTTCCTC CTGGCACCTC 1200  
 AAACGCTGGA CCAAGGTGGA CACAATTGCA GCAGACGAGA GCTTCCCTC CTCTCTCTCC 1260  
 75 TCCTCTCTCT CTCTCTCTCT TGACGCTGG GCTGTGGGAC CCCACGGGGC TGGGACGCGG 1320  
 GCTGAGCTGC AACTGAACGT CAAGAGCGCG AGCTTTGGGC CTCTCACCCA ACGCGGCTTC 1380  
 TACGTGGCTC TCCAGGACAC GGGGCGCTGC CTGGCCCTGG TCGCTGTGAG GCTCTCTCTC 1440  
 TAGACTGCC CTGCCGTGCT CCGATCCTTT GCTTCTTTTC CAGAGACGCA GGCCAGTGGG 1500  
 GCTGGGGGGG CCTCCCTGGT GGCAGCTGTG GGCACCTGTG TGGCTCATGC AGAGCCAGAG 1560  
 80 GAGGATGGAG TAGGGGGCCA GGCAGGAGGC AGCCCCCCCA GGCTGCACTG CAACGGGGAG 1620  
 GGCAAGTGA TGTAGCTGT CCGGGGCTGC CGCTGCCAGC CTGGATACCA ACCAGCAGA 1680  
 GGAGACAAAG CTGCCAAGC CTGCCACCG GGGCTCTATA AGTCTTCTGC TGGGAATGCT 1740  
 CCTGTCTCAC CATGCCCTGC CCGCAGTCAC GCTCCCAACC CAGCAGCCCC CGTTTGGCCC 1800  
 TGCCTGGAGG GCTTCTACCG GGCAGTTCCT GACCCACCG AGGCCCGCTG CACTGTCTCT 1860  
 CCATCGGCTC CCCAGGAGCT TTGGTTTGAG GTGCAAGGCT CAGCACTCAT GCTACACTGG 1920

5 CGCCTGCCTC GGGAGCTGGG GGGTOGAGGG GACCTGCTCT TCAATGTCGT GTGCAAGGAG 1980  
 TGTGAAGGCC GCCAGGAACC TGCCAGCGGT GGTGGGGGCA CTGTGCACCG CTGCAGGGAT 2040  
 GAGGTCCACT TCGACCCCTG CCAGAGAGGC CTGACTGAGA GCGAGTGTGT AGTGGGGGGA 2100  
 CTCGCGGCAC ACGTACCTTA CATCTTAGAG GTGCAGGCTG TTAATGGGGT GTCTGAGCTC 2160  
 AGCCCTGACC CTCTCTAGGC TGCAGCCATC AATGTGAGCA CCAGCCATGA AGTGCCTCT 2220  
 GCTGTCCCTG TGGTGACCA GGTGAGCCGG GCATCCAACA GCATCACCGT GTCTGGCCG 2280  
 CAGCCCGACC AGACCAATGG GAACATCTGT GACTATCAGC TCCGCTACTA TGACCAGGCA 2340  
 GAAGACGAAT CCCACTCTTT CACCCTGACC AGCGAGACCA ACACTGCCAC CGTGACACAG 2400  
 10 CTGAGCCCTG GCCACATCTA TGGTTTCCAG GTGCGGGGCC GGACTGTCTG CGGCCACGGC 2460  
 CCTTACGGGG GCAAGTCTA TTCCAGACA CTTCCTCAAG GGGAGCTGTG TTCCAGCTT 2520  
 CGGAAAGAC TCTCTTGGT GATCGGCTCC ATCCTGGGGG CTTTGGCCCT CCTCTGCTG 2580  
 GCAGCCATCA CCGTGTGGC GGTCTCTTC CAGCGGAAGC GCGTGGGAC TGGCTACAG 2640  
 GAGCAGCTGC AGCAATACAG CAGCCACGGA CTCGGGGTGA AGTATTACAT CGACCCCTCC 2700  
 15 ACCTACGAGG ACCCTGTGCA GGCATCCGA GAACCTGCCG GGAAGTCA TCTGTCTTAT 2760  
 ATCAAGATTG AGGAGTCTAT TGGGACAGGC TCTTTTGGAG AAGTGGGCA GGGCCGCTG 2820  
 CAGCCACGGG GACGAGGGA GCAGACTGTG GCCATCCAGG CCTGTGGGC CGGGGGCGCC 2880  
 GAAAGCCTGC AGATGACCTT CTTGGGCGCG GCGCAGTGC TGGGTCACTT CCAGCACCCC 2940  
 AACATCTGCG GGCTGAGGGG CGTGGTCAAC AAGAGCCGAC CCCTCATGCT GCTGACGGAG 3000  
 20 TTCTAGGAGC TTGGCCCCCT GGACAGCTTC CTCAGGCAGC GGGAGGGCCA GTTCAGCAGC 3060  
 TGGCAGCTGC TGGCATGCA GCGGGGAGTG GCTGCTGCCA TGCACTACCT GTCCAGCTTT 3120  
 GCCTTCGTCC ATCGCTCGCT GTCTGCCAC AGCGTGTCTG TGAATAGCCA CTTGGTGTGC 3180  
 AAGGTGGCCC GTCTTGGCCA CAGTCTCTAG GGCCTAAGTT GTTGTCTTG CTGGGACGCC 3240  
 CCAGAGGTCA TTGCACATGG AAAGCATAACA ACATCCAGTG ATGTCTGAG CTTTGGGATA 3300  
 25 CTCTATGTTG AAGTGTGAG TTATGGAGAA CGGCCTTACT GGGACATGAG TGAGCAGGAG 3360  
 GTAATAATG CAATAGAGCA GGAATTCCGG CTGCCCGCCG CTCAGGCTG TCCTCTGGA 3420  
 TTACTATCTA TTATGTGGA CACTTGGCAG AAGGACCGTG CCGGGCGGCC TCATTTTGAC 3480  
 CAGCTGTGGT GTCGATTTGA CAAGATGATC CGCAAGCCAG ATACCTTGCA GCTGGCGGG 3540  
 GACCCAGGGG AAAGGCTTTC CCAGGCCCTT CTGACCCCTG TGGCCCTGGA CTTTCTCTGT 3600  
 30 CTGGACTCAC CCCAGGCTTG GCTTTCAGCC ATTGGACTGG AGTGCTACCA GGAACAATTC 3660  
 TCCAAGTTTG GCCTCTGTAT CTTCACTGAT GTGGCTCAGC TCAGCCTAGA AGACTGCTT 3720  
 GCCTGGGCA TCACCTTGCG TGGCCACAG AAGAAGCTGC TGACCCACAT CCAGCTCCTT 3780  
 CAGCAACACC TGAGGACAGA GGGCTCAGTG GAGGTCTGAG AATGACGATA CCGGTGACTC 3840  
 AGCCCTGGAC ACTGGTCCGA GAAGGGACAT GTGGGACGTG AGCCGGGCTC CAACAGCCTC 3900  
 35 TGTGAGAGAT GCCCCACACC AAACCCAACC CTCCTGATGG CTGCATTCCT TGGTCTCTCC 3960  
 CCTCTCACCC AGCCCCCTCC TCATTAAAGG GAAAGAAGGG AATTGTCAAA 4010

Seq ID NO: C213 DNA Sequence  
 Nucleic Acid Accession #: XM\_043340.4  
 Coding sequence: 195..1067

40 1 11 21 31 41 51  
 GGGCGGGGCC CAATGGGCTG CGCGGAGCGT CACTTCCCGG CAGCGGGAGG CGAGTGGGGA 60  
 GTGCGGAGTG GCGAGTGCTA GGGGGGCGGC CGGCGGGGCG GGGCGGGCGG GAGGAGGGGT 120  
 45 TGGCAGCGGG CTCGAGCCCA CGCGGCGCGG CGGCGCGCCT GGCCTGCAAG GCTCCACACC 180  
 CCGGCGGCGG CAGGATGCCC TTGACTTCA GAGAGTTTGA CATCTACAGG AAGGTGCCCA 240  
 AGGACCTTAC GACGCCAAGG TACACGGGGG CCATTATCTC CATCTGCTGC TGCCTCTTCA 300  
 50 TCTCTTCTCT CTCTCTCTCG GAGCTCACCG GATTTATAAC GACAGAAGTT GTGAACGAGC 360  
 TCTATGTCGA TGAGCCAGAG AAGGACAGCG GTGGCAAGAT CGACGTCAGT CTGAACATCA 420  
 GTTTACCCAA TCTGCACTGC GAGTTGGTTG GGCTTGACAT TCAGGATGAG ATGGGCAGGC 480  
 ACGAAGTGGG CCACATCGAC AACTCCATGA AGATCCCGCT GAACAATGGG GCAGGCTGCC 540  
 GCTCTGAGGG GCAAGTTCAGC ATCAACAAGG TCCCGGCAAA CTTCCAAGTG TCACACACA 600  
 GTGCCACAGC CCAGCCACAG AACCCAGACA TGACGATGAT CATCCACAAG CTCTCTCTTG 660  
 55 GGGACAGCCT ACAGGCTCAG AACATCCACG GAGCTTTCAA TGCTCTCGGG GGAGCAGACA 720  
 GACTCACCTC CAACCCCTTG GCCTCCACG ACTACATCCT GAAGATTGTG CCCACGGTTT 780  
 ATGAGGACAA GAGTGGCAAG CAGCGGTACT CCTACCACTA CAGGTTGGCC AACAGGAAT 840  
 ACGTGGCGAA CAGCCACAGC GGCGGCATCA TCCCTGCAAT CTGGTTCCGG TAGACCTCA 900  
 GCGCCATCAC GGTCAAGTAC ACAGAGAGAC GGCAGCGCT GTACAGATTG ATCAACACGA 960  
 60 TCTGTGCCAT CATTGGCGGG ACCTTCACCG TCGCGGCGAT CCTGGACTCA TGCACTTTCA 1020  
 CAGCCTCTGA GGCCTGGAAG AAGATCCAGC TGGGCAAGAT GCATTGACGC CACACCCAGC 1080  
 CTAATGGCGG AGGACCTTGG GCATCGCCAG CCTGTGCTCC AGTGCCTCTG CTCTTTGGC 1140  
 CCTCAATCTG GTCCCAATC TGGCTGTGTC CCAAGGGTGT TGTGGGAAGT GGGGGGAAAG 1200  
 TAGAGGATGG CTCGATGTTT TGCAGCTACC TCTTTTCCCC GTGTTTCTTT TTAGACAAAT 1260  
 65 TACACTGCCT GAAGTTGAGC TTCCCTTTTC CCTGGGAGC CCCAAGAACA GAGTCAGGCA 1320  
 AGGGGTGGGG AGTCCAGGGG AACATCCAG AATGCATATC GATCAGCTCT CAGCCAGGCT 1380  
 TGACAAATCT CCGACGCCCC ACTAGGTGGA CACATTAATG ATTTGGTTTC TCCCTGGGC 1440  
 AGCCAACTG CCGCAGGCG ACCAGACCTG GGCTTTGAGC TTTGGGACCA GGCTGCCCAA 1500  
 AGGTACTCCT TTATACACC GGCACCTTCC ACGAAAGATG GTACTTCCCA AGCAAGCCCC 1560  
 70 TATGATTGT CACTATAGAT GGAATGTGT GGCATGCACA TGAGTTGAAA TTCTTTTATG 1620  
 CATTTTTTTG AAGAAAAAAA AAAAACAAC TCTGAGGACA TAGGGGATGT CAGTTTCTTA 1680  
 TGAAGAGAC ACCTCTGACC CGTTATTCTT ATAATCAAAA TCTGAAGGGA AAAAAATGTT 1740  
 TTAGTTCTTT CCCACTGCT TGGGTTCAC TAGATTAAAA GGCTGATTTT CAG 1793

Seq ID NO: C214 DNA Sequence  
 Nucleic Acid Accession #: NM\_002151.1  
 Coding sequence: 246..1499

80 1 11 21 31 41 51  
 TOGAGCCCGC TTCCAGGGA CCCTACCTGA GGGCCACAG GTGAGGCAGC CTGGCCTAGC 60  
 AGGCCCCAGC CCACCGCTCT TGCCTCCAG CCGCCGCTG CTGCGGGGCC ACCATGCTCC 120  
 TGCCACGGCC TGGAGACTGA CCGAGCCCG GCACTACCTC GAGGCTCCGC CCCACCTGCG 180  
 TGGACCCAG GGTCCACACC TGGCCACGGA GGTGAGCAG GGAATCATT ACAAGAGGCA 240  
 GTGACATGCG GCAGAAGGAG GGTGGCCGGA CTGTGCCATG CTGCTCCAGA CCCAAGGTGG 300

5 CAGCTCTCAC TGGCGGGACC CTGCTACTTC TGACAGCCAT CGGGGCGGCA TCCTGGGCCA 360  
 TTGTGGCTGT TCTCTCTCAG AGTGACCAGG AGCCGCTGTA CCCAGTGCAG GTCAGCTCTG 420  
 CGGACGCTCG GCTCATGGTC TTTGACAAGA CGGAAGGGAC GTGGCGGCTG CTGTGCTCTC 480  
 CGCGCTCCAA CGCCAGGGTA GCGGACTCA GCTGCGAGGA GATGGGCTTC CTCAGGGCAC 540  
 TGACCCACTC CGAGCTGGAC GTGCGAACGG CGGGCGCCAA TGGCACGTCG GCCTTCTTCT 600  
 GTGTGGACGA GGGGAGGCTG CCCACACCCC AGAGGCTGCT GGAGGTCATC TCCGTGTGTG 660  
 ATTGCCCCAG AGGCCGTTTC TTGGCCGCCA TCTGCCAAGA CTGTGGCCGC AGGAAGCTGC 720  
 CCGTGGACCG CATCGTGGGA GCGCGGGACA CCAGCTTGGG CCGGTGGCCG TGGCAAGTCA 780  
 GCCTTCGCTA TGATGGAGCA CACCTCTGTG GGGGATCCCT GCTCTCCGGG GACTGGGTGC 840  
 10 TGACAGCCGC CCACTGCTTC CCGGAGCGGA ACCGGGTCTT GTCCCGATGG CGAGTGTGTTG 900  
 CCGGTGGCGT GGGCCAGGCC TCTCCCCACG GTCTGCAGCT GGGGGTGCAG GCTGTGGTCT 960  
 ACCACGGGGG CTATCTTCCC TTTCCGGACC CCAACAGCGA GGAGAACAGC AACGATATTG 1020  
 CCTGGTCCA CCTCTCCAGT CCCTGCCCC TCAAGAAATA CATCCAGCCT GTGTGCCTCC 1080  
 15 CAGCTGCGCG CCAGGCCCTG GTGGATGGCA AGATCTGTAC CGTGACGGGC TGGGCGAACA 1140  
 CGCAGTACTA TGGCCAACAG GCGGGGGTAC TCCAGGAGGC TCGAGTCCCC ATAATCAGCA 1200  
 ATGATGTCTG CAATGGCCCT GACTTCTATG GAAACCAAGT CAAGCCCAAG ATGTTCTGTG 1260  
 CTGGCTACCC CGAGGGTGGC ATTGATGCCT GCCAGGGCGA CAGCGGTGGT CCCTTTGTGT 1320  
 GTGAGGACAG CATCTCTGGG ACGCCACGTT GCGCGCTGTG TGGCATTGTG AGTTGGGGCA 1380  
 20 TGGCTGTGTC CTTGGCCAGG AAGCCAGGCG TCTACACCAA AGTCAGTGAC TTCGGGGAGT 1440  
 GGATCTTCCA GGGCATAAAG ACTCACTCCG AAGCCAGCGG CATGGTGACC CAGCTCTGAC 1500  
 CGGTGGCTTC TCCTGCGGCA GCCTCCAGGG CCCGAGGTGA TCCCGTGGT GGGATCCACG 1560  
 TGGGGCCAGG GATGGGAGCT TTTTCTTCTT GGGCCCGGTC CACAGGTCCA AGGACACCTC 1620  
 CCCTCCAGGG TCCTCTCTTC CACAGTGGCG GGGCCACTCA GCCCCGAGAC CACCCAACTC 1680  
 25 CACCTCTCTG ACCCCATGAT AAATAATTGT CTGCTGTCTG GGACTCCTGT CTAGGTGCCC 1740  
 CTGATGATGG GATGCTCTTT AAATAATAAA GATGGTTTGG ATT 1783

Seq ID NO: C215 DNA Sequence  
 Nucleic Acid Accession #: AB037745.1  
 Coding sequence: 26..1744

30 1 11 21 31 41 51  
 | | | | |  
 ATGGTGGAA ACCTGCCCCA CAAACATGGA AACGACCGTT CTCAGTGGGA TCAACTTCGA 60  
 GTACAAGGGC ATGACAGGCT GGGAGGTGGC TGGTGATCAC ATTTACACAG CTGCTGGAGC 120  
 35 CTCAGACAAT GACTTCATGA TTCTCACTCT GGTGTGTCGA GGATTAGAC CTCGCGAGTC 180  
 GGTGATGGCA GACACAGAGA ATAAAGAGGT GGCCAGAAAT ACATTGTCTCT TTGAGACCTC 240  
 CTGTTCTGTG AACTGTGAGC TCTACTTCAT GGTGGGTGTG AATTCTAGGA CCAACACTCC 300  
 TGTGGAGACG TGGAAAGGTT CCAAAGGCAA ACAGTCTCTAT ACCTACATCA TTGAGGAGAA 360  
 40 CACTACACAG AGCTTCACTT GGGCCTTCCA GAGGACCACT TTTCTAGAGG CAAGCAGGAA 420  
 GTACACCAAT GACGTTGCCA AGATCTACTC CATCAATGTC ACCAATGTTA TGAATGGCGT 480  
 GGCTCTCTAC TGCCGTCCTT GTGCCCTAGA AGCCTCTGAT GTGGGCTCCT CCTGCACCTC 540  
 TTGTCTGTCT GGTACTATA TTGACCGAGA TTCAGGAACC TGCCACTCCT GCCCCCTTAA 600  
 CACAATTCTG AAAGCCACCC AGCCTTATGG TGTCCAGGCC TGTGTGCCCT GTGTCCAGG 660  
 45 GACCAAGAAC AACAGATCC ACTCTCTGTG CTACAATGAT TGCACCTTCT CACGCCAACAC 720  
 TCCAACAGAG ACTTTCAACT ACAACTTCTC CGCTTTGGCA AACACCGTCA CTCTTGCTGG 780  
 AGGGCCAAAG TTCACTTCCA AAGGGTTGAA ATACTTCCAT CACTTTACCC TCAGTCTCTG 840  
 TGGAAACCAG GTAGGAAAAA TGTCTGTGTG CACCGACAAT GTCACTGACC TCCGGAATCC 900  
 TGAGGGTGAG TCAGGGTTCT CCAATCTAT CACAGCTAC GTCTGCCAGG CAGTCATCAT 960  
 50 CCCCCAGAG GTGACAGGCT ACAAGGCCGG GGTTCCTCA CAGCCTGTCA GCCTTCTGTA 1020  
 TOGACTTATT GGGGTGACAA CAGATATGAC TCTGGATGGA ATCACCCTCC CAGCTGAATC 1080  
 TTTCCACCTG GAGTCTCTGG GAATACCGGA CGTGATCTTC TTTTATAGGT CCAATGATGT 1140  
 GACCCAGTCC TGCAGTCTG GGAGATCAAC CACCATCCGC GTCAGGTGCA GTCCACAGAA 1200  
 AACTGTCCCT GGAAGTTTGC TGTGCCAGG AACGTGTCTA GATGGGACCT GTGATGGCTG 1260  
 55 CAACTCTCAC TCTCTGTGG AGAGGCGGGC TGTGTGCCG CTCTGCTCAG TGGCTGACTA 1320  
 CCATGCTATC GTCAGCAGCT GTGTGGCTGG GATCCAGAAG ACTACTTACG TGTGGCGAGA 1380  
 ACCCAAGCTA TGCTCTGGTG GCATTCTCT CCCTGAGCAG AGAGTCACCA TCTGCAAAAC 1440  
 CATAGATTTC TGGCTGAAGG TGGGCATCTC TGCCAGGCAAC TGTACTGCCA TCCTGCTCAC 1500  
 CGTCTTGACC TGCTACTTTT GGAAGAAAGAA TCAAAACTA GAGTACAAGT ACTCCAAGCT 1560  
 60 GGTGATGAAT GCTACTCTCA AGGACTGTGA CCGCCAGCA GCTGACAGCT GCGCCATCAT 1620  
 GGAAGGCGAG GATGTAGAGG ACGACCTCAT CTTTACCAGC AAGAAGTCAC TCTTTGGGAA 1680  
 GATCAATCA TTTACCTCCA AGCAGCCAGC TCCTGTCAAC ATCTCTCTTT CAGAGGACTC 1740  
 CTGATGGATT TGACTCAGTG CCGCTGAAGA CATCCTCAGG AGGCCAGAGC ATGGACCTGT 1800  
 GAGAGGCACT GCCTGCCTCA CCTGCCTCCT CACCTTGCTAT AGCACCCTTG CAAGCCTGCG 1860  
 65 GCGATTGGG TCCGACATC CTGCAACACC CACTGCTGGA AATCTCTTCA TTGTGGCCTT 1920  
 ATCAGATGTT TGAATTTTCA ATCTTTTTTT ATAGAGTACC CAAACCTTCC TTTCTGCTTG 1980  
 CCTCAAACT GCCAAATATA CCCACACTTT GTTTGTAAAT TATGCCCTTG CTGTATCTTT 2040  
 GTTCCCAAAA ATGGCCCATC CGCCAGAGCC ATAGCTTCGT CTGCTCATAA TTCTTATAGC 2100  
 TTTGGAATGA AAATATTCTT ATCTTCTTAA GTATAGAAAC TATTTCTCTT GTCTCTTAAC 2160  
 70 TTAAGGCGAG AAACAGCTGG GAGTTTTCTT CGCATGCCCT CAGCTCATGA TCTCTTCAGG 2220  
 AGAGAGGCTG GGTGAGGAGG GTGTGGGGGT TCCTTGGTGG ATAATCTTCA TAGCAGCCTG 2280  
 GATCCATTTC CCCTGGATAA CCAGCTCAAA GGGAGTGAAA ATGGTAGTCT GAGGGCAAGG 2340  
 GGAGCAAGGC TTGGGTGAAG AAAGCCTTGA AAAGCATAAA AAGAGGCCGG GCGCGGTGGC 2400  
 TCACGCCCTG AATCCAGCA CTTTGGGAGG CCGAGGGCGG CAGATCATGA GGTCCGGAGA 2460  
 75 TTGAGACCAT CCGGCTAAC ACGGTGAAGC CCGTCTCTA CTGAAATAC AAAAAATTAG 2520  
 CCGGGCGTGG TGGCGGGTGC CTGTGGTCCC AGCTACTCGG GAGGCTGAGG CCGGAGAATA 2580  
 GCGTGGGCGT GGAAGGGCGA GCTTGCACTG AGCCGAGATC GCGCCACTGC ACTCCATCCA 2640  
 GCCTGGGTGA CAGAGTGAGA CTCTGCCCTCA AAAAAAAGAA AAGCAAAAG 2700  
 AGAGGCAACA AGGAATGTTT TTGTTTTTGA GACAGGCTCT CACTCTGTCA CCTAGGCTGG 2760  
 80 AGTGCACTGG CGTACTCACT GTTCACTGCA GCCTCAAGCT CTTGGGCTCA GGCTATCCTC 2820  
 CCATCTCAGC CTCTCAAGTA GCTGGGACTA CGAGTGTGCA CCACAGGCT CACTAATTTT 2880  
 TGTGTTTTTT GTAGACAGGG GTTTTCAACG TGTGCCCAG GCTGGTCTCC AACTCCTGGG 2940  
 CTCAGTGAAT CTGTCCGCTT CGGCTCCCA AACTGCTGGG ATTACAGGCA TAAGCCACTG 3000  
 CACTCAGCCT TTTATTGTTT TTTTAAACCA CGTAGCTCAT TGCTTCTCT TAAGTAAATG 3060  
 ATAGATATTG TCATGGAAGC CAAAGGAATA AGTTTCATCA GAAATGCCC AAAGCCCTGG 3120

Seq ID NO: C216 DNA Sequence  
Nucleic Acid Accession #: NM\_004864.1  
Coding sequence: 26-952

Seq ID NO: C432 DNA Sequence  
Nucleic Acid Accession #: NM\_052858.1  
Coding sequence: 54..1259

1334

	CGCAGAGGAA	GGGAGACCCC	GGGCGCCGCA	GACCCGAAAG	TGAACCCCT	TCGGAGAGAT	540
	ATCTGCCCTC	GACCCCGAGG	CCTGGACGAG	AGGAGGTGGA	ATATTACCA	TCAGAGGCGG	600
	AAGGACTCCT	GGAATGCCAC	AAATGCAAA	ACTTGTGCAC	TGGGAGAGCC	TGCTGCCAAA	660
5	TGCTGGAGGT	TCTCTGAAC	TTGCTGATCC	TGGCTGCGAG	CTCTGTGTCT	TACAGTTCCA	720
	CAGGGGCTA	CACGGGCATC	ACCAGCTTGG	GGGGCATTTA	CTACTATCAG	TTCGAGGGGG	780
	CTTACAGTGG	CTTTGATGGT	GCTGACGGGG	AGAAGGCCCA	GCAACTGGAT	GTCCAGTTCT	840
	ACCAGTAAA	GCTGCCCATG	GTCACTGTGG	CAATGGCCTG	TAGTGGAGCC	CTCACAGCCC	900
	TCTGCTGCCT	CTTCGTTGCC	ATGGGTGTCC	TGCGGGTCCC	GTGGCATTGT	CCACTGTTGC	960
10	TGGTGACCGA	AGGCTTGTGG	GACATGTCTA	TCGCGGGGGG	GTACATCCCG	GCCTTGTACT	1020
	TCTACTTCCA	TACTCTCTCT	GCTGCCTATG	GCTCTCCTGT	GTGTAAAGAG	AGGCAGGCGC	1080
	TGTACCAAA	CAAAAGCTAC	AGCGGTTTCC	GCTGCAGTTT	CCACGGAGCA	GATATAGGAG	1140
	CTGGAATCTT	TGCTGCCCTG	GGCATTGTGG	TCTTTGCCCT	GGGGGCGGTC	CTGGCCATAA	1200
	AGGGCTACCG	AAAAGTTAGG	AAGCTAAAAG	AGAAGCCAGC	AGAAATGTTT	GAATTTTAAG	1260
15	GGTTTCTAAA	ACGCTCTGAC	AGATGCAAGT	GGTGGTGGAA	GGTAGTCTGA	GCCACTGCCT	1320
	TTCCCAAGAG	TCCTTGTGG	TGGAAGTTTC	CAATGCTGGA	AAAGCAGCGA	CCGACGCTTG	1380
	GTGTGGTGGG	CGGAGCTCCC	AGTCGCTATG	AGCGGTGTTC	ATGGATGCAA	CAGACCCCTG	1440
	CTTCTGGAGT	CTCTGTGAG	TGAGGGACCA	ATCAAAATTA	TTTTTCAAAA	AGCAAAAAAA	1500
	TGGCGGGCCT	CGGCGGCTCA	CACCTGTAA	CCAGCAGCTT	TGGGAGGCTG	AGGTGGGTGG	1560
20	ATCACTTGAG	GTGAGGAGCT	CGAGACGAGC	TTGGCCAAAC	TGGTGAGCCC	CCGTCTCTAC	1620
	TAAATAACAA	AAAAATTAGC	CAGGCGTGGT	GGCGGGCGCC	TGTAATCCCA	GCTACTTGGG	1680
	AGGCTGAGGC	AGGAGAATCG	CTTGAATCTG	GGAGGCGGAG	ATTGCACTGA	GCCGAGATCC	1740
	CGCCACTGCA	CTCCAGCCCA	GGTGACAGAG	CGAGACTCCA	TCTCAAAAA	AAAAAAAAAA	1800
25	Seq ID NO: C434 DNA Sequence						
	Nucleic Acid Accession #: Eos sequence						
	Coding sequence: 261..2861						
	1	11	21	31	41	51	
30	GAGCTAGCGC	TCAAGCAGAG	CCCAGCGCGG	TGCTATCGGA	CAGAGCCTGG	CGAGCGCAAG	60
	CGGCGCGGGG	AGCCAGCGGG	GCTGAGCGCG	GCCAGGGTCT	GAACCCAGAT	TTCCAGACT	120
	AGCTACCATT	CCGCTTGCCC	ACGCCCGGGG	AGCTCGCGCG	GCCTGGCGGT	CAGCGACCAG	180
	ACGTCCGGGG	CCGCTGCGCT	CCTGGCCCCG	GAGGCGTGAC	ACTGTCTCGG	CTACAGACCC	240
	AGAGGGAGCA	CAGTGCAGAG	ATGGGAGCTG	CTGGGAGGCA	GGACTTCTCT	TTCAAGGCCA	300
35	TGCTGACCAT	CAGCTGGCTC	ACTCTGACCT	GCTTCCCTGG	GGCCACATCC	ACAGTGGCTG	360
	CTGGGTGCCC	TGACAGAGC	CCTGAGTTGC	AACCTCGGAA	CCCTGGCCAT	GACCAAGACC	420
	ACCATGTGCA	TATGGCCAG	GGCAAGACAC	TGCTGCTCAC	CTCTTCTGCC	ACGGTCTATT	480
	CCATCCACAT	CTCAGAGGGA	GGCAAGCTGG	TCATTAAAGA	CCACGACGAG	CCGATTGTTT	540
40	TGGGAACCCG	GCACATCCTG	ATTGACAAAG	GAGGAGAGCT	GCATGCTGGG	AGTGCCCTCT	600
	GCCTTTTCCA	GGGCAATTTT	ACCATCATTT	TGTATGGAAG	GGCTGATGAA	GGTATTGAGC	660
	CGGATCCTTA	CTATGGTCTG	AAGTACATTG	GGGTGGTAA	AGGAGGCGCT	CTTGAAGTGC	720
	ATGGACAGAA	AAAGCTCTCC	TGGACATTTT	TGAACAAGAC	CCTTCACCCA	GGTGGCATGG	780
	CAGAAGGAGG	CTATTTTTTT	GAAAGGAGCT	GGGCCCACCG	TGGAGTTATT	GTTCATGTCA	840
45	TCGACCCCAA	ATCAGGCACA	GTCACTCCAT	CTGACCGGTT	TGACACCTAT	AGATCCAAGA	900
	AAGAGAGTGA	ACGTCTGGTC	CAGTATTGGA	ACGCGGTGCC	CGATGGCAGG	ATCCTTTCTG	960
	TTGCAAGTAA	TGATGAAGGT	TCTGAAATTC	TGGATGACAT	GGCCAGGAAG	GGCATGACCA	1020
	AATTGGGAAG	CAACACTCTC	CTGCACCTTG	GATTTAGACA	CCCTTGGAGT	TTTCTAACTG	1080
	TGAAGGAAAA	TCCATCATCT	TCAGTGGGAG	ACCATATTGA	ATATCATGGA	CATCGAGGCT	1140
50	CTGCTGCTGC	CCGGGTATTC	AAATTGTTCC	AGACAGAGCA	TGGCGAATAT	TTCAATGTTT	1200
	CTTTGTCCAG	TGAGTGGGTT	CAAGACGTGG	AGTGGACGGA	GTGGTTGAT	CATGATAAAG	1260
	TATCTCAGAC	TAAAGGTGGG	GAGAAATTTT	CAGACCTCTG	GAAAGCTCAC	CCAGGAAAAA	1320
	TATGCAATGC	TCCCATTGAT	ATACAGGCCA	CTACAATGGA	TGGAGTTAAC	CTCAGCACCG	1380
	AGGTTGTCTA	CAAAAAAGGC	CAGGATTATA	GGTTTGCTTG	CTACGACCGG	GGCAGAGCCT	1440
55	GCCGGAGCTA	CCGTGTACGG	TTCTCTGTG	GGAAGCCTGT	GAGGCCCAAA	CTCACAGTCA	1500
	CCATTGACAC	CAATGTGAAC	AGCACCATTC	TGAACCTGGA	GGATAATGTA	CAGTCAATGGA	1560
	AACCTGGAGA	TACCTGGTCT	ATTGCCAGTA	CTGATTACTC	CATGTACCAG	GCAGAGAGGT	1620
	TCCAGGTGCT	TCCCTGCAGA	TCTGCGCCCC	CCAACCAAGT	CAAAGTGGCA	GGGAACCAAA	1680
	TGTACCTGCA	CATCGGGGAG	GAGATAGACG	GCCTGGACAT	GCGGGCGGAG	GTGGGCTTTC	1740
60	TGAGCCGGAA	CATCATAGTG	ATGGGGGAGA	TGGAGGACAA	ATGCTACCCC	TACAGAAACC	1800
	ACATCTGCAA	TTTCTTTGAC	TTGATACCTT	TTGGGGGCCA	CATCAAGTTT	GCTCTGGGAT	1860
	TTAAGGCAGC	ACACTTGGAG	GGCACGGAGC	TGAAGCATAT	GGGACAGCAG	CTGGTGGGTC	1920
	AGTACCGGAT	TCACCTCCAC	CTGGCCGGTG	ATGTAGACGA	AAGGGGAGGT	TATGACCCAC	1980
	CCACATACAT	CAGGACCTTC	TCCATCCATC	ATACATTCTC	TCGCTGCTGC	ACAGTCCATG	2040
65	GCTCCAATGG	CTTGTGTATC	AAGGACGTTG	TGGGCTATAA	CTCTTTGGGC	CAGTCTTCTT	2100
	TCAOGGAAGA	TGGGCCGGAG	GAAOCGAACA	CTTTTGACCA	CTGTCTTGGC	CTCCTTGTCA	2160
	AGTCTGGAAC	CCTCTCTCCC	TCGGACCGTG	ACAGCAAGAT	GTGCAAGATG	ATCACAGAGG	2220
	ACTCCTACCC	AGGGTACATC	CCCAAGCCCA	GGCAAGACTG	CAATGCTGTG	TCCAACCTCT	2280
	GGATGGCCAA	TCCCAACAA	AACCTCATCA	ACTGTGCCCG	TGCAGGATCT	GAGGAAACTG	2340
70	GATTTTGGTT	TATTTTTCAC	CACGTACCAA	CGGGCCCCCT	CGTGGGAATG	TACTCCCCAG	2400
	GTTATTTCAGA	GCACATTCCA	CTGGGAAAAAT	TCTATAACAA	CCGAGCACAT	TCCAACCTACC	2460
	GGGCTGGCAT	GATCATAGAC	AACGGAGTCA	AAACCAACCGA	GGCCTCTGCC	AAGGACAAGC	2520
	GGCGTTCTCT	TCTCATCATC	TCTGCCAGAT	ACAGCCCTCA	CCAGGACGCG	GACCCGCTGA	2580
	AGCCCCGGGA	GCCCGCCATC	ATCAGACACT	TCATTGCTTA	CAAGAACCAG	GACCAAGGGG	2640
75	CCTGGCTGGC	CGGCGGGGAT	GTGTGGCTGG	ACAGCTGCCA	TTTCAGAGGG	GAGGCTCAGG	2700
	AAGGCTTCTT	GCTTACAGGA	ATGAAGGCTG	GGGGCATTIT	GCTGGGGGGA	GATGAGGCGG	2760
	CCTCTGGAAT	GGCTCAGGGA	TTTACCCCTC	CCTGCCGCTG	CCTGCTGAAG	CTGGTGACTA	2820
	CGGGGTGCGC	CTTTGCTCAC	GCTCTCTGCG	CCCACTCATG	ATGGAGAAGT	GTGGTCAGAG	2880
	GGGAGCAATG	GGCTTTGTCT	CTTATGAGCA	CAGAGGAATT	CAGTCCCCAG	GCAGCCCTGC	2940
80	CTCTGACTCC	AAGAGGGTGA	AGTCCACAGA	AGTGAGCTCC	TGCCTTAGGG	CCTCATTTGC	3000
	TCTTATTCAGA	GGGAACCTAG	CACAGGGGGC	CTCCAGGAGA	CCCTAGATGT	GCTGTACTAC	3060
	CCTCGGCTCG	GGATTTTCAGA	GCTGGAAATA	TAGAAAATAT	CTAGCCCAAA	GCCTTCATTT	3120
	TAAACAGTTG	GGAAGTGAAG	CCCCAAGAT	GGGAAAGAAC	CACACAGCTA	AGGGAGGGCC	3180
	TGGGAGAGCC	CACCTAGGCC	CTTGTCTGCC	CACCACATTG	CCTCAACCA	CGGCCCCAGG	3240
	GTGCCAGGCG	ACTCCTGAGG	TAGCTTCTGG	AAATGGGGAC	AAGTCCCCCT	GAAGGAAGG	3300

5  
 10  
 15  
 20  
 25

```

AAATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCCTGCTCCC AGCGCACACA 3360
AACCCGCCCT CCCCTTGGTG TTGGCGGTCC CTGTGGCCTT CACTTTGTTC ACTACCTGTC 3420
AGCCGAGCCT GGGTGCAACAG TAGCTGCAAC TCCCATTGGT TGCTACCTGG CTCTCCTGTC 3480
TCTGCAGCTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTCGCCATGT TTCTGGTGAG 3540
CCAATTTGGC TGAATCTTGGG TGTCTGAACA GCTATTGGGT CCACCCCACT CCCTTTTCAGC 3600
TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGCCCAA AGAGCTCCTG 3660
TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGACAG AGGCACCAGA GTCTCCCTGG 3720
GTCTTGATGAT GAACTACATT TATCCCTTTT CTGCCCCCAA CCACAACTC TTTCCTTCAA 3780
AGAGGGCCTG CTGCGCTCCC TCCACCAAC TGACCCCATG AGACTCGGTC CAAGAGTCCA 3840
TTCCCCAGGT GGGAGCCCAAC TGTGAGGAG GTCTTTCCCA CCAACATCT TTCAGCTGCT 3900
GGGAGGTGAC CATAGGGCTC TGTCTTTAAA GATATGGCTG CTTCAGAGGC CAGAGTCACA 3960
GGAAGGACTT CTTCCAGGGA GATTAGTGGT GATGGAGAGG AGAGTTAAAA TGACCTCATG 4020
TCCTTCTGTG CCACGGTTTT GTTGAGTTTT CACTCTTCTA ATGCAAGGCT CTCACACTGT 4080
GAACCACTTA GGATGTGATC ACTTTGAGGT GGCCAGGAAT GTTGAATGTC TTTGGCTCAG 4140
TTCATTTAAA AAAGATATCT ATTTGAAAGT TCTCAGAGT GTACATATGT TTCACAGTAC 4200
AGGATCTGTA CATAAAGATT TCTTCTCTAA ACCATTCAAC AAGAGCCAAT ATCTAGGCAT 4260
TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAAATT TCCTCTTGT TATTCTGTIT 4320
TGTAAGACTT AAGTGAGTTA GGTCTTTAAG GAAAGCAACG CTCCTCTGAA ATGCTTGTCT 4380
TTTTTCTGTT GCCGAAATAG CTGGTCCCTT TTGGGGAGTT AGATGTATAG AGTGTCTGTA 4440
TGTAACCATT TCTTGTAGGC ATCACCATGA ACAAGAGAT ATTTCTATT TATTATTAT 4500
ATGTGCACTT CAAGAAGTCA CTGTGAGAGA AATAAGAAAT TGTCTTAAT GTCATGATTG 4560
GAGATGCTCT TTGCTATTCT TGAAGGGGT GTACCTAGAG CCAAGGAAT TGGCTCTGTT 4620
TTGAAAAAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAAAAA 4680
AAAAAAAAA AAAAAAAAAA AA 4702
  
```

Seq ID NO: C217 Protein Sequence  
 Protein Accession #: NP\_005805.1

30  
 35

```

1 11 21 31 41 51
| | | | |
MVGKMWPLVW TLCAVRVTDV AISVETPQDV LRASQKSVT LPCTYHTSTS SREGLIQWDK 60
LLLTTERVW IWFENKQYI HGELYKNRVS ISNNAEQSDA SITIDQLTMA DNGTYECSVS 120
LMSDLEGNTK SRVRLVLVLP PSKPECGIEG ETIIGNNIQL TCQSKESGPT PQYSWKRYNI 180
LNQEQPLAQP ASGQPVSLKN ISTDTSGYYI CTSSNEBGTQ FCNITVAVRS PSMNVALYVG 240
IAVGVAALI IGIIIIYCCC CRGKDDNTED KEDARPNREA YEEPPEQLRE LSREEREEDD 300
YRQEEQRSTG RESPDHLQD 319
  
```

Seq ID NO: C218 Protein Sequence  
 Protein Accession #: Eos sequence

40  
 45  
 50  
 55  
 60

```

1 11 21 31 41 51
| | | | |
MGSRTPEPSP HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSPF 60
GFSVEFYRFG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEPVEYKSLQ WPGATVRAHG SSILACAPLY SWRTEKEPLS DPGVGTCTYST 180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ QQILSATQEQ 240
IAESYYPEYL INLVQQLQT RQASSIYDDS YLGYSVAUGE FSGDDTEDEV AGVPKGNLTY 300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLVVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDGFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
QQGVVFVFPF GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDGNG YPDLTIVGSPG 480
VDKAVVYRGR PIYSASASLT IFFAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GFTVELQLDW QKQKGVVRA LPLASRQATL TQTLIIQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALNMF SLDPQAPVDS HGLRPAHYQ SKSRIEDKAQ ILLDCGEONI CVPDLQLEVF 660
GEQNHVYLGQ KNALNLTFAH QNVGEGGAYE AELRVTPAPE AEYSGLVRHP GNPFSLSCDY 720
FAVNFQRLIV CDLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFQILSK NLNNSQSDVY 780
SFRLSVEAQA QVTLNGVSKP EAVLPFVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLESCPQ QALGEGQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QOKREAPSR 900
SASSGQPIK CPEAECEFLR CELGPLHQQE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
YKALQMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
YKLGFFKRSL PYGTAMEKQA LKPPATSDA 1049
  
```

Seq ID NO: C219 Protein Sequence  
 Protein Accession #: NP\_002412.1

65  
 70  
 75

```

1 11 21 31 41 51
| | | | |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDRD NSPFDGPGGN 180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSLSHST DIGALMYP 240
TFSGDVQLAQ DDIDIGIAIY GRSONFVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
PYMRTNPFYF EVELNFIISVF WPQLENGLEA AYEAFADREDEV RFFKGNKYWA VQGNVLHGY 360
PKDIYSSFGF PRYVKHIDAA LSEENTGKTY FFFVANKYWRV DEYKRSMDPG YPKMIAHDPF 420
GIGHKVDVAF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRQ 469
  
```

Seq ID NO: C220 Protein Sequence  
 Protein Accession #: Eos sequence

80

```

1 11 21 31 41 51
| | | | |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGOADIM ISFVRGDRD NSPFDGPGGN 180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSLSHST DIGALMYP 240
  
```

TFSGDVQLAQ DDIDGIIQAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
 PYMRTNFFYP EVELNFTISVF WFQLENGLEA AYEFAADRDEV RFFKGNKYWA VQGQNVLHGY 360  
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDDP YPKMIAHDFP 420  
 GIGKVDVAVF MKDGFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence  
 Protein Accession #: NP\_055146.1

1 11 21 31 41 51  
 MVRKPVVSTI SKGGYLGQNV NGRPLSLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA 60  
 GIFISPKGVL QNTGSVGMSL TIWTVCCVLS LFGALSYAEL GTTIKSGGH YTYILEVFGP 120  
 LPAPVRVWVE LLIIRPAATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180  
 SMSVSWASARI QIFLTFCCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240  
 YGMYAYAGWF YLNFVTEEVE NPEKTIPLAI CISMATITGV YULTNVAYFT TINAELLLS 300  
 NAVAVTFSEF LLGNFSLAVP IFVALSCFES MNGGVFAVSR LFYVASREGH LPEILSMIHV 360  
 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSPARWLFI GLAVAGLIYL RYKCPDMHRP 420  
 FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480  
 SEKIITRLQI ILEVPEEDK L 501

Seq ID NO: C222 Protein Sequence  
 Protein Accession #: NP\_003237.1

1 11 21 31 41 51  
 MGLAWGLGVL FLMHVCGTNR IPESGGDNSV FDIFELTGAA RKSGRRLVK GPDPSSPAFR 60  
 IEDANLIPPV PDDKQDLVD AVRAEKGFLI LASLRQMKKT RTGLLALERK DHSQVQSVV 120  
 SNGKAGTLDL SLTVQGGQHV VSVEALLAT GQNKSTILFV QEDRAQLYID CEKMEAEID 180  
 VPIQSVFTRD LASIARLRIA KGGVNDNFQG VLQNVRFVFG TTPEDILRNK GCSSTSVLL 240  
 TLNNVWVNG SPAIRTYIG HKTDLQAIC GISCELSM VLELRGLRTI VTTLQDSIRK 300  
 VTEENKELAN ELRRPPLCYH NGVQYRNEE WTVDSCTECH QNSVTICK VSCPIMPEN 360  
 ATVPDGECCP RCWPSDSADD GWSWSEWTS CSTSCGNGIQ QGRSCDSL NRCGSSVQT 420  
 RTCHIQCEDK RFKQDGGWSH WSPWSSCSVT CGDGVITRIR LCNSPSPQMN GKPCGEARE 480  
 TKACKIDACP INGGWGPWSP WDICSVTGGG GVQKRSRLCN NPAPQPGKD CVGDVTENQI 540  
 CNKQDCPIDG CLSNPCFAGV KCTSYPDGSW KCGACPPGYS NGIQCCTDVD ECKEVPDACP 600  
 NHNGEHCEN TDGYNCLPC PPRFTGSQPF GQGVHATAN KQVCKPRNPC TDGTHDCNKN 660  
 AKCNYLGHSY DPMYRCECKP GYAGNGIICG EDTDLGWN ENLVCVANAT YHCKKDNCFN 720  
 LPNSGQEDYD KDGIGDACCDD DDDNDKIPDD RDNCPPHYNP AQYDYDRDDV GDRCDNCPYN 780  
 HNPDAQDTDN NGEGDACAAD IDGDGILNER DMCQYVYVND QRTDMDGVG DQCDNCPLEH 840  
 NPDQLSDSD RIGDTCDNNQ DIEDGHQNN LDNCPYVYVNA NQADHDKQK GDAADHDDN 900  
 DGIPEDDKMC RLVENPDQKD SDGDGRGDAC KDDFDHDSV DIDDICPENV DISETFRRF 960  
 QMIPLDPKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDFSG TFFINTERDD 1020  
 DYAGFVFGY SSSRFYVVMV KQVTQSYWDT NPTRAQYSG LSVKVVNSTT GPGEHLRNAL 1080  
 WHTGNTPGQV RTLWHDPRHI GWKDTAYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD 1140  
 KTYAGGRGLL FVFSQEMVFP SDLYECRDP 1170

Seq ID NO: C223 Protein Sequence  
 Protein Accession #: NP\_002183.1

1 11 21 31 41 51  
 MPLLWLGRFL LASCWIIVR SPTPGSEHGS AAPDCPCAL AALPKDVNS QPEMVEAVKK 60  
 HILNMLHLK RPDVTQVPVK AALLNAIRKL HVKGKGVNGY VEIEDDIGRR AEMNEMEQT 120  
 SEIITFAESG TARKTLHFEI SKEGSDLSV ERAEVLFLK VPKANRTRTK VTIRLFQKQK 180  
 HPQGLSDTGE EAEVGLKGE RSELLSEKV VDARKSTWHV FVSSSIQRL LDQKSSLDV 240  
 RIACEQCQES GASLVLLGKK KKEEKEGEGK KKGEGGEGAG ADEEKEQSHR PFLMLQARQS 300  
 EDHPPHRRRR GLECDGKVIN CCKQOFFVVF KDIGWNDWII APSGYHANYC EGECPSHIAG 360  
 TSGSSLSFHS TVINHYMRG HSPPANLKSC CVPTKLREMS MLYYDDGQNI IKKDIQNMIV 420  
 BECCGS 426

Seq ID NO: C224 Protein Sequence  
 Protein Accession #: NP\_000086.1

1 11 21 31 41 51  
 MYPDTACVLL LTLAALGASG QGQSPGSDL GPQMLRELQE TNAALQDVVD WLRQQVREIT 60  
 FLKNTVMEDC ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120  
 NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180  
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQRGAQRFCP DGSPSECH 240  
 ADCVLERDGS RSCVCRVWGA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSSQ 300  
 EDVDRDGDG ACDPDADGDG VFNEDKNCPL VRNPDQRNTD EDKWDGACDN CRSQKNDDQK 360  
 DTDQDGRGDA CDDIDIDGRI RNQADNCPRV FNSDQKDSG DGIGDADNOC POKSNPDQAD 420  
 VDHDVFGDAG DSDQDQDGDG HQDSRDNCPV VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480  
 RDNCRVLPNP GQEDADRQGV GDVCQDDFDA DKVVDKIDVC PENAETLTLD PRAPQTVVLD 540  
 PEGDAQIDPN WQVLNQGRIE VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDYAGFI 600  
 PGYQDSSFFY VVMWQKMBQY YWQANPFRAV AEPGIQLKAV KSTGPGEQL RNALWHTGDT 660  
 ESQVRLWKD PRNVGKDKK SYRWFLQHRP QVGYIRVRY EGPELVADSN VVLDTTMRGG 720  
 RLGVFCFSQE NIWANLRYR CNDTIPEDYE THQLRQA 757

Seq ID NO: C225 Protein Sequence  
 Protein Accession #: NP\_612464

1 11 21 31 41 51

MRPQGPASP QRLRGLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSPG ANGIPGTPGI PGRDGFKEGK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120  
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECGSL PIAIILYLDQ 180  
 GSPENNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGADSTGW NSVSRIIEE 240  
 LPK 243

Seq ID NO: C226 Protein Sequence  
 Protein Accession #: NP\_003216.1

1 11 21 31 41 51  
 MATMENKVIC ALVLVSMAL GTLAEAQDET CTVAPRERQN CGFPGVTPSQ CANKGCCFDD 60  
 TVRGVPWCFY PNTIDVPPEE ECEF 84

Seq ID NO: C227 Protein Sequence  
 Protein Accession #: NP\_056234.1

1 11 21 31 41 51  
 MPKRAHWGAL SVVLILLNGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60  
 NLGFSNIQAL SETSFAGLTK LELLMIHGNE IPSIPDGALR DLSSLQVFKF SYNKLRVITG 120  
 QTLQGLSNLM RLHIDHNKIE FIHPQAFNGL TSLRLHLLEG NLLHLQHPST FSTFTFLDYP 180  
 RLSTIRHLYL AENMVRTLPA SMLRNMPLEL NLYLQGNPWT CDCEMRWFLE WDAKSRGILK 240  
 CKDKKAYEGG QLCAMCFSPK KLYKHEIHLK KDMTCLKPSI ESPLRQNRSR SIEEEQEQEE 300  
 DGGSQLILEK FOLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHNLQT DPPDIDINAT 360  
 VALDFECMPT RENYKELNKL IAYYSEVPVK LHRELMLSKD PRVSQYVRQD ADEEALYYTG 420  
 VRAQILAEPE WVMQPSIDIQ LNRROSTAKK VLLSYTYQYS QTISTKDTRO ARGSRWVMIE 480  
 PSAGAVORDQ VLEGGPCQLS CNVKASESPS IFWVLPDGSJ LKAPMDPPDS KFSILSSGWL 540  
 RIKSMEPSDS GLVQCIQVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN 600  
 ALAIPAEHLIS WLIPNRIIN DLANTSHVYM LFNGLTSLIPK VQVSDSGYYR CVAVNQGGAD 660  
 HFTVGTITVK KGSGLSPKRG RRPKAKALSR VREDIVEDEG GSGMGDEENT SRRLHHPKQD 720  
 EVPLKTKDDA INGDKKAKKG RRLKLMWHS EKEPETNVAE GRRVFESRRR INMANKQINP 780  
 ERWADILAKV RGNLPPKGT E VPLIKTTSP PSLSLEVTPP FFAVSPSPAS PVQTVTSAAE 840  
 SSADVPLLEG EEHVLTGIS ASMGLEHNHN GVILVEPEVT STPLEEVVDD LSEKTEEITS 900  
 TEGDLKGTAA FTLISEPYEP SPTLHTLDTV YEKPTHEETA TEGWSAADVG SSPEPTSSEY 960  
 EPFLDAVSLA ESEPMQYFDP DLETKSQDE DKMKEDTFAH LTPTPTIWN DSSTSOLFED 1020  
 STIGEPGVPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPHPS 1080  
 RSSESEQES KSITLDPDST GIMSSMSFPK KPAETTVGTL LDKDTTIVTT TPRQKVAPSS 1140  
 TMTSTPSSRR PNGRRRLRPN KFRHRHKQTP PTTFAPSETF STQPTQAPDI KISSQVSSL 1200  
 VPTAWDNTV NTPKQLEMEK NAEPTSKGTP RRRKHKRPNK HRYTPSTVSS RASGSKPSPS 1260  
 PENKRNIVT PSSETILLPR TVSLKTEGTY DSDLYMTTTR KIYSSYPKVQ ETLFVITYKPT 1320  
 SDGKEIKDDV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKEESS FVGFGTPTW 1380  
 NPSRTAQPPR LQTDIPVITS GENLTDPLLL KELEDVDFTS EFLSSLTVST PPHQEBAGSS 1440  
 TLLSSIKVEV ASSQAETTL DQDHELTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500  
 MSLGQTTTK NLPAPSRISQ ASRDSKENVF LNYVGNPETE ATPVNNEGTQ HMSGPNELST 1560  
 PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620  
 LPEMSTQAS RYFVTSQSPR HWTNKPEITT YPSGALPENK QFTTPTLST TIPLPLHMSK 1680  
 PSIPSKFTDR RTDQFNYSK VFGNNNIFEA RNPVGKPPSP RIPIHNSGRL PFTTNTKLSF 1740  
 PQLGVTRRPQ IPTSPAPVMR ERKVIPGSYN RIHSHSTFHL DFGPPAPPLL HTPTQTGSPS 1800  
 TNLQNIWMS STQSSISGIF SSVQSSGSFH QSSSKFFAGG PPASKFWSLG EKPQILTKSP 1860  
 QTVSVTAETD TVFPCBATGK PKPFVTWTKV STGALMTPTNT RIQRFEVLKN GTLVIRKVVQ 1920  
 QDRGQYMTA SNLHGLDRMV VLLSVTVQQP QILASHYQDV TVYLGDTIAM ECLAKGTAP 1980  
 QISWIFPDRR VMOQTVSPVES RITLHENRTL SIKEASFSDR GVIKCVASNA AGADSLAIRL 2040  
 HVAALPPVIH QLEKLENSLP PGLSIHICT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100  
 VFPNGTLYIR NLAPKDSGRY ECVAANLVGS ARRTVQLNVQ RAAANARITG TSPRRTDVRY 2160  
 GGTLKLDCA SGPDPWPRILW RLPSKRMIDA LPSFDSRIKV FANGTLVVKV VTDKADGDL 2220  
 CVARNKVGDD YVVLKVDVVM KPAKIEHKEE NDHKVYFGD LKVDCAVATG LNPSEIWSLP 2280  
 DGLSVNSFMQ SDDSGGRTRK YVVFNNGLY FNEVGMREEG DYTCAFAENQ GKDEMRVRVK 2340  
 VUTAPATIRN KTYLAVQVY GDVVTVACEA KGEPMKPVTV LSPTNKVIPT SSEKYQIYQD 2400  
 GTLLIQAQR SDSGNYTCLV RNSAGEDRKT VWIHVNVQPP KINGNPNPIT TVREIAAGGS 2460  
 RKLIDCKAEG IPTPRVLWAF PEGVVLPAFY YGNRITVHGN GSLDIRSLRK SDSVQLVOMA 2520  
 RNEGGEARLI VQLTVLEPME KPIPHDPISE KITAMAGHTI SLNCSAAGTP TPSLVVVLN 2580  
 GTDLQSGQQL QRFYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVLGLKPEAN 2640  
 KQYHNLVSII NGETLKLPCP PPGAGQGRFS WTLFNGMHLE GPQTLGRVSL LDNGTLTVRE 2700  
 ASVFDGRGYV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVITYTRPGNT VKLNCMAMGI 2760  
 PKADITWELP DKSHLWAGVQ ARLYGNRPLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820  
 KTTYIHVF 2828

Seq ID NO: C228 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MPGKTLRTG APADYRVILK TSQEDELDPV DDISVRVMSS QSVLVSVDVP VLEKQKKVVA 60  
 SRQYTVRYRE KGLARWDYK QIANRRVLIE NLIPDVTYEF AVRSQGERD GKWSTSVQPR 120  
 TPESAPTTAP ENLNVVFWNG KPTVVAASWD ALPETEGKVK VCLLDLTGLFS VSSFQPSAKS 180  
 FQNTFFHTPR LSNHLEQSPS PILETLLLPW MWVCSLGNAI FSKSGPQTGE AWDLTTPKPSL 240  
 SLQQECSCCT QKDFSCLAYL IDIQTKQVKN DPQLEGSVFG PCFLFYFLTF MLDIGGFSPI 300  
 MCYEDPVSS LTGNSLKSVA ASKADVQNT EDNGKPEKPE PSSPSRAPA SSQHPSPVAS 360  
 PQGRNAKDLL LDLNKILAN GGAPRKPLR AKKAEELDLQ STEITGEEEL GSREDSPMSP 420  
 SDTDQKRTL RPPSRHGHVS VAPGRATVRA RMPALPRREG VDKPGFSLAT QRRPGAPPSA 480  
 SASPAHAST QGTSHRPSLF ASLNDNDLVD SDEDERAVGS LHPKGAPAP RPALSPSRQS 540  
 PSSVLDRSS VHPGAKPASP ARRTPHSGAA EEDSSASAPP SRLSPPHGGS SRLLETPQHL 600  
 SSPLSKGGKD GEDAPATNSN APSRSTMSSS VSHLSSRTQ VSEGAASDG ESHGDGDRED 660



5 GGRQAEATAQ TLRARPASGH FHLLRHKFFA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR 720  
AHPVPVSHSD SHPKLSSGIH GDEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPORG 780  
ASLHRKEPI ENPKSTGADT HPQGYSSLA SKAQDVQOST DADTEGHSFK AQGSDTRHA 840  
SPARPPAARS QQHPSPVPRM TPGRAPEQQP PPPVATSQHH PGQSRDAGR SPSPQRLSLT 900  
10 QAGRPRPTSQ GRSHSSSDPY TASSRGMFLP ALQNQDEDAQ GSYDDDDSTEV EAQDVRAPAH 960  
AARAKEAAS LPKHQQVESP TGAGAGGDHR SORGHASPA RPSRPGGPQS RARVPSRAAP 1020  
GKSEPPSKRP LSSKSQQSVS AEDEEEDAG FFKGGKEDLL SSSVPKWPS STPRGGKAD 1080  
GSLAKEEREP AIALAPRGGS LAPVKRPLFP PPGSSPRASH VPSRPPPSA ATVSFVAGTH 1140  
PWPRYTTRAP PGHFTTTPML SLRQRMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVL 1200  
10 GSNQKPNQGR IINGPQGTW VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDLE 1260  
GTFVVSVDGL PLFGQGRHGT PLANAQDKPI LSLGKGKPLVG LEVIKKTTHP FTTTMMPTTT 1320  
TTPLPTTTT RPTTATTMQP TTTTTPLTTP TPRETTATT TTTTTRPTT VRTTTRTTT 1380  
TTPKPTTPIP TCPPGTLEH DDDGNLIMS NGIFECYAE DEFSGLETDT AVPTTEAYVI 1440  
15 YDEDEYFETS RPTTTEPST TATTTPRVI EGAISSEFEE EPDLAGRKRF VAPYVTVLNK 1500  
DPSAPCSLQD ALDHFPQVDSL DEIIPNDLKK SDLPQHAHR NITVVAVEGC HSFVIVDWDK 1560  
ATFGDLVTGY LVYSASYEDF IRNKFSTQAS SVTHLPIENL KPNTRYFVKV QAQNPHGYGP 1620  
ISPSVSFVTE SDNPLLVVRP PGGELSGSHS LSNMIPATRT AMDGNM 1666

Seq ID NO: C229 Protein Sequence

Protein Accession #: NP\_003005.1

20  
25  
30  
1 11 21 31 41 51  
MFLSILVALC LNLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHST QENAILAIEQ 60  
YEELVDVNC AVLRFFFCAM YAPICTLEFL HDPIKPKCKSV CQRARDDCEP LMKMYNHSWP 120  
ESLACDELIV YDRGVCISPE AIVTDLPELV KNIDITEDMM VQERPLDVDC KRLSPDRCKC 180  
KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVDV KEIFKSSSPI PRTOVPLITN 240  
SSQCPCPHLP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300  
KKKTAGRTSR SNPPKPKGKP PAKPASPKK NIKTRSAQKR TNPKRK 346

Seq ID NO: C230 Protein Sequence

Protein Accession #: NP\_005931.1

35  
40  
45  
1 11 21 31 41 51  
MAPAAWLRS AARALLPPML LLLQPPPLL ARALPPDVH LHAERRGPQ WHAALPSSPA 60  
PAPATQEA PR PASSLRPPRC GVPDPDSGLS ARNRQKRFVL SGRWRKXTDL TYRILRFPWQ 120  
LVQEQVRQTM AEALKVNSDV TPLTTFTEVH GRADIMIDFA RYWHGDDLP DPGGGLAHA 180  
FFPKTHREGD VHFYDETWT IGDDQGTDL QVAHEFEHGV LGLQHTTAAK ALMSAFYTFR 240  
YPLSLSDDDC RGVQHLVQGP WFTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300  
VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHQWGLP SPVDAAFEDA QGHIWFFQGA 360  
QYVYDGEKP VLGPAPLTEL GLVRFVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVD 420  
VVPERRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDV VKVKALEGFP RLVGPDFFGC 480  
AEPANTFL 488

Seq ID NO: C231 Protein Sequence

Protein Accession #: NP\_076927

50  
55  
60  
1 11 21 31 41 51  
MGENDPPAVE AFFSFRSLFG LDDLKISPA PDADAVAAQI LSLPLKFFP IIVIGIALI 60  
LALAIGLGIH FDCSGKYRCR SSFKCIBLIA RCDGVSDCKD GEDEYRCVRV GQONAVLQVF 120  
TAASWKTMCS DDWKGHYANV ACAQLGFPYS VSSDNLRVSS LEGQFREFFV SIDHLLPDDK 180  
VIALHSHYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWFP QASLQFGYH 240  
LOGGSVITPL WIIIAHCVY DLYLPKSWTI QVGLVSLLEN PAPSHLVEKI VYHSKYKPKR 300  
LGNIDIALMKL AGPLITNEMI QPVCLNSEE NFPDGVKVCNT SGWGATEDGG DASFLNHAA 360  
VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420  
GIGCAEVNKP GUYTRVTSFL DWIHEQMERD LKT 453

Seq ID NO: C232 Protein Sequence

Protein Accession #: NP\_003211

65  
70  
75  
1 11 21 31 41 51  
MLWKLTDNIK YEDCEDRHG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP 60  
PYQPIYPSQ DPYSHVNDPY SLNPLHAQPO POHPGWFGQR QSQESGLLHT HRGLPHQLSG 120  
LDPRRDYRRH EDLLHGPHAL SSGLDLSTH SLPHAIIEVP HVEDPGINIP DQTVIKKGPV 180  
SLSKNSNAV SAIPINKDNL FGGVVNPNV PCSVPGRSL LSSTSKYKVT VAEVQRLSP 240  
PECLNASLLG GVLRRAKSKN GGRSLREKLD KIGLNLPAQR KKAANVTLLT SILVEGEAVHL 300  
ARDFGVVCET EPPAKAVAEF LNRQHSQDNE QVTRKNMLLA TKQICKFTD LLAQDRSPLG 360  
NSRPNPILEP GIQSCILTFN LISHGFGSPA VCAAVTALQ YLTELKAMD KMYLSNNFNS 420  
HTDNNKSSD KEEKHRK 437

Seq ID NO: C233 Protein Sequence

Protein Accession #: NP\_002979.1

80  
1 11 21 31 41 51  
MKGLAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCPKPGVI 60  
LLTKRGRQIC ADPNKWKVQK YISDLKANA 89

Seq ID NO: C234 Protein Sequence

Protein Accession #: NP\_004054.1

1 11 21 31 41 51  
 5 MILQAHLSL CLMLYLATG YGQEGKFSGP LKPMTFISIYE GQEPSQIIIFQ FKANPPAVTF 60  
 ELTGETDNIF VIEREGLLYY NRALDRETRS THNLQVAALD ANGIIVEGPV PITIEVKDIN 120  
 DNRPTFLQSK YEGSVQRNSR PGKPFLLVNA TDLDPPATPN GQLYYQIVIQ LPMINNVMYF 180  
 QINNKTGAIS LTREGSQELN PAKNPSYNLV ISVKDMGGQS ENSPSDITTS DIIVTENIWK 240  
 APKPVEMVEN STDPHPKIT QVRWNDPGAQ YSLVDKEKLP RFPFSIDQEG DIYVTPQLDR 300  
 10 EEKDAYVFYA VAKDEYKPL SYPLEIHVKV KDINDNPPTC PSPVTVEVQ ENERLGNISIG 360  
 TLTAHRDEE NTANSFLNRY IVEQTPKLFM DGLFLIQTYA GMLQAKQSL KKQDTPQYNL 420  
 TIEVSDKDFK TLFQVQINVI DINDQIPIFE KSDYGNLTAL EDTNIGSTIL TIQATDADEP 480  
 FTGSSKILYH IIKGDSERGL GVDTPHTNT GYVVIKKPLD FETAAVSNIV FKAENPEPLV 540  
 FGKYNASSF AKFTLIVTDV NEAPQFSQHV FQAKVSEDVA IGTKVGNVTA KDPEGLDISY 600  
 15 SLRGDTRGWL KIDHVTGEIF SVAPLDREAG SPYRVQVAT EVGSSSLSSV SEFHLLIADV 660  
 NDNPPRLAKD YTLGFFCHPL SAPGSLIFEA TDDQHLFRG PHFTFSLGSG SLQNDWEVSK 720  
 INGTHARLST RHTEFEEREY VVLRINDGG RPFLEGIVSL PVTFCSCVEG SCFRPAGHQT 780  
 GIPTVGMVAV ILLTLLLVIG IILAVVFIRI KKDKGKDNVE SAQASEVKPL RS 832

20 Seq ID NO: C235 Protein Sequence  
 Protein Accession #: NP\_004434.1

1 11 21 31 41 51  
 25 MARARPPPPP SPFPGLLPLL PPLLLLPLLL LPAGCRALEE TLMDTKWVTS ELAWTSHPES 60  
 GNEEVSGYDE AMNIRTYQV CNVRESSQNN WLRTGFIWRR DVQRYVELK FTVRDCNSIP 120  
 NIPGSCKETP NLFYYEADSD VASASSPFWM ENFYVKVDIT APDESFSRLD AGRVNTKVRS 180  
 FGPLSKAGFY LAFQDQGACM SLISVRAPYK KCASTTAGFA LFPETLTGAE PLSLVIAPGT 240  
 CIPNAVEVSF PLKLYCNGDG ENMVVPGACT CATGHEPAAK ESQCRPCPPG SYKAKQGEPP 300  
 30 CLPCPPNSRT TSPAASICTC HNNFYRADSD SADSACTTVP SPFRGVISNV NETSLILEWS 360  
 EPRDLGGRDD LLYNVICKKC HGAGGASACS RCDDNVEFVP RQLGLTERRV HISHLLAHTR 420  
 YTFEVQAVNG VSCSKPLPPR YAAVNITNQ AAPSEVPTLR LHSSSGSSLT LSWAPPERPN 480  
 GVILDYEMKY FEKSEGIASV VTSQMNVSQV DGLRPDARYV VQVRARTVAG YQYSRPAEF 540  
 ETTSESGSA QQLQQLPLI VGSATAGLVF VVAVVVIIV CLRKQRHGSD SEYTEKLQY 600  
 35 IAPGMKVYID PFTYEDPNEA VREFAKEIDV SCVKIEEIVG AGEFGEVCRG RLKQPGRRREV 660  
 FVAIKTLKVG YTERORRDFL SEASIMGQFD HPNIIRLEGV VTKSRPVMIL TEFMENCALD 720  
 SPLRLNDGQF TVIQLVGLMR GIAAGMKYLS EMNVYHRDLA ARNILVNSML VCKVSDFLGS 780  
 RFLDDPSDP TTTSSLGSKI PIRWTAPEAI AYRKFTSASD VWSYGIVMME VMSYGERPYW 840  
 DMSNQDVINA VEQDYRLPPP MDCPTALHQL MLDCCWVRDRN LRPKFSQIVN TLDKLRNAA 900  
 40 SLKVIASAQS GMSQPLDRT VPDYTTFTTV GDWLDIAKMG RYKESFVSAG FASFDLVAQM 960  
 TAEDLLRIGV TLAGHQKXIL SSIQDMRLQM NQTLFPVQV 998

Seq ID NO: C236 Protein Sequence  
 Protein Accession #: NP\_001795.1

45 1 11 21 31 41 51  
 MYGVYVLDKD SPVYGPAPR ASLGLGPANY GPPAPPPAPP QYPDFSSYSH VEPAPAPPTA 60  
 WGAPFPAPKD DWAAAYGPGP AAPAASPASL APGPPPDFSP VPAPPGPGPG LLAQPLGGPG 120  
 50 TPSSPGARQ TPYEWRRSV AAGGGGGSGK TRTKDKYRVV YTDEQRLELE KEFHYSRYIT 180  
 IRRKSELAAN LGLTERQVKI WQNRRAKER KVNKKGQQQQ QPPQPPMAHD ITATPAGPSL 240  
 GGLCPNNTSL LATSSPMPVK EEFLP 265

Seq ID NO: C237 Protein Sequence  
 Protein Accession #: NP\_068813.1

55 1 11 21 31 41 51  
 MGS DRARKGG GPKDFGAGL KYNRHEKVN GLEEGVEFLP VNNVKVKEH GPGRWVVLAA 60  
 VLIGLLLVLL GIGFLVWHIQ YRDVRVQKVF NGYMRITNEN FVDAYENSNS TEFVSLASKV 120  
 60 KDALKLLYSY VPLFLGPHYKE SAVTAFSEGS VIAYYWEFS IPQHLVEEAE RVMAEERVMV 180  
 LPPRARSLKS FVVTSVVAFV TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA 240  
 HARCQWALRG DADSVLSLTF RSPFLASCD E RGSOLVTVYN TLSPEMPEHAL VQLCGTYPPS 300  
 YNLTFHSSQN VLLITLITNT BRRHPGFAT PFQLPRMSSC GGRIRKAQGT FNSPYYPGHY 360  
 65 PPNIDCTWNI EVPNQHVKV RFKFFYLLEP GVPACTCPKD YVEINGEKYC GERSQFVVT 420  
 NSNKITVRFH SDQSYTDTGF LAEYLSYDSS DPCPGQFTCR TGR CIRKELR CDGWADCTDH 480  
 SDELNCSCDA GHQPTCKNF CKPLFWVCD S VNDGDSNDE QGCSCAQTF RCSNGKCLSK 540  
 SQQNGKDDC GDGSDASCP KVNVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSEK 600  
 DDCGLRSPT RQARVVGTD ADEGEWPGVQ SLHALGQGHI CGASLISPNW LVSAHCYID 660  
 70 DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH PPFNDFTFDY DIALLELEKP 720  
 AEYSSMVRPI CLPDASHVFP AGKAIWVTGW GHTQYGGTGA LILQKGEIRV INQTTCEML 780  
 PQQITPRMMC VGLFSGGVDS CQDSSGGPLS SVEADGRIFQ AGVWSWGDGC AQRNKPQVYT 840  
 RLPLFRDWIK ENTGV 855

75 Seq ID NO: C238 Protein Sequence  
 Protein Accession #: Eos sequence

80 1 11 21 31 41 51  
 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMNCSAAV DIMFLLDGSN 60  
 SVKGSGFERS KEFAITVCDG LDISPERVRV GAFQFSSTPH LEFLDPSFT QQEVKARIK 120  
 MVFKGGTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180  
 FAVGVRRFRW EELHALASEP RGQHVLLABQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDS SAGTTLDGFL 360

5 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVDPDLVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT QGDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480  
 EAVRAELEEI TGSFPHVMVY SDPQDLFNQI PELQGLCSR QRPQCRTQAL DLVFMMLDTSA 540  
 SVGPENFAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRRNGI 660  
 SVLVVGVGPV LSEGLRRLAG PRDSLHVA YADLRYHQDV LIEWLGEAK RPNVNLCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP 755

10 Seq ID NO: C239 Protein Sequence  
 Protein Accession #: Eos sequence

15 1 11 21 31 41 51  
 | | | | | |  
 MPPFLLLEAV CVPLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMPLLDGSN 60  
 SVGKGSFERS KHAFTVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120  
 MVFKGGRRET ELALXYLLHR GLPGGRNASV PQILIIITDG KSQGDVALPS KQLKERGVTV 180  
 FAVGRVFRPW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REPAGNAPCW RGSRRTLAVL AAHCPFYSNK RVFLTHPATC YRTTCPGPCD 300  
 20 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLPLDLS SAGTTLDGFL 360  
 RAKVPVVRV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVDPDLVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT QGDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480  
 EAVRAELEEI TGSFPHVMVY SDPQDLFNQI PELQGLCSR QRPQCRTQAL DLVFMMLDTSA 540  
 SVGPENFAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 25 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRRNGI 660  
 SVLVVGVGPV LSEGLRRLAG PRDSLHVA YADLRYHQDV LIEWLGEAK RPNVNLCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCVVCVS QGWILETPLR HMAFVQEGSS 780  
 RTPPSNYREG LGTEMYPTFW NVCAPGP 807

30 Seq ID NO: C240 Protein Sequence  
 Protein Accession #: XP\_097386.1

35 1 11 21 31 41 51  
 | | | | | |  
 MPKSEPLGCL SPASRAPGSA AATGAWLPAA SGGPGPLGPP CTCPPRSLGR GRAGSRAGSS 60  
 PSGCVCVSGI LRVVSVGDPA SRRWVDLDSN SEDLSLLTLP MIVGTGGVGG GWARGWVPAQ 120  
 EKEVAEGSGH AGRNGRRRLQ RVYGARSWIL GRKPCIQRL PASGGPVQPQ PCPSPATACR 180  
 WGFKFGVAFW GAAQHPLPCR LGGGRAVPSA TRTLDGF 217

40 Seq ID NO: C241 Protein Sequence  
 Protein Accession #: CAC03433

45 1 11 21 31 41 51  
 | | | | | |  
 MLSSDTDFTA SWELVVRVDH PNEEQQKQDV LRVSGDLHVG GVMLKLVEQI NISQDWSDF 60  
 LWWEQKHNL LKTHWTLDKY GVQADAKLLF TPQHKMLRLR LFNLMVRLR VFSFVAVFKA 120  
 VSDICKILNI RRSEELSLK PSGDYFKKK KCKNNKEPI IEDILNLESS PTASGSSVSP 180  
 GLYSKMTPI YDPFNGTPAS STMTWFSDSP LTEQNCSTLA FSQPPQSPEA LADMYQPRSL 240  
 VDKAKLNAGW LDSSRSLMEQ GIOEDEQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300  
 50 LLEEIDCTEE EMLIPALQY HISKLSLSAE TQDFAGESEV DEIEAALSNL EVTLEGGKAD 360  
 SLLEDITDIP KLDADNLKLF PKLLPKAPK QYWFIFKDT IAYFNKELE QGEPLKLNIL 420  
 RGCEVVPDYN VAGKFGIKL LIPVADGME MYLRCDHENQ YAQWMAACML ASKGTMTADS 480  
 SYQPEVLNLI SFLMKNRNS ASQVASSLEN MDMNPECFVS PRCARHKHSK QLAARILEAH 540  
 QNVAQMPLVE AKLRFIQAWQ SLPEFGLTYY LVRFKSGKID DILGVSYNRL IKIDAATGIP 600  
 55 VTWRFTNIK QHNNWETRQ VVIEFDQNVF TAFTCLSDAC KIVHEYIGGY IFLSTRSKDQ 660  
 NETLDEDLFH KLTGGQD 677

60 Seq ID NO: C242 DNA Sequence  
 Nucleic Acid Accession #: NM\_005170  
 Coding sequence: 337..918

65 1 11 21 31 41 51  
 | | | | | |  
 GGGCGTGAGA AAGCGCAGCG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TTAAAAACCA 60  
 GCCGCCCTGC CGCGCCCTGC GGAGACCTGC GAGAGTCCGC CGCACGCGC GGGACACGAG 120  
 CGTCCACGCG TCCCTGGCGC GTACGCGCTG CCACCACTAG GCCTCCTATC CCGGGGCTCC 180  
 AGACGACCTA GGAGCGGTGC CCTGGGAGT TGCTGGGCG CGCGGTGCCA GAAGCCCTCT 240  
 TGGGGCGCCA CGATTTCCTC CGTCGCTCC GGTTCCTCTG CTGCACTT CTGCGGCGC 300  
 GCGGCGACCT GAGGCGGCGG GGTGGATGCA GGCGCGATGG ACGGCGGAC ACTGCCAGG 360  
 70 TCCGCGCCCC CTGCGCCCCC CGTCCTCTGC GGTGCGCTG CCGGCGGAG ACCCGGCTCC 420  
 CCGGAACCTG TGCGCTGCAG CCGGCGGCGG CGACCGGCCA CGCAGAGAC CGGAGGCGGC 480  
 GCAGCGGCGG TAGCGCGGCG CAATGAGGCG GAGCGCAACC GCGTGAAGCT GGTGAACCTG 540  
 GGCTTCAGG CGCTCGGCGA GCACGTGCGG CACGCGGCGG CCAGCAAGAA GCTGAGCAAG 600  
 75 GTGAGAGAC TGCGCTCAGC CGTGGAGTAC ATCCGCGCGC TGCAGCGCT GCTGGCGGAG 660  
 CACGAGCGCG TGCGCAAGCG GCTGGCGGGA GGGCTGAGGC CGCAGGCGGT GCGGCGCTCT 720  
 GCGCCCGCGG GCGCGCGGAG GACCAACCGG GTGCGCGCT CGCCCTCCCG CGCTTCTCTG 780  
 TCCCGGCGCG GCGGCGGCGG CTCGGAGCCC GGTCCCGCGC GTTCCGCTTA CTCGTGGGAC 840  
 GACAGCGGCT GCGAAGGCGG GCTGAGTCTT GCGAGCGCG AGCTACTCGA CTCTCTCCAGC 900  
 80 TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence  
 Protein Accession #: NP\_060233.1

1 11 21 31 41 51

5  
10  
15

MSGGHQLQLA	ALWPLIMAT	LQAGFGRITGL	VLAADVESER	SAEQKAVIRV	IPLKMDPTGK	60
LNLTLEGVFA	GVAEITPAEG	KLMQSHPLYL	CNASDDDNLE	PGFISIVKLE	SPRRAPRPCL	120
SLASKARMAG	ERGASAVLFD	ITEDRAAAEQ	LQQPLGLTWP	VVLINGNDAE	KLMEFVYKNO	180
KAHVRIELKE	PPAWPDYDVW	ILMTVVGTIF	VIIASVLR	RCRPRHSRPD	PLQORTAWAI	240
SQLATRRYQA	SCROARGEWP	DSGSSCSAP	VCAICLEEPS	EGQELRVISC	LHEFHRCNVD	300
PWLHQHRTCP	LCVFNITEGD	SFSQSLGPSR	SYQEPGRRLH	LIRQHPGHAH	YHLPAAYLLG	360
PSRSAVARPP	RPGPFLPSQE	PGMGPRHHRF	PRAAHPRAPG	EQQLLAGAQH	PYAQGWGMSH	420
LQSTSQHPAA	CPVPLRRARP	PDSSSGSGESY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
NCTDISLQGV	HGSSSTFCSS	LSSDFDPLVY	CSPKGDPPQRV	DMQPSVTSRP	RSLSVSVPTG	540
ETQVSSVHYH	HRHRHHYK	RFQWHGRKPG	PETGVQPSRP	PIPRTPQPE	PPSPDQQVTG	600
SNSAAPSRL	SNPQCPRALP	EPAPGPVDAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRRGGP	660
SEPTPGSRPQ	DATVHPACQI	FPHYTPSVAY	PWSPEAHPLI	CGPPGLDKRL	LPETPGPCYS	720
NSQPVVWCLT	PRQPLEPHPP	GEGPSEWSSD	TAEGRPCPYP	HCQVLSAQPG	SEEELEELCE	780
QAV						783

Seq ID NO: C244 DNA Sequence  
Nucleic Acid Accession #: NM\_004289  
Coding sequence: 493..1695

20  
25  
30  
35  
40  
45  
50  
55  
60

1	11	21	31	41	51	
GC	CG	AG	G	CG	CG	60
CG	CG	CG	CG	CG	CG	120
G	A	G	A	G	A	180
G	A	G	A	G	A	240
A	A	T	G	A	A	300
A	A	C	A	A	A	360
A	G	A	C	A	A	420
T	C	A	G	C	A	480
A	T	C	A	G	C	540
C	A	G	A	T	G	600
C	C	A	A	G	A	660
A	A	T	C	T	C	720
C	A	T	A	G	A	780
G	A	G	A	T	G	840
C	T	T	T	T	G	900
T	C	T	C	A	T	960
A	C	T	A	G	T	1020
G	A	A	C	C	A	1080
T	T	T	C	A	A	1140
T	C	T	G	A	T	1200
A	C	A	G	A	T	1260
G	T	A	G	A	T	1320
C	T	G	A	C	A	1380
G	C	T	G	C	A	1440
T	G	T	A	C	T	1500
A	T	T	A	C	A	1560
G	A	T	G	A	C	1620
A	G	T	A	C	T	1680
G	A	A	G	A	T	1740
G	A	A	C	T	T	1800
C	T	G	C	A	T	1860
C	T	T	C	A	T	1920
A	T	A	C	A	A	1980
C	A	T	C	T	T	2040
G	G	A	T	A	G	2100
A	G	T	T	G	T	2160
A	A	T	T	T	G	2174

Seq ID NO: C245 Protein Sequence  
Protein Accession #: NP\_004433

65  
70  
75  
80

1	11	21	31	41	51	
M	L	E	T	L	M	60
V	C	N	F	S	R	120
D	S	A	T	K	P	180
Y	G	G	C	M	S	240
C	N	G	D	E	M	300
T	N	C	V	R	N	360
I	C	K	S	G	S	420
S	P	Q	F	A	S	480
Y	N	A	T	A	I	540
L	P	L	I	I	G	600
F	T	Y	E	D	P	660
T	E	K	Q	R	R	720
V	I	Q	L	V	G	780
Y	T	S	A	L	G	840
E	Q	D	R	L	P	900
I	N	L	P	L	L	960
L	A	G	H	Q	K	987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP\_114148.1

```

1      11      21      31      41      51
5  MDARRVPQKD LRVIKQNLKKE RYVKLISMET SSSSDSDSDS FASDNFANTR LQSVREGCRT 60
   RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNDSDEDES GMNFLEKRAL 120
   NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180
   TRSRRLILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMVE DDLPRSSRRS SSVTLPHIIR 240
   FVEEITEGGV GERLQQPSKR RYITVHWALL VINAVRRLLI PKQTAETQTA GAFAESSVAP 300
10 AFETVMVKRS GMLCWIRTGI ARLVEESATA VSAGSEMDGV RLGSGLCI 347

```

Seq ID NO: C247 Protein Sequence  
Protein Accession #: NP\_036577.1

```

15 1      11      21      31      41      51
   MENPSPAAL GKALCALLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60
   PLPRPPAQWS SLLGAHSSD YSMWRKNQYV SNGLRDPFAER GEAWALMKEI EAAGEALQSV 120
   HAVFSAPAVP SGTGQTSAEL EVQRRHSLVS FVVRIVPSPD WFGVVDLSDL CDGDRWREQA 180
20 ALDLYPYDAG TDSGTFSSP NFATIPQDTV TEITSSSPSH PANSFYFRL KALPPIARVT 240
   LVRLLQSERA FIPPAVLPS RNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTSK 300
   RTRYVRVQPA NNGSPCELE EEAECVPDNC V 331

```

Seq ID NO: C248 Protein Sequence  
Protein Accession #: NP\_063947.1

```

25 1      11      21      31      41      51
   MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
   YFLCGQPLHF IPKQQLCDGE LDCPLGEDEE HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120
   GWFSAACFDN FTEALAEAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
   GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDSNFWQV SIQYDKQHC GGSILDPHWV 240
   LTAACHCFRKH TDVFNKVRRA GSDKLGSPFS LAVAKIIIE FNPMPKOND IALMKLQFPL 300
   TFSGTVRIPC LPFFDEELTP ATPLWIGWG FTQNGGKMS DILLQASVQV IDSTRCNADD 360
35 AYQGEVTEKM MCAGIEGGV DTCQGDSSGP LMYQSDQWHV VGIWSWGYGC GGPSTPGVYT 420
   KVSAYLNWIY NVWKAL 437

```

Seq ID NO: C249 Protein Sequence  
Protein Accession #: NP\_003036.1

```

40 1      11      21      31      41      51
   MGCKVLLNIG QQLRRKVVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60
   NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELMA FITGWNILIS 120
45 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGV L AENPDIFAVI IILILTGLLT 180
   LGVKESAMYN KIFTICINLV LGFIMVSGFV KGSVKNQWLT EEDFGNTSGR LCLNNDTKEG 240
   KPGVGGFMFP GFSGVLSGAA TCFYAFVGFD CIATTGEEVK NPQKAIPVGI VASLLICFIA 300
   YFGVSAALTL MPMYFCLDNN SPLPDAFKHV GHEGAKYAVA VGSLCALSAS LLGSMFPMFR 360
   VIYAMAEGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLDV LMSIGTLAY 420
50 SLVAACVLVL RYQPEQNLV YQMASTDEL DPADQNELAS TDSQLGLFLP EAEMFSLKTI 480
   LSPKNMEPSK ISGLIVNIST SLIAVLIITE CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540
   VVTGVIWRQP ESKTKLSFKV PFLPVLPILS IFVNVYLAMQ LDQGTWVRFA VMMLIGFIY 600
   FGYGLWHESE ASLDADQART PDGNLDQCK 629

```

Seq ID NO: C250 Protein Sequence  
Protein Accession #: NP\_002767.1

```

55 1      11      21      31      41      51
   MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPMQ 60
   VSLFNGLSFH CAGVLVDQSW VLTAAHCGNK PLWARVGGDH LLLLQGEQLR RTRRSVVHFK 120
60 YHQGSGPILP RRTDEHDLML LKLARFVVFG PRVRALQLPY RCAQPGDQCQ VAGWGITAAR 180
   RVKYNKGLTC SSITILSPKE CEVFYPGVVT NNNICAGLDR QQDPCQSDSG GPLVCDETLQ 240
65 GLSWGVYPC GSAQHPAVYT QICKYMSWIN KVIRSN 276

```

Seq ID NO: C251 Protein Sequence  
Protein Accession #: XP\_095088.3

```

70 1      11      21      31      41      51
   MTRAATAEPG RVSPASPARS TAGLPRAFLQ SLRTLDDILD DWQRCVHLR EIQSLWVEAR 60
   ELPSGVLEGL SQRGPGQGA AVRSRRGGAV PRGARAVPER CAGTETRGR RCSGLQLRG 120
   GFRGCPADPC ARGEHRRHTI TSGVDCGLLK QMKELEQKE VLLQGLEMA QGRDWYQQQL 180
75 QVQVERQCRL GQSRASADFG AVGSPPRLGR LLPKVQEVAR WLGLLEAEAC AGRALPTSSS 240
   GPCCSALTST SSPGWQQQII LMLKEQNRLL TQEVTEKSR ITQLEQKSAL IKQLFEARAL 300
   SQQDGGLSPA GPHEIPLTRF RLPVLTWAGA LLSFSPQLL LPLSADSGGP LHELPDTWFP 360
   AVLLWVSPG KRTAHARLHF HQRPAEGAWQ LGCGAAEAP E TCGTLPHFES HKTCEPDSL 420
   GGPCPQEGDR SWSHLGAAPD VAPAVAKVTP NREDAAGSRH GDICPLCPKG LLTPFDIAIE 480
   FSLAEWQCLD HAQNLRYRDV MLENYRNLFS LGMTVSKPDL IACLEQNKEP QNKRNEMAA 540
80 KHPVTCSEFN QDLQPEQSIK DSLQKVIPT YGKCGHENLQ LKCKCKRVDE CEVHKGGYND 600
   LNQCLSTNQ KIFQTHKCVK VFSKFSNSNR HNARYTGKXH LKCKKYGKSF CMFSLNQHQ 660
   IHTKEKSYK CEECKSPNH SSGTTHKRI LTGEKPYRCE ECGKAFRWS NLTRHKRIHT 720
   GEKPYACEC GQAFRRSSTL TNHKRIHTGE RPYKCEBCK AFSVSSALY HKRIHTGEK 780
   YTCBEOGKAF NCSSTLTKTHK IHTGEKPYT CEECGRTFNC SSTVKAHKRI HTGEKPYKCE 840

```

5 ECDKAFKWHK SLAKHKIIHT GEKPYKCSDS KALAKSSEVQ KVSXGDGNG IRVHKKKETQ 900  
 10 GWLVRNKNEN RTGLFQIRAA VRPNRDPSSG QQEGSLTDPI QRKEEPLDQV HYDHQNALED 960  
 QRTQGVGGLL TFRDVVIEFS LEWQCLDHA QNLYRDVML ENYRNLVSLG IAVSKPDLIT 1020  
 CLEQNKPEWN IKRNMVTKH PDLPPLEGIK DSLQKVIPRR YGKSGHDNLQ VKTCKSMGEC 1080  
 EVQKGGCNEV NQCLSTQNK IFQTHKCVK FGKFSNSNRH KTRHTGKKHF KCKKYGKSFC 1140  
 MVSQHLHQHI IHTRENSYQC EEOGKPFNCS STLSKHKRIH TGEKPYRCEE CGKAFWSSST 1200  
 LTKHRRHHTG EKPYTCEECG QAFSRSSSTA NKKRIHTGEX PYTCEECGKA FSLSSSLTYH 1260  
 KRIHTGEKPY TCEECGKAFN CSSTLKKHKI IHTGEKPYKC KECGKAFAPS STLNTHKRIH 1320  
 TGEKPYKCEE CDKAFKWSST LANHKSMTGT EKPYPKCE 1357

Seq ID NO: C252 Protein Sequence  
 Protein Accession #: NP\_114433.1

15 1 11 21 31 41 51  
 MASRSMRLLL LLCLAKTGV LGDIIMRPSG APGWFFYHKS CYGYFRKLRL WSDAELECOG 60  
 YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120  
 KSMGGNKHCA EMSSNNFLIT WSSNECNKRG HFLCKYRP 158

20 Seq ID NO: C253 Protein Sequence  
 Protein Accession #: XP\_051860.2

25 1 11 21 31 41 51  
 MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK FVRPKLTVTI DTNVNSTILN 60  
 LEDNVQSWKP GDTLVIASST YSMYQAEFQ VLPSCRSCAPN QVKVAGKPMY LHIGEEIDGV 120  
 DMRAEVGLLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIFKALGFK AAHLEGTELK 180  
 HMQQLVGGY PIHFHLAGDV DERGGYDPPT YIRDLSEIHT FSRCVTVHGS NGLLIKDVVG 240  
 YNSLGHCFPT EDGPEERTFP DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300  
 30 DCNAVSTFPM ANPMNNLINC AAAGSEETGF WFIFHHVPTG PSVGMYSPTY SEHIPLGKPY 360  
 NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLISIISARYS PHQDADPLKP REPAIRHFI 420  
 AYKNQDHGAW LRGGDVWLDG CRFADNGIGL TLASGGTFPY DDGSKQEIKN SLFVGESGNV 480  
 GTEMMDNRIW GPGGLDHSGR TLPICQNFPI RGIQLYDGPQ NIQNCFTFRK VALEGRHTSA 540  
 LAFLRLNAWQ SCPHNNVTGI AFEDVPITSR VFFGEPGPWF NQDMDGDKT SVFHDVDGVS 600  
 35 SEYPGSYLTK NDNMLVLRHPD CINVDWRGA ICSGCYQMY IQAYKTSNLR MKIINKDFPS 660  
 HPLYLEGALT RSTHYQQYQP VVTLOKGYTI HMDQTAPEL AIWLINFNKG DWIRVGLCYP 720  
 RGTTFSLSD VHNRLKQTS KTGVPVRLTQ MDKVEQSYPG RSHYYWDEDS GLLFLKLAQ 780  
 NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKRLFGSQLK 840  
 40 TKDHPLEVKM ESSKQHFPHL WNDFAFIEVD GKYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900  
 NSILQGIPIWQ LFNVTATIPD NSIVLWASKG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV 960  
 GPKGSFRPIW VTLDTEDHKA KIFQVVPPIV VKKKKL 996

Seq ID NO: C254 Protein Sequence  
 Protein Accession #: NP\_055188.1

45 1 11 21 31 41 51  
 MTALSSENCN FQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT QQNFMEYPCI 60  
 SLAFVDLILL VNISILLYFR DFVLLSIRPT KYHICLFTQI ISFTYGLFHY PVFLTACIDY 120  
 50 CLNFSKTKKL SFKQKLFYF FTVILIWISV LAYVLGDPAL YQSLKAQNAV SRHCFFYVSI 180  
 QSYWLSFFMV MILFVAFITC WEEVTTLVQA IRITSYMNNT ILYFPFSSHS SYTVRSKKIP 240  
 LSKLIVCFLS TWLPFVLQV IIVLLKQVPI AYIEMNIPWL YFVNSFLIAT VYWNCEKLN 300  
 LKIDGLPLDP FVNWKCCPIP LTIPLNEQIE KPTISIMIC 338

55 Seq ID NO: C255 Protein Sequence  
 Protein Accession #: Eos sequence

60 1 11 21 31 41 51  
 MALVLGSLLL LGLCGNSPSG GQPSSTDAPK AMNYELPATN YETQDSHAG PIGILFELVH 60  
 IFLYVVQPRD FPEDTLRKFL QKAYESKIDY DKIVVYEAGI ILCCVLGLLF IILMPLVGYP 120  
 FCMCRCCNKC GGMHQHQKE NGPFLRCKFA ISLVICIII SIGIFYGFVA NHQVTRIKR 180  
 SRKLADSNFK DLRTLLNETP EQIKYILAQY NTKDKAFTD LNSINSVLGG GILDRLRPN 240  
 65 IPVLDEIKSM ATAIKETKEA LENMNSTLKS LEQOSTQLSS SLTSVKTSLR SSLNDPLCLV 300  
 HPSSETCNSI RLSSLQNSN PELRQLPFVD AELDNVNNVL RTDLGLVQVQ GYQSLNDIPD 360  
 RVQRQTITTV AGIKRVLSNI GSDIDNVTR LPIQDILSAF SVYVNNTESY IHRNLTLEE 420  
 YDSYWWLGL VICSLTLIV IFYLLGLLGG VCGYDREATP TTRGCVSNTG GVFLAVGVGL 480  
 SFPLCWILMI IYVLTFFVGA NVEKLICEPY TSKELFVILD TPYLLNEDWE YVLSGKLPNK 540  
 SKMKLTFEQV YSDCKNRTG YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNINIFL 600  
 70 LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLIS PAYDLEAKN SLPPGNLRNS 660  
 LKRDAQTIKT IHQQRVLPIS QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFQNFITN 720  
 NTSSVIISET KKYGRITIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID 780  
 75 PLNLPWFGIG KATVFLPAL IPAVKLAKY RMDSSEDVYD DVETIPMKNM ENGNNGYHKD 840  
 HVGIGHNPVM TSPSQH 856

Seq ID NO: C256 Protein Sequence  
 Protein Accession #: NP\_149038.1

80 1 11 21 31 41 51  
 MKAIHLTLT ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60  
 PSFPTATSPA PPIIISTHSS TIPTPAPPII STHSSSTIPI PTAADSESTT NVNSLATSDI 120  
 ITASSPNDGL ITMVPSSTQS NNEMSPPTED NQSSGPPTGT ALLETSTLNS TGPSNCPQDD 180  
 PCADNSLCVK LNTSFCLCL EGYVNSSTC KKGKVFPGKI SVTVSETFDP EERKSMAYQD 240

5 LHSSEITSLFK DVFQTSVYQG TVILTVSTSL SPRSEMRADD KFNVTIVTI LAETTSNEK 300  
 TVTEKINKAI RSSSSNFLNY DLTILRCOYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360  
 VASSLKCPDA CNAQHKQCLI KKSOGAPECA CVPQYQEDAN GNCQKCAFY SGLDCKDKFQ 420  
 LILITVGTIA GIVILSMIIA LITVARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480  
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY 512

Seq ID NO: C257 Protein Sequence  
 Protein Accession #: NP\_001423.1

10 1 11 21 31 41 51  
 | | | | | |  
 MTAGRRMEML CAGRVPALLL CLGFHLLQAV LSTTVIPSCI PGESSEDNCTA LVQTEDNPRV 60  
 AQVSITKCSS DMNGYCLHQG CIYLVDMSON YCRCEVGYTG VRCEHFFLTV HQPLSKEYVA 120  
 15 LTVILILFL ITVVGSTYYP CRWYRNKRSK EPKKEYERVY SGDPELRQV 169

Seq ID NO: C258 Protein Sequence  
 Protein Accession #: AAC63902.1

20 1 11 21 31 41 51  
 | | | | | |  
 MDRSKENCIS GPVKATAPVG GPKRVLVTQQ IPCQNPLPVN SGQAQRVLCV SNSSQVRVLIQ 60  
 AQKLVSSHAP VQNKQKQKQLQ ATSVPHPVSR PLNNTQKSKQ PLPSAPENNP EEBELASKQKN 120  
 EESKQRQWAL EDFEIGRPLG KKGKFGNVYLA REKQSKFILA LKVLFAQLE KAGVEHQLRR 180  
 25 EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL 240  
 ANALSYCHSK RVIHRRDIKE NLLLSAGEL KIADFGWSVH APSSRRITLC GTLDYLPPEM 300  
 IEGRMHDEKV DLWSLGLVLCY EFLVGKPPFE ANTYQETVKR ISRVEFTFPD FVTEGARDLI 360  
 SRLKHNPSQ RPLRLREVLEH PWITANSSKP SNCQNKESAS KQS 403

30 Seq ID NO: C259 Protein Sequence  
 Protein Accession #: NP\_037504.1

35 1 11 21 31 41 51  
 | | | | | |  
 MSRTAYTVGA LLLLLGLTLLP AAEGKKKGSQ GAIPPPDKAQ HNDSEQTQSP QPQSRNRGR 60  
 GQGRGTAMPG EEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCY 120  
 QCNSEFYIPRH IRKEEGSFQS CSFCKPKKFT TMMVTLCNCP LQPPTKKRVR TRVKQCRCIS 180  
 IDLD 184

40 Seq ID NO: C260 Protein Sequence  
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51  
 | | | | | |  
 MKVGVWLWIS FFTFTDGHGG FLGKNDGIKT KKEILVNKKK HLGPFVEEYQL LLQVITYRDSK 60  
 EKRDRLNFKL LKPPPLWWSH GLIRIIRAKA TTDCNSLNGV LQCTCEDSYT WFPSPCLDPQ 120  
 NCYLHTAGAL PSCECHLNHL SQSVNFCERT KINGTFKINE RPTNDLLNSS SAIYSKYANG 180  
 IEIQLKKAYE RIQGFESVQV TQPRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALEK 240  
 LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300  
 50 LSLLEELNKN FSGMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNIISSLSL 360  
 ASHPRVSNST MEDVISIADN ILSASVTNW TVLLREEKYA SSRLLLETLEN ISTLVPTTAL 420  
 PLNFSRKPID WKGIPVKNQK LKRGYSYQIK MCPQNTSIP I RGRVLIGSDQ FQRLPETII 480  
 SMASLTGNI LPSVKNQNAQ VNGPVISTVI QNYSINEVFL PFSKIESNLS QPHCVFWDPS 540  
 HLQWMDAGCH LVNETQDITV CQCTHLTSFS ILSPPFVPT IFFVVKWITY VGLGISIGSL 600  
 55 ILCLIIELAF WQIHKKSQTS HTRRICMVNI ALSLLIADWV FIVGATVDTT VNPSGVCTAA 660  
 VFFTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQHLMA VGFCLYGCP LIISVITIAV 720  
 TQPSNTYKRK DVCWLNWSNG SKFLAFVVP ALAIVAVNPF VVLLVLTKLM RPTVGERLSR 780  
 DDKATIIIRVG KSLLLITPL GLTWGFGIGT IVDSQNLAWH VIFALINAFQ GPFILCFGIL 840  
 LDSKLRLFP NKLKLSLSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA FSHGDSDDN 900  
 60 IMLTQFVNSE 910

Seq ID NO: C261 Protein Sequence  
 Protein Accession #: NP\_000575.1

65 1 11 21 31 41 51  
 | | | | | |  
 MTSKLAVALL AAPLISAALC EGAVLPRSAK ELRCQCIKTY SKPFPKFIK ELRVIESGPH 60  
 CANTEIIVKL SDGRELCLDP KENWVQRVVE KPLKRAENS 99

70 Seq ID NO: C262 Protein Sequence  
 Protein Accession #: NP\_005594.1

75 1 11 21 31 41 51  
 | | | | | |  
 MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGSV EPEQNRVNRE AEENREPFRK 60  
 ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAFTPIPM NLFEQFKRAA 120  
 NLYFLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTECV 180  
 IKDGRPFVAK WKEIQVGDVI RLKKNDFVPA DILLSSSEP NSLCYVETAE LDGETNLKFK 240  
 MSLEITDQYL QREDTLATFD GFICEEPPNN RLDKFTGTIL WRNTPPLDA DKILLRGCVI 300  
 80 RNTDFCHGLV IFAGADTKIM KNSGKTRPKR TKIDYLANYM VYTIFFVLLI LSAGLAIGHA 360  
 YWEAQVGNSS WLYLDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLQSHFIN 420  
 WDLQMYAEK DTPAKARTTT LNEQLGQIHY IPSDKTGTLT QNIMTFKKCC INQIYGDHR 480  
 DASQHNHNKI EQVDFSWNTY ADGKLAFYDH YLIEQIQSGK EPEVRQFFFL LAVCHTMVD 540  
 RTDGLQNYQA ASFDEGALVN AARNFGPAFL ARTQNTITIS ELGTERTYNV LAILDPNSTR 600  
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIPANET LRTLCCLCYKE 660

5  
10  
15  
20  
25  
30

```

IEEKEFTWVN KKFMAASVAS TNREALDKV YEEIEKDIL LGATAIEDKL QDGVPEITISK 720
LAKADIKIWN LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
KFAPVQESF FPPGGRNALI ITGSMNLIL LEKTKRINKI LKLFPRTEE ERRMRQSKR 840
RLEAKKEQRQ KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVM 900
IKTAHIGVGI SQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNFA 960
FTLVHFWYSP FNGYSAQTAY EDWFTILYNV LYTSLPVLML GLLDQDVSDK LSLRFPGLYI 1020
VGQRDLLENY KRFFVSLHLG VLTSMILFFI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL 1080
VITVNFQIGL DTSYNTFVNA FSIFGSIALY FGIMFDFHSA GIHVLFPSAF QFTGTASNAL 1140
RQFYIWLITII LTVAVCLLPV VAIRFLSMTI WPSSEDKIQK HRKRLKAEEQ WQRRQVFR 1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPDLAIVAD GTAEYRRTGD S 1251

```

Seq ID NO: C263 Protein Sequence  
Protein Accession #: XM\_044533

15  
20  
25  
30

```

1 11 21 31 41 51
| | | | |
MLRTAMGLRS WLAAPWGAIP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
RFAEHISNY TALLLSRDRG TLVVGAREAL FALSSNLSPF PGGEYQELLW GADAEKKQCC 120
SFKGKDPQPD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY IMENFTLAR DEKGNVLLED 180
GKGRCPDPDN PKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SINWLQDPAF 240
VASAIPESL GSLQGDDEKI YFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
TSFLKAQLLC SRPDDGFFPN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
FTMKDVQRFV SGLYKEVNR E TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
NFLKDHFLMD GQVSRMILL QPQARYQVVA VHRVPGLLHT YDVLFLGTGD GRHLKAVSVG 480
PRVHIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
PYCAWSSGSS KHVSILQPOL ATRFWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
FQNTVNTILA CPLLSNLATR WLENGAPVN ASASCHVLT GDLLLVGTQQ LGFEQCWSLE 660
EGFQQLVASY CPEVVEDGVA DQTEGGSSVP VIISTSRVSA PAGGKASWGA DRSYNKEFLV 720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
PLDHRGYQSL SDSPGSRVFP TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV 837

```

Seq ID NO: C264 Protein Sequence  
Protein Accession #: NP\_008950.1

35  
40

```

1 11 21 31 41 51
| | | | |
MASQNRDPA TSVAAARKGA EFGGGAARGP VGKRLQQLM TLMMSGDKGI SAFPESDNLF 60
KWWGTHGAA GTTYEDLRYK LSLFPPSGYP YNAPTVMKLT PCYHENVDTQ GNICLDILKE 120
KWSALYDVRT ILLSIQSLLG EPNIDSPLNT HAAELWKNPT AFKXYLQETY SKQVTSQEP 179

```

Seq ID NO: C265 Protein Sequence  
Protein Accession #: NP\_055399.1

45  
50  
55

```

1 11 21 31 41 51
| | | | |
MGRGWGFLFG LLGAVLLSS GHGEEQPPET AAQRFCQVVS GYLDDCTCDV ETIDRFNNYR 60
LFPRLQKLE SDYFRYKVN LKRPCPFWD ISQCGRRDCA VKPCQSDVDP DGIKSASYKY 120
SEENANLIEE CEQAEELGAV DESLSEETQK AVLQWTKHDD SSDNFCEADD IQSPEAEVVD 180
LLLNPERYTG YKGPDAWKI NVIYEENCFK PQTIKRPLNP LASGQQTSEE NTFYSWLEGL 240
CVERAPFYL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEFQQRFDG ILTEGEGPRR 300
LKNLYFLYLI ELRLSKVLP FFERPDQLF TGNKIQDEEN KMLLEILHE IKSPLHFDPE 360
NSFPAGDKKE AHKLKEDFRL HFRNISRIMD CVGCKFCRLW GKLTQQLGT ALKILFSEKL 420
IANMPESGPS YEFILTRQEI VSLFNAFGRI STSVKELENF RNLLQNIH 468

```

Seq ID NO: C266 Protein Sequence  
Protein Accession #: NP\_002879.1

60

```

1 11 21 31 41 51
| | | | |
MQPRRQLRPA FWSGPRGRPR TAPLLALLL LAFVAAPAGS GGPDDPGQPQ DAGVPRRLIQ 60
QKARAALHFF NFRSGSPSAL RVLAEVQGR AWINPKEGCK VHVVFSTERY NPESLLQEGE 120
GRIGKCSARV FFKQKPRPT INVTCTRLIE KKKRQQEDYL LYKQMKQLKN PLEIVSIPDN 180
HGHIDPSLRL IWDLAPLGSS YVMWEMTTQV SHYLLAQLTS VRQWVRKT 228

```

65  
70

```

Seq ID NO: C267 Protein Sequence
Protein Accession #: NP_005400.1

1 11 21 31 41 51
| | | | |
MSVKGMAIAL AVILCATVVQ GPFMFKRGRC LCIGPGVKAV KVADIEKASI MYPNNCDKI 60
EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

```

Seq ID NO: C268 Protein Sequence  
Protein Accession #: PGENESH predicted

75  
80

```

1 11 21 31 41 51
| | | | |
MLRQVLRRGL QSFCHRLGLC VSRHPVFFLT VPAVLITITF LSALNRPOPE GDLERLVAPS 60
HSLAKIERSL ASSLFPLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120
VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIISVLEDL RQAAVSNKTT ARVQVRYFNT 180
KLKVCSCML LPKEAALHF LP 202

```

Seq ID NO: C269 Protein Sequence  
Protein Accession #: NP\_002429.1



	1	11	21	31	41	51	
5	MRLPLLLVFA	SVIPGAVLLL	DTRQFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	60
	VSESIQMSVA	FKLCIGVPSK	TDWVAITLYA	CDKSEBFQKW	ECKNDTLLGI	KGEDLFFNYG	120
	NRQEQINIMLY	KGSGLWSRWK	IYGTDDNLCS	RGYEAMYTL	GNANGATCAF	PFKFNKMYA	180
	DCTSAGRSDDG	WLWCGITTDY	DTDCLFGYCP	LKFEGSESLW	NKDPLTSVSY	QINSKSALTW	240
	HQARKSCQQQ	NAELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNSLSFNSGW	QMSDRSPFRY	300
10	LNLWPGSPSA	EPGKSCVSLN	PGKNKAWENL	ECVQKLGYSIC	KKGNTTLNSF	VIPSESDVPT	360
	HCPSQWKPYA	GHCYKIHRRDE	KKIQRDALTT	CRKEGGDLTS	IHTIEELDFI	ISQLGYEPND	420
	ELWIGLNDIK	IQMYFWSDDG	TPVTFTKWLR	GEPSEHNRRQ	EDCVVMKGKD	GYWADRGCEN	480
	PLGYICKMKS	RSQGPETIVEV	EKGCRCGWKK	HHFYCYMIGH	TLSTFAEANK	TNNENAYLT	540
	TIEDRYEQAF	LTSFVGLRPE	KYFWTGLSDI	QTKGTFFQWTI	EEEVRFTHWN	SDMPGRKPGC	600
	VAMRTGIAGG	LWDVLKCDK	AKFVCKHWA	GVTHPPKPTT	TPEPKCPEDW	GASSRTSLCF	660
15	KLYAKGKQW	KTFESRDRC	RALGGDLASI	NNKEEQQTW	RLITASGSYH	KLFWLGLTYG	720
	SPSEGGTWD	GSPVSYENWA	YGEFNNYQNV	EYCGELKGD	TMSWMDINCE	HLNWNICQIQ	780
	KGQTPKPEPT	PAPQDNPPVT	EDGWVIYKDY	QYFYSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESEKPLMKY	VNRNDAQSAY	FIGLLISLSD	KFAWMDGSKV	DYVSWATGEP	NFANEDENCV	900
20	TMYSNSGFWN	DINGCPNPAF	ICQRHNSIN	ATTVMPTMPS	VPSGCKEGWN	FYSNCKPKIF	960
	GFMEERQW	QEARAKCIGF	GGNLVSIQNE	KEQAFITYHM	KDSTPSAWTG	LNDVNSEHTF	1020
	LWTDGRGVHY	PMWKGYPGG	RRSSLSYEDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPSLTNP	TAQITQDGFV	KYKSSYSLSM	RQKFCWHEAE	TYCKLHNSLI	ASILDIFYSNA	1140
	FAWLQMETSN	ERVHIALNSN	LTDNQYTWD	KWRVRYTNWA	ADEPKLSAC	VYLDLDGYWK	1200
25	TAHCNESFYQ	LCKRSDEIPA	TEPPQLPGR	PESDHTAWIP	FHGHCYIYES	SYTRNMGQAS	1260
	LECLRMGSSL	VSISAAESS	FLSYRVEPLK	SKTNFWIGLF	RNVEGTWLIW	NNSPVSVFNW	1320
	NTGDPGGERN	DCVALHASSG	FWSNIHCSSY	KGYICKRPKI	IDAKPTHELL	TTKADTRKMD	1380
	PSKPSNVAG	VVIIVILLIL	TGAGLAAYFF	YKRRVHLPO	EGAPENTLYF	NSQSSPGTSD	1440
	MKDLVGNIEQ	NEHSVI					1456

Seq ID NO: C270 Protein Sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LLFPLSSRTQ	KLPTRDEELF	QMQIRDKAFF	HDSSVIPDGA	EISSYLFRDT	60
	PKRYFFVVEE	DNTPLSVTVT	PCDAPLEWKL	SLQELPEDRS	GGSGDLEPL	EQKQKQIINE	120
	BGTLEFSYKG	NDVYEFISS	SPSGLYQLDL	LSTEKDTHEK	VYATTPESD	QYPPELPYDP	180
	RVDVTSLGRT	TUTLAWKPSP	TASLLKQPIQ	YCVVINKEHN	FKSLCAVEAK	LSADDAFMA	240
40	PKPGLDFSPF	DFAHFGFPSP	NSGKERSFQA	KPSPKLGRHV	YSRPKVDIQK	ICIGNKNIFT	300
	VSDLKPDQY	YDFVFNIN	SNMSTAYVGT	FARTKEBAKQ	KTVELKDGKI	TDVFKRKGA	360
	KFLRFAFVSS	HQKVTFFIHS	CLDAVQIQVR	RDGKLLLSQN	VEISIQOQLR	GKPKAKYLVR	420
	LKGNKKGASM	LKILATTRPT	KQSFPSLPED	TRIKAFDKLR	TCSSATVAML	GTQERNKFCI	480
	YKKEVDNIN	EDQKQRENOQ	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTE	TIKGLQPGKS	540
45	YLLDVYVIGH	GGHSVKYQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence  
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QMEKKLQEP	RSTRNKEKED	RESSEYWNKS	GKVGKLVNQS	YMSQNKGNV	60
	VKFSAGKVKL	KLLKQIQEP	VKPTVNYKMA	NSSECEKPKI	NGKVCQCEN	KAALLVCLEB	120
	GEDYCSGCPA	NVHQKQALKL	HRTTLLQARS	QILFNVLDA	HQPKVDNPD	EPKEENSTK	180
55	ETSKIQHKPK	SVLLQSSSE	VEITTMKRAQ	RTKPRKSLLC	EGSFDEEASA	QSFQEVLSQW	240
	RTGNHDDNKK	QNLHAAVNDK	LEECEVQTNL	KIWRREPLNIE	LKEDILSYMB	KLWLKXHRR	300
	PQEQLFKCYQ	IRSHHMKPL	VMHSVLKMK	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence  
Protein Accession #: NP\_078963.1

	1	11	21	31	41	51	
60	MEKLNKXKR	RTPQEQLFQM	LSDTFFPHPE	TTGDAQCSQN	ENDEDSGDEE	TKVQHTALLL	60
	PVETLNIERP	EPSLKIVELD	DTYEEEFEEA	ENIVPYKVKL	ADADSQRSCA	PHDCQKNSFP	120
65	YENGIIQHVV	FDKGRDPLN	LCLANSSTYY	KDNKSGETSN	TDFDNIIVDP	VYSSDIEKIE	180
	ESTSPERNLK	EKNIGLESNQ	KSDSDCVSLE	SKDTLLGRDL	EKAPIEEKLS	QDIKESLELS	240
	NLYKRPSPFE	SKTTKSSLLL	QEIACRSKPI	TKQYQGLERF	FIFDTNERLN	LLPSHRLCEN	300
	NSSTRITLAE	DREWIPDHS	SEYADNAIVL	GVLQGAQSPS	SSRKQKQMGQ	KSQRFPSTANF	360
70	PLNSVSKESS	SCLSSSHPRS	RSAAAQSSSR	AASEISEIEY	IDITDQNELS	LDDTTDQHTL	420
	DNLEKELQVL	RSLADTSEKL	YSLTSEFPD	FSSQSLNISQ	ISTDFLKTSH	VRGPCGVVEEL	480
	SCSGRDTKIQ	SLSLSESST	DEEEDFLNK	QHVITLPSK	ST		522

Seq ID NO: C273 Protein Sequence  
Protein Accession #: NP\_005399.1

	1	11	21	31	41	51	
75	MKVSALLCLL	LLMTAAFNPO	GLAQPDALNV	PSTCCFTFSS	KKISLQRLKS	YVITTSRCPO	60
80	KAVIFRTKLK	KICADPKEK	WVQNYMKHLG	RKAHTLKT			98

Seq ID NO: C274 Protein Sequence  
Protein Accession #: BAC05158.1

	1	11	21	31	41	51
--	---	----	----	----	----	----

15 Seq ID NO: C275 Protein Sequence  
Protein Accession #: AAA60212.1

Seq ID NO: C276 Protein Sequence  
Protein Accession #: NP\_631911.1

Seq ID NO: C277 Protein Sequence  
Protein Accession #: NP\_473364.1

45 Seq ID NO: C278 Protein Sequence  
Protein Accession #: FGENESH predicted

Seq ID NO: C279 Protein Sequence  
Protein Accession #: XP\_168571.1

Seq ID NO: C280 Protein Sequence  
Protein Accession #: NP\_005257.2

1 11 21 31 41 51  
| | | | |  
MGDWSPLGNF LEEVHKHSTV VGKVLTLVLF IFRMLVLGTA ARSSWGDBQA DFRCDTIQPG 60  
CONVCYDOAF PISHIRYWVL OIFVSTPSL VVMGHAMHTV RMOEKKRLRE ASRAKEVRGS 120

GSYEYPVAEK AELSCWEEGN GRIALQGTLL NTYVCSILIR TTMEVGFIIVG QYFIYGIFLT 180  
 TLHVCRNSPC PHVNVYVSR PTEKNVFIVF MLAVAALSLL LSLAELYHLG WKKIRQRFVK 240  
 PRQHMAKQCL SGSPVGIVQS CTPPPDFNQC LENGPGGKFF NPFSNNMASQ QNTDNLVTEQ 300  
 VRGQEQTPGE GFIQVRYGQK FEVFNVSVP GRLPHGYHSD KRRLSKASSK ARSDDLVS 358

Seq ID NO: C281 Protein Sequence  
 Protein Accession #: NP\_055274.2

1 11 21 31 41 51  
 | | | | |  
 MYLSICCCFL LWAPALTKN LNYSVPEEQG AGTVIGNIGR DARLQPLFP AERGGGGRSK 60  
 SGSYRVLENS APHLLDWDAD SGLLYTKQRI DRESLCRHNA KCQLSLEVFA NDKEICMIKV 120  
 EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDPD AGENGLRITYL LTRDDHGLFG 180  
 LDVKSREGDT KFPELVIQKA LDREQQNHHT LVLTAIDGGE PPRSATVQIN VKVIDSNDNS 240  
 15 PVFEAPSYLV ELPENAPLGT VVIDLNATDA DEGNNGEVLY SFSSYVPPDRV RELFSIDPKT 300  
 GLIRVKGNDL YEENGLMELD VQARDLGPNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA 360  
 LSEAPPGTV IALVRVTRD SGKNGQLQCR VLGGGGTGGG GGLGGPGGSV PFKLEENYDN 420  
 FYTVVTRDPL DRETQDEYN TIVARDGGSP PLNSTKSFAP KILDENDNPP RFTKGLYVLQ 480  
 VHENNIPGEY LGSVLAQDPD LQNGTVSYS ILPSHIGDVS IYTYVSVNPT NGAIYALRSP 540  
 20 NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTVLDVNDNA FVIVLPTLQN DTAELQVPRN 600  
 AGLGYLVSTV RALSDRGES GRLTYEIVDG NDDHLFEIDP SSGEIRTLP FWEDVTPVVE 660  
 LVVKVTDHGK PTLSAVAKLI IRSVSGSLPE GVPVRNGEQH HWDMSLPLIV TLSTISIILL 720  
 AAMITIAVKC KRENKEIRTY NCRIAESYSH QLGCGGKGGK KINKNDIMLV QSEVEERNAM 780  
 NVMNVSSPS LATSPPMYFDY QTRLPLSSPR SEVMYLPAS NNLTVPPQGA GCHTSFTGQG 840  
 25 TNASETPAIR MSIIQTDNFP AEPNYMGSRO QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence  
 Protein Accession #: NP\_005592.1

1 11 21 31 41 51  
 | | | | |  
 MELCRSLALL GSSLGLMFCL IALSTDFWFE AVGFTHSAHS GLNPTGHGDI ISGYIHTQT 60  
 FSIMAVLWAL VSVSEFLVLS FSLFPPGHG PLVSTTAFAA AAISMVVAMA VYTSEWDQP 120  
 35 PHPQIQTFPS WSPYLGWVSA ILLCTGALS LGAHCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence  
 Protein Accession #: NP\_006424.2

1 11 21 31 41 51  
 | | | | |  
 MATWALLLLA AMLLGNPGLV FSRLSPEYYD LARAHLRDEE KSCPCLAQEG PQGDLLTKTQ 60  
 ELGRDYRTCL TIVQKLKXKV DKPTQRSVSN AATRVCTGR SRWRDVCNRF MRRYQSRVTQ 120  
 40 GLVAGETAQQ ICEDLRLCIP STGPL 145

Seq ID NO: C284 Protein Sequence  
 Protein Accession #: NP\_005594.1

1 11 21 31 41 51  
 | | | | |  
 MKVSAALAV ILIATLAP ASASPYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP 60  
 50 AVVFTRKMR QVCANPEKKW VREYINSLEM S 91

Seq ID NO: C285 Protein Sequence  
 Protein Accession #: NP\_071437.1

1 11 21 31 41 51  
 | | | | |  
 MAPGRAVAGL LLLAAAGLGG VAECPGLAFS EDVLSVPGAN LSLSAAQLQH LLEQMGAASR 60  
 VGVPEPGQLH FNQCLTAEEI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPKHK 120  
 TRPSHSEVWG YGFLSVTIIN LASLLGLILT PLIKKSYFPK ILTFFVGLAI GTLFSNAIFQ 180  
 LIPEARGFDP KVDSYVEKAV AVFGGFYLLP FFERMLKMLL KTYGQNGHGH PGNDNFGPQE 240  
 KTHQPKALPA INGVTCYANP AVTEANGHIH FDNVSVVSLQ DGKKEPSSCT CLKGPKLSEI 300  
 65 GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSIAT LCEEPFHELQ DVFILLNAGM 360  
 STRQALLFNF LSACSCYVGL AFGILVGNF APNIIIFALAG GMFLYISLAD MFPFEMNDMLR 420  
 EKVTRKRTDF TFFMIQNAGM LTGFTAILLI TLYAGEIELE 460

Seq ID NO: C286 Protein Sequence  
 Protein Accession #: NP\_004175.1

1 11 21 31 41 51  
 | | | | |  
 MPNSEPASLL ELFNISATQG ELVRSKAGN ASKDEIDSAV KMLVSLKMSY KAAAGEDYKA 60  
 75 DCPFGNPAFT SNHGDATEA EEDFVDPWTV QTSSAKGIDY DKLIVRFGSS KIDKELINRI 120  
 ERATGQRPHH FLRRGIFFSH RDMNQVLDAY ENKKPFYLYT GRGSPSEAMH VGHLPFFIFT 180  
 KWLQDVFNVE LVIQMTDEK YLWKDLTDQ AYGDVAENAK DIIACGFDIN KTFIFSDLDY 240  
 MGMSSGPYKN VVKIQKHVTF NQVKGIFGFT DSDCIGKISF PAIQAAPSFS NSPPQIFRDR 300  
 80 TDIQCLIPCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF 360  
 LTDTAQIKT KVNKHAFSGG RDTIEHRQF GGCNDVDVSF MYLTFFLEDD DKLEQIRKDY 420  
 TSGAWLTGEL KKAIEVLQP LIAEHQARRK EVTDEIVKEF MTPRKLSDFF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP\_004929.1

	1	11	21	31	41	51	
5	MTVFRQENV	DYDTEGEE	LGSGQFAVVK	KREKSTGLQ	YAKFIKRRRT	KSSRRGVS	RED 60
	IEREVSILKE	IQHPNVITLH	EVYENKTDVI	LILELVAGGE	LFDFLAEKES	LTEEEATEPL	120
	KQILNGVYYL	HSLQIAHFDL	KPENIMLLDR	NVPKPRIKII	DFGLAHKIDF	GNEFKNIFGT	180
	PEFVAPEIVN	YEPLGLEADM	WSIGVITYIL	LSGASPLFGD	TKQETLANVS	AVNYEFEDEY	240
10	PSNTSALAKD	FIRRLVVKDP	KKRMTIQDSL	QHPWIKPKDT	QQALSRKASA	VNMEKFKKFA	300
	ARCKWKQSVR	LISLQQLRSR	SFLSRSNMSV	ARSDDTLDEE	DSFVMKAIH	AINDDNVPGI	360
	QHLGLSLSNY	DVNQPNKHGT	PPLLIAAGCG	NIQILQLLIK	RGSRIDVDQK	GGSNNAVWAA	420
	RHGHVDTLKF	LSENKCPLDV	KDKSGEMALH	VAARYGHADV	AQVTCASAAQ	IPISRTKEEE	480
	TPHCAAWHG	YYSVAKALCE	AGCNVNIKNR	EGETPLLTAS	ARGYHDIVCE	LAEHGADLNA	540
	CDKDGHIALL	LAVRRQCMVE	TKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPVIVVACEA	600
15	NCNLDISKNY	GRTPHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSBQHEHVA	660
	GLLARLRKDT	HRGLFQQQLR	PTQNLQPRIK	LKLFQHSQSG	KTTLVESLKC	GLLSFFRRR	720
	RPRLSSTNSS	RFPSPPLASK	PTVSVSINN	YPCENVSVR	SRSMMFEPGL	TKGMLVFEVA	780
	PTHHPHCSAD	DQSTKAIDIQ	NAYLNGVGDF	SVWEFSGNPV	YFCYDYFAA	NDPTSIHVVV	840
	FSLEEPYEIQ	LNPIVFWLSP	LKSLVPVEEP	IAFGGKLQNP	LQVVLVATHA	DIMNVPRPAG	900
20	GEFGYDKDTS	LLKEIRNRFG	NDLHISNKL	FVLDAGASGSK	DMKVLNRHLQ	EIRSQIVSVC	960
	PPMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQLHSTG	1020
	EINIMQSETV	QDVLLLDPRW	LCTNVLGKLL	SVETPRALHH	YRGYTVEDI	QRLVPSDSVE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPALIKT	DNLHRSWADE	EDEVMYGGV	RIVPVEHLTP	1140
	FPGGIFHKVQ	VNLCRWIHQQ	STEGDADIRL	WVNGCKLANR	GAEILVLVNV	HGGQIEVQVR	1200
25	GLETEKIKCC	LLLSVCSVTI	ENVMAITLPG	LLTVKHVYLS	QQLREHHEPV	MIYQPRDFPR	1260
	AQTLKETSIT	NTMGGYKESF	SSIMCFGCHD	VYSQASLGMD	IHASDLNLLT	RRKLSRLLD	1320
	PDPLGKDWCL	LAMNLGLPDL	VAKYNTNNGA	PKDFLPSPLH	ALLREWTTPY	ESTVGTLMSE	1380
	LRELGRDDAA	DLILKASSVF	KINLDGNGQE	AYASSCNSGT	SYNSISSVVS	R 1431	

Seq ID NO: C288 Protein Sequence  
Protein Accession #: NP\_002072.1

	1	11	21	31	41	51	
35	MELRARGWWL	LCAAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSDVP	QAEISGEHLR	60
	ICPGGYTCCT	SEMEENLANR	SHAELETALR	DSSRVQLAML	ATQLRSFDDH	FQHLNDSESR	120
	TLQATFPFAP	GELYTQNARA	FRDLYSELRL	YRGRANLHLE	ETLAEFWARL	LERLFKQLHP	180
	QLLLPDDYLD	CLGKQAEALR	PFGAEAPREL	LRATRAFAVA	RSEFVQGLVA	SDVVRKVAQV	240
40	PLGPECRAV	MKLVYCAHCL	GVPGARPCPD	YCRNVLGKCL	ANQADLDAEW	RNLDSMVL	300
	TDKFWGTSGV	ESVIGSVHTW	LAEAINALQD	NRTDLTAKVI	QCGGNPKVNP	QGGPPEEKRR	360
	RGKLAPRERP	PSGTLEKLVS	EAKAQLRDVQ	DFWISLPGTL	CSEKMAISTA	SDDRCNNGMA	420
	RGRYLPEVMG	DGLANQINNP	EVEVDITKPD	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDPPQ	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence  
Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILIYFLFL	LWEDTQGWGF	KDGIFHNSIW	LERAAAGVYHR	EARSQKYKLT	YAEAKAVCEP	60
	EGGHLATYKQ	LEAARKIGFH	VCAAGWMAKQ	RVGYPIVKPG	PNCQGFQGTI	IDYGIRLNRS	120
	ERWDAYCYNP	HAKCEGCVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFGVGRYC	GDELPPDDIIS	TGNVMTLKPL	SDASVTAGGF	240
55	QTKYVAMPDV	SKSSQCKNTS	TTSTGNKNFL	AGRFPSHL			277

Seq ID NO: C290 Protein Sequence  
Protein Accession #: NP\_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLFSLAGRS	EVGNSQAVCP	GTLNGLSVTG	DAENQYQTLY	KLYERCEVVM	60
	GNLEIVLTGH	NADLSPLQWI	REVTGVVLVA	MNEFSTLPLR	NLRVVRGTQV	YDGKFAIFVM	120
	LNNTNNSSHA	RQLRLTQTLT	EILSGGVYIE	KNDKLCHMDT	IDWRDIVRDR	DAEIVVKDNG	180
	RSCPPCHEVC	KGRCWGPGSE	DCQTLTKTIC	APQCNHCFPG	PNPQCCCHDE	CAGGCSGPQD	240
65	TDCFACRHFN	DSGACVPRCP	QPLVYNKLT	QLEPNPHTKY	QYGGVCVASC	PHNFVVDQTS	300
	CVRACPPDKM	EVDKNGLKMC	EPCGGLCPKA	CEGTGSGSRE	QTVDSNNIDG	FVNCTKILGN	360
	LDPLITGLMG	DPWHKIPALD	PEKLNVERTV	REITGYLNIQ	SWPPHMHNFS	VFSNLTITGG	420
	RSLYNRGFSL	LIMKNLNVTS	LGFRSLKEIS	AGRIYISANR	QLCYHHSINW	TKVLRGPTEE	480
	RLDIKHNRPR	RDCVABGKVC	DPLCSSGGCW	GPQPGQCLSC	RNYSRGGVCV	THCNFLNGEP	540
70	REFPAHEAECF	SCHPECPQMG	GTATCNGSGS	DTCAQCAHFR	DGPHCVSSCP	HGVLGAKGPI	600
	YKYPDVQNEC	RPCHENCQOG	CKGPELQDCL	GQTLVLIGKT	HLTMALTVIA	GLVVIFFMLG	660
	GTFLYWRGRR	IQNKRAMRRY	LERGESIEPL	DPSEKANKVL	ARIFKETELR	KLKVLGSGVF	720
	GTVHKGWVIP	EGESIKIPVC	IKVIEDKSGR	QSFQAVTDEM	LAIGSLDAH	IVRLGLGCPG	780
	SSLQLVTQYL	PLGSLLDHVR	QHRGALGPQL	LLNMGVQIAK	GMYYLEEHGM	VHRNLAARNV	840
75	LLKSPSQVQV	LEEDVADLLP	PDDKQLLYSE	AKTPIKWMAL	ESIHFQKYTH	QSDVNSYGV	900
	VWELMTFGAE	PYAGLRLAEV	PDLLEKGERL	AQPICTIDV	YVMVVKCMI	DENIRPTFKE	960
	LANEFTRMAR	DPPRYLVIKR	ESGPGIAPGP	EPHGLTNKKL	EVELEPELD	LDLDLEAED	1020
	LNATTILGSA	LSLPVGTILNR	PRGSQSLLSP	SSGYMPMNQ	NLGGSCQESA	VSGSSERCPR	1080
	PVSLHMPPRG	CLASESEBEG	VTGSAELQ	KVSMCRSRSR	SRSRPRGRDS	AYHSQRHSL	1140
80	TPVTPLSPPG	LEEDVNGYV	MPDTHLKGTP	SSREGTLSSV	GLSSVLGTEE	EDEDEEYEM	1200
	NRRRRHSFPH	PPRPSLEEL	GVEYMDVGS	LSASLGSTQS	CPLHVPVIMP	TAGTTPDEDY	1260
	EYMNRRQDGG	GPGGDYAAAG	ACPAEQGYE	EMRAPQGGH	QAPHVHYARL	KTLSLEATD	1320
	SAFDNPDYWH	SRLFPKANAQ	RT				1342

Seq ID NO: C291 Protein Sequence  
Protein Accession #: NP\_001207.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MAPLCSPWL PLLIPAPAG LTVQLLSLL LLMPVHPQL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
ELLGFLQPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
10    VEGHRFPAL HVHLSTAF RVEALGRPG GLAVLAAPLE EGPEENSAYE QLLSRLEEIA 300
EEGSETQVPG LDISALLPSD PSRYFYEGS LTPPCAQGV INTVFNQTM LSAKQLHTLS 360
DTLWGPQDSR LQLNFRATQP LNRGVIEASF PAGVDSSPRA AEFVQLNSCL AAGDILALVF 420
GLLFAVTSVA FLVQMRQRHR RGTGKGVSRY PAEVAETGA 459

```

Seq ID NO: C292 Protein Sequence  
Protein Accession #: NP\_004198.1

```

20      1      11      21      31      41      51
      |      |      |      |      |      |
MGGAVVDEGP TGVKAPDGGW GMAVLEGCFF ITGFSYAFPK AVSVFFKELI QEFGIGYSYT 60
AWISSILLAM LYGTGPLCSV CVNRFGCRPV MLVGGLPASL GMVAASPCRS IIQVYLTGV 120
ITGLGLALNP QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGRWGCV 180
LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFRDRGFVL YAVAASVMVL 240
25    GLFVPPVFFV SYAKDLGVPD TKAAPLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSP 300
SMFFNGLADL AGSTAGDYGG LVVFCIPFGI SYGMVGALQF EVLMAIVGTH KFSASIGLVL 360
LMEAVAVLVG PPSGKLLDA THVVMYFVIL AGAEVLTSSL ILLGNFFCI RKKPKPQPE 420
VAAEEEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

```

Seq ID NO: C293 Protein Sequence  
Protein Accession #: NP\_000349.1

```

30      1      11      21      31      41      51
      |      |      |      |      |      |
MALFVRLAL ALAALGPAF TLAGPAKSPY QLVLQHSRLR GRQHGNVCA VQKVIGTNRK 60
YFTNCKQWY RKICCKSTVI SYECCPGYEK VPGEKGCFAA LPLSNLYETL GVVGGTTTQL 120
YTDREKLRP EMEGPGSFTI FAPSNEAWAS LPAEVLDSL SVNIELLNA LRYHVMGRRV 180
LTDELKHMT LTSMYQNSNI QIHYPNGIV TVNCARLLKA DHATNGUVH LIDKIVSTIT 240
35    NNIQQIIEIE DTFETLRAAV AASGLNTMLE GNGQYTLAP TNEAFKIPS ETLNRLGDP 300
EALRDLNHN ILKSAMCAEA IVAGLSVETL EGTTLLEVCS GDMLTINGKA IISNKDILAT 360
40    NGVIHYDEL LIPDSAKTLF ELAASDVST AIDLFRQAGL GNHLSGSERL TLLAPLNSVF 420
KDGTPPIDAH TRNLRLNHI KDQLASKYLY HGQTLETGG KKLRFVYRN SLCIENS CIA 480
AHDKRGRYGT LFTMDRVLT PMGTVMVLK GDNRFMSLVA AIQSAGLTET LNREGVYTVF 540
APTNEAFRAL PPRERSRLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
45    LKQNVVSVNK EPVAEPDIMA TNGVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660
SRASQSVRL APVYQKLLER MKH 683

```

Seq ID NO: C294 Protein Sequence  
Protein Accession #: NP\_006527.1

```

50      1      11      21      31      41      51
      |      |      |      |      |      |
MTQRSIAGPI CNLKFVTLV ALSSLEPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISN 60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGHA 120
GDDPYTLQYR GCGKEGKYIH FTFNPLNDN LTAGYGSRRG VVFEHWAHLR WGVFDEYNND 180
55    KPFYINGNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
MFMQSLSSVV EPCNASTHNQ EAPNLQNM C SLRSAMDVIT DSADFHSFP MNGTELP PPP 300
TFSLVQAGDK VVCLVLVDS KMAEADRLQ LQQAAPFLM QIVEIHTFVG IASFDSKGEI 360
RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLEKGF EVVEKLANGKA YGSVMILVTS 420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSLRT GGLKFPVPDI SNSNSMIDAF 480
60    SRISSTGDI PQOHIOLEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540
FDPDGRKYIT NNFTINLTPR TASLWIPGTA KPGHWYTYLN NTHSLQALK VTVTSRASNS 600
AVPPATVEAF VERDSLHFPF PVMYIANVKQ GFYPILNATV TATVEPETGD PVTLLRLDDG 660
AGADVIKNDG IYSRYFFSPA ANGRYSKLVH VNHSFSTSTP AHSIPGSHAM YVPGYTANGN 720
IQMNAFRKSV GRNEEBERKWG PSRVSSGSGF SVLGVPAGPH PDVFPCKII DLEAVKVEEE 780
65    LTLSTAPGE DFDQGGATSY EIRMSKSLQN IQDDFNAIL VNTSKRNFQQ AGIREIFTFS 840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
LILKGVLTAM GLIGIICLII VVTHETLSRK KRADKENG T KLL 943

```

Seq ID NO: C295 Protein Sequence  
Protein Accession #: Eos sequence

```

70      1      11      21      31      41      51
      |      |      |      |      |      |
MKFLILLILQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFF REMPGGPVWR KHYITYRINN 120
YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAGD FHAFDGKGGI 180
LAHAFPGSG IGGDAHFDED EFWTHSGGT NLFLTAVHEI GHSGLGHSS DPKAVMFPY 240
KYVDINTFRL SADDIRGIQS LYGDPEKQR LPNPDNSEPA LCDPNLSFDA VTVGNKIFP 300
75    FKDRFFNLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
EENYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
NQQIGPKID AVFYSKNKY YFPQGSNQFB YDFLLQRTK TLKSNSWFGC 470

```

Seq ID NO: C296 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 5 MKFLLILLQ ATASGALPLN SSTLEKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60  
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHVF REMPGEFVWR KHYITYRINN 120  
 YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAGHD FFAFDGKGGI 180  
 LAHAFPGSG IGGDAHFDED EFWTTHSGGT NLPLTAVHAI GHSILGLGHSS DPKAVMFPTY 240  
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300  
 10 FKDRFPWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360  
 EPNYPKSIHS FGPFNVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420  
 NFQIGIGPKID AVFYSKQKY YFFQGSNQFE YDFLLQRIK TLKSNSWFGC 470

Seq ID NO: C297 Protein Sequence  
 Protein Accession #: NP\_008883.1

1 11 21 31 41 51  
 15 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60  
 IGIFVIGICLF CLSVLIGIVI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFPTPNL 120  
 20 FLKQMLERYQ NNSPPLNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAPRTENN 180  
 DADYPNPRQC CVMNKLKEPL NLEACKLGVF GFYHNNQCYE LISGPMNRHA WGVAVFGFAI 240  
 LCWTFNVLG TMFYNSRIEY 260

Seq ID NO: C298 Protein Sequence  
 Protein Accession #: NP\_001784.2

1 11 21 31 41 51  
 25 MGLPRGPLAS LLLIQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPQQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120  
 30 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180  
 YELFGHASE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYTYN GUVAYSISHS EPKDPHOLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 35 TDMGDGSGTT TAVAVVEILD ANDNAPMFDQ QKYEAHVPEN AVGHVQRLT VTDLDAPNSP 360  
 AWRATYLLMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEVPC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLTLTLID 540  
 40 VNDEGFPVEP RQITICNQSP VRQVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNEEGD 600  
 TVLSLKKFL KQDTYDVHLS LSDHGKKEQL TVIRATVCDQ HGHVETCPGP WKGGFPLPVL 660  
 GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720  
 GLEAPPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRPKKLA DMYGGEEDD 829

Seq ID NO: C299 Protein Sequence  
 Protein Accession #: NP\_005620.1

1 11 21 31 41 51  
 45 MAKKAENGI YSVSGDEKKG FLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD 60  
 50 FIMSCVGFV IFSVGGMIGS LCYKNGGGVF LIPYVLIALV GGIPIFFLEI SLGQFMKAGS 120  
 INWNICPLF KGLGYASMI VFYCNYYIM VLAWGFYLV KSFTTLTPWA TCGHTWNTPD 180  
 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVL RSGGLEVPGA LNWEVTCLL 240  
 ACWVLVYPCV WKGVKSTGKI VYFTATFPYV VLVVLLVRGV LLPGALDGI YLKPDPWSKL 300  
 55 GSPQWIDAG TQIFPSYAIG LGALTALGSY NFNNNNCKYD AILALINS TSPFAGFVVF 360  
 SILGFMKAEQ GHIKVAES GPGLAFIAYP RAVTIMPVAP LMAALFFPML LLLGLDSQV 420  
 GVEGFITGLL DLLPASYFR FOREISVALC CALCFVIDLS MVTDDGMVYF QLFYYYSASG 480  
 TLLWQAWE CVVVAWVGA DREMDIACM IGYRCPWMK WCHSFPTPLV CMGIFIENNV 540  
 60 YVEPLVYMT YVYPWGEAM GWAPALSSML CVPLHLGLCL LRAKGTMAER WQHLTQPIWG 600  
 LHLLEYRAQD ADVRLTLTIT PVSESSKVVV VESVM 635

Seq ID NO: C300 Protein Sequence  
 Protein Accession #: NP\_006507.1

1 11 21 31 41 51  
 65 MEPSSKKLTG RLMLAVGGAV LGSLLQFGYNT GVINAPQKVI EEFYNQTVWH RYGESILPTT 60  
 LTLNLSLVA IFSVGGMIGS FSVGLFVNRF GRNNSMLMMN LLAFFSAVLA GFSKLKGSPE 120  
 70 MLILGRPIIG VYQGLTTGPFV PMYVGEVSPT AFRGALGTLH QLSIVVGILI AQVFGLD SIM 180  
 GNKOLWPLL SIIFIPALLQ CIVLPFCPE PRLLINRNE ENRAKSVLKK LRGTADVTHD 240  
 LQEMKEESRQ MMREKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYSTSIFEK 300  
 AGVQPEVYAT ICGSIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLE 360  
 75 LPWMSVLSIV AIFGVAFVE VGPPIPWFI VAEFLSQGPR PAALAVAGFS NWTNPNFVGM 420  
 CFQYVEQLCG FYVFIIFTVL LVLFIFTYF KVPETKGRTP DEIASGRFQ GASQSDKTPE 480  
 ELFHLGADS QV 492

Seq ID NO: C301 Protein Sequence  
 Protein Accession #: XP\_035292.2

1 11 21 31 41 51  
 80 MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60  
 GTIIGSGIFV TAPVGLKEAG SPGLALVWA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120  
 LEVYGSPLAF LKLWIELLII RPSSQYIVAL VPATYLLKPL PTCFVPEEA AKLVACLCLV 180  
 LLTAVNCYSV KAATRVQDAF AAKALLALAL IILLGFVQIG KGDVSNLDPN FSEFETKLDV 240

5 GNIVLALYSQ LFAYGGWNYL NFVTEEMINP YRNPLAIIII SLPIVTLVYV LTNLAYFTTL 300  
 STEQMLSSSEA VAVDGNVYHL GVMWIIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360  
 SILSMIHQQL LTPVPSLVFT CVMITLLYAFS KDIFSVINFF SFFNWLVAL AIGMIWLRH 420  
 RKPELERPIK VNLALPVFFI LACFLIAVS FWKTPVECGI GFTIILSGLP VYFPGVWKN 480  
 KFKWLLQGIF STTVLCQKLM QVVPQET 507

Seq ID NO: C302 Protein Sequence  
 Protein Accession #: NP\_005259.1

10 1 11 21 31 41 51  
 MNWSIFEGLL SGVKNYSTAF GRWLVLVFI FRVLVYLTA ERVNSDDHKD FDCNTRQPGC 60  
 SNVCPDEFFP VSHVRLMALQ LILVTCPSLL VVMHVAYREV QEKHREAHG ENSGRLYLNP 120  
 15 GKRGGLMWT YVCSLVFKAS VDIAPLYVFH SFYPKYLPP VVKHADPCF NIVDCPISKP 180  
 SEKNIFTLFM VATAICILL NLVELIYLV KRCHECLAAR KAAQAMCTGH PHGTTSSCKQ 240  
 DDLLSGDLIF LGSDSHPLL PDRPRDHVK TIL 273

Seq ID NO: C303 Protein Sequence  
 Protein Accession #: NP\_005121.1

20 1 11 21 31 41 51  
 MKICSLTLLS FLILAAQVLL VEGKKVKVNG LHSKVSEQK DTLGNTQIKQ KSRPGNKGF 60  
 VTKDQANCRW AATEQEEGIS LKVECTQLDH BFSCVFAGNP TSCLKLKDER VYWKQVARNL 120  
 25 RSQKIDICYS KTAVKTRVCR KDFPESLKL VSSTLFGNTK PRKEKTEMSP REHKGKETT 180  
 PSSLAVTQM ATKAPECVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence  
 Protein Accession #: AAH22542

30 1 11 21 31 41 51  
 MCSEIILRQE VLKDGFRDL LIKVKFCESI EDLHTCRLLI KQDIPAGLYV DPEYASLRE 60  
 RNITEAVMVS ENFDIEAPNY LKSESEVLIY ARRDSQCIDC FQAPLPVHCR YHRPHSEDEG 120  
 35 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180  
 WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence  
 Protein Accession #: NP\_004985.1

40 1 11 21 31 41 51  
 MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEYLY RYGYTRVAEM 60  
 RGEKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDIGRFQTF EGDLLKWHHN 120  
 45 ITYKIQNYSE DLPRAVIDDA PARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180  
 FDGKGLLAH AFPPGPIQG DAHFDDELW SLGKGVVPT RFGNADGAAC HFFPIFEGRS 240  
 YSACTDGRS DGLPWCSTTA NYDDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS 300  
 ACTTDGRSDG YRNCATTANY DRDKLFGFCP TRADSTVMOG NSAGELCVFP FTFIGKEYST 360  
 CTSEGRGDGR LWCATTNPD SDKKWGFCD QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420  
 50 PMYRFTGEPF LHKDDVNGIR HLYGPRPEPE PRPPTTTTQP PTAPPTVCPT GPPTVHPSE 480  
 PTAGTGPPTS AGPTGPPTAG PSTATTVPLS FVDDACNVNI FDAIAEIGNQ LYLFDKDKYW 540  
 RFSGRGSRP QGPPLIADKW PALPRKLDV FEEPLSKLF PFSGRQVWVY TGASVLGPRR 600  
 LDKLGLGADV AQVYGAIRSG RGMMLFPGR RLWRFDVKAQ MVDPRSASEV DRMPGVPPLD 660  
 55 THDVFPYREK AYFQDRFYW RVSSRSNLQ VDQVGYVTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence  
 Protein Accession #: NP\_000204

60 1 11 21 31 41 51  
 MAGPRPSPFA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVKDCAY CTDEMFRDRR 60  
 CNTQAEALLA GQRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPEERHFEL 120  
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SOLTSDYITG PGKFVDKVS 180  
 65 PQDTMRPEKL KEFVNSDPP FSPKNVISLT EDVDEPRNKL QGERISGNLD APEGGFDAIL 240  
 QTAVCTRDIG WRPDSTHLLV PSTESAFHYE ADGANVLGI MSRNDERCHL DTTGTYTQYR 300  
 TQDYPSVPTL VRLLAGHNII PIPAVTNYSY SYYEKLHTYF FVSSLGVLQE DSSNIVELLE 360  
 EAFNRIRSNL DIRALDSPRG LRTEVTSKMF OKTRTGSFHI RRGVEGVIQV QLRALEHVDG 420  
 THVQQLPEDQ KGNHLPKSP SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVQCQCV 480  
 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHVCYGEGR YEGQFCEYDN 540  
 70 FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCEGR 600  
 CHCHQSSLYT DTICEINYSI IHPGLCEDLR SCVQCAWGT GEKKGRTECE CNPKVRMVD 660  
 LKRAEIVVVR CSFRDEDDC TYSYTMEDG APGPNSTVLV HKKDCPPGS FWWLIPLLLL 720  
 LLPLALLLLL LCWKYCACCK ACLALLPCCN RGHMVGFEKD HYMLRENLMA SDHLDTPLR 780  
 SGNLKGKRDV RWKVNTNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840  
 75 AQLRQEVEN LNEVYRQISG VHKLQQTFR QQPNAGKQD HTIVDTVLMA PRSAKPAK 900  
 LTEKQVEGRA FHDLVAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVFLI RPEDDDEKQL 960  
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQEPFS VSRGDQVARI FVIRRVLDGG 1020  
 KSQVSRYTQD GTAQNRDVI FVEGELLQFP GEAWKELQVK LLELQEVDSL LRGRQVRRPH 1080  
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLAGP QNPNAKAAGS 1140  
 80 RKIHFNWLP SGKPMGYRVK YWQGDSESE AHLDSKVPVS VELTNLYPYC DYEMKVCAYG 1200  
 AQEGEPYSSL VSCRTHQEVV SEPGRLAFTV VSSTVTQLSW AEAETNGEI TAYEVCYGLV 1260  
 NDDNRPIGFM KKVLDVNDPN RMLLIENLRE SQPYRYTVKA RNGAGWGPFR BAIINLATOP 1320  
 KRPMISPIIP DIIIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSDDTG CGWKFEPLLG 1380  
 EELDRLRRVTW RLPELIPRL SASSGRSSDA EAPTAPRTTA ARAGRAAAMP RSATPGPPGE 1440

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45

HLVNGRMDF	FPGSTNSLHR	MITTSAAAYG	THLSPHVPHR	VLSTSSLTTR	DYNSLTRSEH	1500
SHSTTLPRDY	STLTSVSSHD	SRLTAGVPDT	PTRLVFSALG	PTSLRVSWQE	PRCERPLQGY	1560
SVEYQLLNGG	ELHRLNLPNP	AQTSVVVEDL	LPNHSYVFRV	RAQSQEGWGR	EREGVITIES	1620
QVHPQSPLCP	LFGSAFTLST	PSAPGPLVFT	ALSPDSLQLS	WERPRRPNGD	IVGYLVTCEM	1680
AQGGGPATAF	RVDGDSPEER	LTVPGISENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	1740
FFPQLGSRAG	LFQHPLOQSEY	SSITTTHTSA	TEPFLVDGLT	LGAQHLEAGG	SLTRHVTQEP	1800
VSRTLTSTGT	LSTHMDQQFF	QT				1822

Seq ID NO: C307 Protein Sequence  
 Protein Accession #: NP\_076404.1

15  
 20

1	11	21	31	41	51	
MGFNLTLAKL	PNNELHGQES	HNSGNRSDGP	GKNTTLHNEF	DTIVLPVLYL	IIFVASILLN	60
GLAVWIFPHI	RNKTSPIFYI	XNIVVADLIM	TLTFFPRIVH	DAGFGPWYFK	FILCRYTSVL	120
FYANMYTSIV	FLGLISIDRY	LKVVKPFQDS	RMYSITPTKV	LSVCVWVIMA	VLSPNIIILT	180
NGQPTEDNIH	DCSKLKSPLG	VKWHITAVTV	NSCLFVAVLV	ILIGCYIAIS	RYIHKSSRQF	240
ISQSSRRKRH	NQSIRVVAVV	FFTCLPYHL	CRIPFTFSEH	DRLLDESAQK	ILYYCKEITL	300
FLSACNVCLD	PIIYFMCERS	FSRRLPKKSN	IRTRSESIRS	LQSVRRSEVR	IYYDYTDV	358

Seq ID NO: C308 Protein Sequence  
 Protein Accession #: NP\_065840.1

25  
 30  
 35  
 40  
 45

1	11	21	31	41	51	
MVWCLGLAVL	SLVISQGADG	RGKPEVVSVV	GRAEESVVLG	CDLLPPAGRP	PLHVIEWLRF	60
GPLLPFIQF	GLYSPRIDPD	YVGRVRLQKG	ASLQIEGLRV	EDQGWYECRV	FFLDQHIPPED	120
DFANGSVVHL	TWNSPPQFQE	TPPAVLEVQE	LEFVTLRCVA	RGSPLPHVTW	KLRGKDLGGQ	180
QGVQVQNGT	LRIRRVERGS	SGVYTQASS	TEGSATHATQ	LLVLGPPVIV	VPPKNSVTNA	240
SQDVSLACHA	EAYPANLITYS	WFQDNINVFH	ISRLQPRVQI	LVDGSLRLLA	TQFDDAGCYT	300
CVPSNGLLHP	PSASAYLTVL	CMPGVIRCPV	RANPPLLFVS	WTKDGKALQL	DKFPWGSQGT	360
EGSLIIALGN	EDALGEYSCT	PYNSLGTAGP	SPVTRVLLKA	PPAFIERPKE	EYFQEVGREL	420
LIPCSAQGDP	PPVSVWTKVG	RGLQGOAQVD	SNSSLILRLP	TKEAHGHNEC	SASNAVARVA	480
TSTNVVYVLT	SHVVTNVSV	VALPKGANVS	WEPGFDGGYL	QRFVSWYTPL	AKRPDRMHHD	540
MVSLAVPVGA	AHLLVPLQLP	HTQYQFSVLA	QNKLGSGPFS	EIVLSAPEGL	PTTPAAPGLP	600
PTEIPPLSP	PRGLVAVRTP	RGVLLHWDPP	ELVPKRLDGY	VLEGRQGSQG	WEVLDPVAVG	660
TETELLVPLG	IKDVLVEFRL	VAFAGSFVSD	PSNTANVSTS	GLEVYFSRTQ	LPGLLPQPVV	720
AGVVGVCFL	GVAVLVLSLA	GCLLNRRRAA	RRRRKRLROD	PPLIFSPTGK	SAAPSALGSG	780
SPDSVAIKKL	QGSFVPSLRQ	SLWGDPAQT	PSPHDPDPSS	RGPLPLEPIC	RQPDGRFVMG	840
PTVAAPQERS	GREQAEPRTP	AQRLARSFDC	SSSSPSGAPQ	PLCIEDISPV	APPPAAPPSP	900
LPFGPGLLQY	LSLPFFREMN	VDGDWPPLEB	PSPAAPPDYM	DTRRCTPTSS	LRSPETPPVS	960
PRESLPGAVV	GAGATAPBPY	TALADWTLRE	RLLPGLLPAA	PRGSLTSQSS	GRGSASFRLP	1020
PSTAPSAGGS	YLSAPAGDTS	SWASGPERWP	RREHVVTYSK	RRNTSVSDENY	EMDSEFPQDM	1080
ELLETLHLGL	ASSRLRPEAE	TELGVKTPPE	GCLLNTAHTV	GPBARCAALR	EEFLAFRRRR	1140
DATRRLPAY	RQVPHPEQA	TLL				1163

Seq ID NO: C309 Protein Sequence  
 Protein Accession #:

50  
 55

1	11	21	31	41	51	
MLTKPLQGP	APPGTPTPPP	GGKDREAFAE	EYRLGPLLKG	GGFGTVFAGH	RLTDRLQVAI	60
KVIPRNRLV	WSPLSDSVTC	PLEVALLWKV	GAGGGHGGVI	RLLDWFETQE	GFMLVLERPL	120
PAQDLFDYIT	EKGPLGEGPS	RCFFGQVVAA	IQCHSRGVV	HRDIKDENTL	IDLRRCGACL	180
IDFGSGALLH	DEPYTFDFTG	RVYSPPPEWIS	RHQYHALPAT	VWSLGLILLYD	MVCGDIPFER	240
DQEILEAEHL	FFAHVSPDCC	ALIRRLCLAPK	PSSRPSLEBI	LLDPWMTQPA	EDVTPQPLQR	300
RPCPFGLVLA	TLSLAWPLGA	PNGQKSHFMA	MSQG			334

Seq ID NO: C310 Protein Sequence  
 Protein Accession #: NP\_002501.1

60  
 65  
 70  
 75

1	11	21	31	41	51	
MECLYYFLGF	LLLAARLPLD	AAKRFHDVLG	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
VNKRGMRWK	NSWKGGRVQA	VLTSDSPALV	GSNITFAVNL	IFPRCQKEDA	NGNIVYERMC	120
RNEAGLSADP	YYYNWTAWSE	DSGGENGTGQ	SHHNVPDGGK	PPPHHPGWRR	WNFIYVFFTL	180
GQYFQKLGRC	SVRVSVNTAN	VTLGSQLMEV	TVYRRHGRAY	VPIAQVKDVY	VVTDQIFVEV	240
TMFQKNDRNS	SDETFLLKDL	IMFDVLIHDP	SHFLNYSTIN	YKWSFGDNTG	LFVSTNHTVN	300
HTYVLNGTFS	LNLTVKAAAP	GPCPPPPPPP	RPSKPTPSLG	PAGDNPLELS	RIPDENCQIN	360
RYGHFQATIT	IVEGILEVNI	IQMTDVLMVP	PWESSLIDF	VVTCQGSIPT	EVCTIISDPT	420
CEITQNTVCS	PVDVDEMCLL	TVKRTFNGSG	TYCVNLTGSD	DTSLALTSTL	ISVPDRDPAS	480
PLRMANSALI	SVGCLAFVTV	VISLLVYKKH	KEYNPIENSP	GNVVRSGKLS	VFLNRKAVFV	540
PPGNQEKDPL	LKNQEFKGV					560

Seq ID NO: C311 Protein Sequence  
 Protein Accession #: Eos seq

80

1	11	21	31	41	51	
MRILKRFLAC	IQLLCVCRID	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
QSPINIDEDL	TQVNVNKKL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCPDA	DRFSSFEAAV	KGKGLKRLAS	180
ILPEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYIY	YNGSLTSPPC	240
TDTVDWIVFK	DTVSISESQ	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	300



5	TGKEEIHAEV CSSEPEVQA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360
	HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNPDLDFPE 420
	LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
	RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
	GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
	ENISQGYIFS SENPETIITYD VLIPESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSSTDI 660
	TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
	TEVTPHAFPT SSRQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
10	LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
	IKHFPKHVAD LHASSGFTEE FEEVQSCITVD LGITADSSNH PDNKHKNRYI NIVAYDHSRV 900
	KLAQLAEKDG KLTIDYINANY VDGYNRPKAY IAAQGPLKST AEDPWRMINE HNVEVIMIT 960
	NLVEKGRKRC DQYWPADGSE EYGNFLVTQK SVQVLAYYTV RNPTLRNTKI KKGSKQGRPS 1020
	GRVVTQYHYT QWPDGMVPEY SLFVLTFVRK AAYAKRHAVG PVVHCSAGV GRTGTIYIVLD 1080
15	SMLQQIQHEG TVNIFGFLKH IRSQRNYLVQ TEEQYVFIHD TLVEAILSKE TEVLDSHIHA 1140
	YVNALLIPGP AGKTYKLEQF QLLSQSNIQQ SDYSAALKQC NREKNRTSSI IPVERSRVGI 1200
	SSLSGEGTDY INASYIMGYI QSNFIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDGQNM 1260
	AEDEFVYWFN KDEPINCESF KVTLMAAEHK CLSNEEKLI QDFILEATQD DYVLEVHRFQ 1320
	CPKWNPDSP ISKTFELISV IKBEAANRDG PMIVHDEHGG VTAGTFALIT TLMHQLKEN 1380
20	SVQVQVAKM INLMRPGVFA DIBQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI 1440
	AESLESIV 1448

Seq ID NO: C312 Protein Sequence

Protein Accession #: XP\_031379

25	1 11 21 31 41 51	MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
		QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
30		FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKGLRLS 180
		ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
		TDTVDMIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSY 300
		TGKEEIHAEV CSSEPEVQA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360
		HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNPDLDFPE 420
35		LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
		RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
		GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
		ENISQGYIFS SENPETIITYD VLIPESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSSTDI 660
		TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
40		TEVTPHAFPT SSRQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
		LNTTPAASS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSE LFRHLHTVSO 840
		ILPQVTSATE SDKVLHASL PVAGGDLLE PSLAQYSDVL STTHAASETL EFGSEGVLY 900
		KTLMFQVEP PSSDAMMHAR SSGPEPSYAL SDNBSQHIP TVSYSSAIPV HDSVGVTYQG 960
		SLFSGPSHF IPKSLITPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS 1020
45		PVSVAEFTYT TSFVGDNDKA LSKSEIIYGN ETELQIPSFN EMVYPSSESTV MPMYDYNVK 1080
		LNASLQETS SISSTKGMFP GLAHTTTKV FDHEISQVPE NNFVQPTHT VSQASGDTSL 1140
		KPVLANSSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200
		AVPSDPIIVE TPKVDKISST MLHLIVNSA SSENMLHSTS VPVFDVSPTS HMHSASLQGL 1260
		TISYASEKYE FVLLKSESSH QVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID 1320
50		EPLNTLINKL IHSDELITST KSSVTGKVAF GIPTVASDTF VSTDHVPVIG NGHVAITAVS 1380
		PHRDGSVTST KLLFPKSKATS ELSHSAKSDA GLVGGGEDGD TDDGDGDDDD DRGSDGLSIH 1440
		KCMSCSYRE SQEKVMDND THENSLMDQN NPISYSLSEN SEEDNRVTSV SSDSQTGMDR 1500
		SPGKSPSANG LSQKMDGKE ENDIQTGSAL LPLSPESKAW AVLTSEDESG SQGQTSDSL 1560
		ENETSTDFSF ADTNEKADG ILAAGDSEIT PGFPQSPTSS VTSENSEVFR VSEAEASNS 1620
55		HESRIGLAEG LESEKKAVIP LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR 1680
		VISTPPTPIF PISDDVGAIP IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCITVDGI 1740
		TADSSNHDPN KHKRYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA 1800
		QGPKLSTAEF FWRMIWEHNV EVITMITNLV EKGRRKCDQY WPADGSEYQ NPLVTQKSVQ 1860
		VLAYTYVRNF TLNKTIGKG SKGRPSGRV VTQYHYTQWP DMGVPEYSLE VLTVPVRKAY 1920
60		AKRHAVGPVV VHCASAGVGT GTYIVLDSML QQIQHEGTVN IFGFLKHRS QRNYLVQTEE 1980
		QYVFIHDTLV EALLSKETEY LDSEIHAYVN ALLIPGPAGK TKLEKQFOLL SQSNIQSDY 2040
		SAALKQCNE KNRSTSSIIP ERSRVGISSL SGEGTDYINA SYIMGYQSN EFIITQHPLL 2100
		HTIKDFWMI WDHNALQVVM IPDQGNMAED EFVWPNKDE PINCESPKVT LMAEHEKCLS 2160
		NEEKLIQDF ILEATQDDYV LEVRFQCPK WFNPDSPISK TPELISVIKE EAANRDGPMI 2220
65		VHDEHGGVTA GTFCALITLM HQLEKENSVD VYQVAKMINL MRPGVFADIE QYQFLYKVIL 2280
		SLVSTRQEN PSTSLDNGA ALPDGNIAES LESLV 2315

Seq ID NO: C313 Protein Sequence

Protein Accession #: NP\_002842

70	1 11 21 31 41 51	MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
		QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
		FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKGLRLS 180
75		ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
		TDTVDMIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSY 300
		TGKEEIHAEV CSSEPEVQA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360
		HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNPDLDFPE 420
		LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
80		RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
		GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
		ENISQGYIFS SENPETIITYD VLIPESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSSTDI 660
		TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
		TEVTPHAFPT SSRQDLVST VNVVYSQTQ PVYNEASNS HESRIGLAEG LESEKKAVI 780

5 PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
 PIKHFPHKVA DLHASSGFTE EFETLKEFYQ EVQSCVDLGI ITADSSNHPD NKHKRNYINI 900  
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
 VEIVVMITNL VEKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYTYVRN FTLRNTKIKK 1020  
 10 GSQKGRPSGR VVTQHYHTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGVP VVHCSAGVGR 1080  
 TGTIYVLDSM LQIQIHEGTV NIFGFLKHIR SQRNYLVQTE EQYVFIHDTL VEAILSKETE 1140  
 VLDSDHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
 VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260  
 MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320  
 VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380  
 MHQLEKENS SVDYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440  
 AALPDGNIAE SLESIV 1456

Seq ID NO: C314 Protein Sequence  
 Protein Accession #: Eos sequence

15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 MVFKASKITF HWGKCNMSSD GSEHSLGQK FPLEMQIYCF DADRFSFEE AVKKGKGLRA 180  
 LSILFEVGTB ENLDFKAIID GVESVSRFGK QAALDPFILL NLLPNSTDKY YIYNGSLTSP 240  
 PCTDWDIVF KDTVSISESQ LAVFCEVLTM QSGYVLMMD YLQNNFREQQ YKFSRQVFSS 300  
 YTGKEEIHFA VCSSEFENVQ ADPENYTSLL VTWERPRVY DTMIEKFAVL YQQLDGEDQT 360  
 KHEFLTDGYQ DLGAILNLL NMSYVLQIV AICTNGLYK YSDQLIVDMT DNPELDLFP 420  
 ELIGTEEIIK EEEEGKDIEE GAIVNPGRDS ATNQIRKKEP QISTTTHYNR IGTKYNEAKT 480  
 NRSPTRGSEF SGKGDVPNTS LNSTSQPVTK LATEKDISLT SQTVELPPH TVEGTSASLN 540  
 DGSKTVLRSP HMLSGTAES LNTVSITEYE EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600  
 SENISQGIYF SSENPEITTY DVLPESARN ASEDSTSSGS EESLKDPMS EGNVFPSTSD 660  
 ITAQPDVSGS RESFLQNTYT IRVDESEKT KSFSAAGPVM SQGPSVTDLE MPHYSTFAYF 720  
 PTEVTPHAPT PSSRQQLVSV TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAVI 780  
 PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
 PIKHFPHKVA DLHASSGFTE EFETLKEFYQ EVQSCVDLGI ITADSSNHPD NKHKRNYINI 900  
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
 VEIVVMITNL VEKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYTYVRN FTLRNTKIKK 1020  
 GSQKGRPSGR VVTQHYHTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGVP VVHCSAGVGR 1080  
 TGTIYVLDSM LQIQIHEGTV NIFGFLKHIR SQRNYLVQTE EQYVFIHDTL VEAILSKETE 1140  
 VLDSDHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
 VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260  
 MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320  
 VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380  
 MHQLEKENS SVDYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440  
 AALPDGNIAE SLESIV 1456

Seq ID NO: C315 Protein Sequence  
 Protein Accession #: Eos sequence

50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITPHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEEAV KKGKGLRALS 180  
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVLMMDY LQNNFREQQY KFSRQVFSSY 300  
 TGKEEIHFAV CSSEFENVQ DPENYTSLLV TWERPRVYD TMIEKFAVL YQQLDGEDQT 360  
 HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYKGY SDQLIVDMPT DNPELDLFP 420  
 LIGTEEIIKE EEEEGKDIEE AIVNPGRDSA TNQIRKKEPQ ISTTTHYNR IGTKYNEAKT 480  
 RSPTRGSEFS KGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT HVEGTSASLN 540  
 GSKTVLRSPH MNLSGTAESL NTVSITEYEE EESLLTSFKL DTGAEDSSGS PATSAIPFIS 600  
 ENISQGIYFS SENPETITTY VLIPESARNA SEDSTSSGSE EESLKDPMS EGNVFPSTSDI 660  
 ITAQPDVSGS RESFLQNTYT IRVDESEKT KSFSAAGPVM SQGPSVTDLE MPHYSTFAYF 720  
 TEVTPHAPT PSSRQQLVSV TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAVI 780  
 LVIIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
 IKHFPHKVA DLHASSGFTE EFETLKEFYQ EVQSCVDLGI ITADSSNHPD NKHKRNYINI 900  
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
 VEIVVMITNL VEKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYTYVRN FTLRNTKIKK 1020  
 GSQKGRPSGR VVTQHYHTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGVP VVHCSAGVGR 1080  
 TGTIYVLDSM LQIQIHEGTV NIFGFLKHIR SQRNYLVQTE EQYVFIHDTL VEAILSKETE 1140  
 VLDSDHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
 SRVAGTILLS QSNIQQSDYS AALKQCNREK NRTSSIIIPVE RSRVGISSLS GEGTDYINAS 1260  
 YIMGYYSQNE FIITQHPLH TIKDFWRM IWDHNAQLVMI PDQGNMAE DEFVYWPNDK 1320  
 INCESFKVTL MAEEHKCLSN EEEKLIQDPI LEATQDDYVL EVRHFQCPK KWPNDPSPIS 1380  
 FELISVKEE AANRDGPMIV HDEHGGVTAG TFCALTTLH QLEKENSVDV YQVAKMINLM 1440  
 RGPVFADIEQ YQFLYKVI LS LGVTRQENP STSLDSNGAA LPDGNIAESL ESLV 1494

Seq ID NO: C316 Protein Sequence  
 Protein Accession #: Eos sequence

80

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITPHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEEAV KKGKGLRALS 180  
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240

5	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPEASNSSH	420
	ESRIGLAESL	ESEKKAIVPL	VIVSALTFIC	LVVLVGILY	WRCKFQTAHP	YLEDSTSPRV	480
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGFTEEP	ETLKEFYQEV	QSCITVDLGI	540
	ADSSMHEDNK	HKRNYINIVA	YDHSRVKLAQ	LAEKDGKLT	YINANYVDG	NRPKAYIAAQ	600
	GPLKSTAEDE	WRMIWEHNV	VIVMITNLVE	KGRRKCDQYW	PADGSEBYGN	FLVTQKSVQV	660
	LAYYTVRNF	LRNTKIKKGS	QKGRPSGRV	TQYHYTQWPD	MGVPEYSLPV	LTFVRKAAYA	720
10	KRHAVGPVVV	HCSAGVGRG	TYIVLDSMLQ	QIQHEGTVNI	FGFLKHIRSQ	RNYLVQTEEQ	780
	YVFIHDTLVE	AILSKETEVL	DSHIHAYVNA	LLIPGPAGKT	KLEKQFQLLS	QSNIQSDYS	840
	AALKQCNEK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	YIMGYQSN	FIITQHPLH	900
	TIKDFWRMIW	DHNAQLVVM	PDGQNMAEDE	FVYWPKNDEP	INCESFKVTL	MAEEHKCLSN	960
	EELKLIQDFI	LEATQDDYVL	EVRFHQCPKW	PNPDSPISKT	FELISVIKEE	AANRDGPMIV	1020
15	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	RPGVFADIEQ	YQFLYKVILS	1080
	LVSTRQENP	STSLDSNGAA	LPDGNIAESL	ESL			1113

Seq ID NO: C317 Protein Sequence  
Protein Accession #: Eos sequence

20	1	11	21	31	41	51	
	MRILKRFAC	QLLVCVRLD	WANGYYRQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKLL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
25	FKASKITFW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEAAV	KGKGLRALS	180
	ILFEVGTEN	LDKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPE	420
30	LIGTEEIIKE	EEEGKDIEEG	AINVPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QVTLEPPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
35	TEVTPHAFIP	SSRQDVLVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHPPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCITVDLGI	TADSSNHDPN	HKRNYINIV	900
	AHDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAEDE	FWRMIWEHNV	960
	EVIVMITNLV	EKGRRKCDQY	WPADGSEEYG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
40	SQKGRPSGRV	VQYHYTQWPD	DMGVPEYSLP	VLTFRKAAY	AKRHAVGPVV	VHCSAGVGRG	1080
	GTIVLDSML	QIQHEGTVNI	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	BAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	TLSRPLECRG	TISAHCNLPL	PGLTDPPTSA	1200
	SRVARTILLS	QSNIQSDYS	AALKQCNEK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYQSN	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMAEDE	FVYWPKNDEP	1320
45	INCESFKVTL	MAEEHKCLSN	EELKLIQDFI	LEATQDDYVL	EVRFHQCPKW	PNPDSPISKT	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	1440
	RPGVFADIEQ	YQFLYKVILS	LVSTRQENP	STSLDSNGAA	LPDGNIAESL	ESL	1493

Seq ID NO: C318 Protein Sequence  
Protein Accession #: Eos sequence

50	1	11	21	31	41	51	
	MRILKRFAC	QLLVCVRLD	WANGYYRQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKLL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
55	FKASKITFW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEAAV	KGKGLRALS	180
	ILFEVGTEN	LDKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
60	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPE	420
	LIGTEEIIKE	EEEGKDIEEG	AINVPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QVTLEPPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
65	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFIP	SSRQDVLVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHPPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCITVDLGI	TADSSNHDPN	HKRNYINIV	900
	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAEDE	FWRMIWEHNV	960
70	EVIVMITNLV	EKGRRKCDQY	WPADGSEEYG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
	SQKGRPSGRV	VQYHYTQWPD	DMGVPEYSLP	VLTFRKAAY	AKRHAVGPVV	VHCSAGVGRG	1080
	GTIVLDSML	QIQHEGTVNI	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	BAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	QSNIQSDYS	SAALKQCNE	NRTSSIIPE	1200
	ERSRVGISS	SGEGTDYINA	SYIMGYQSN	FIITQHPLH	TIKDFWRMIW	WDHNAQLVVM	1260
75	IPDGQNMAED	EVYWPKNDEP	PINCESFKVT	LMMAECHKLS	NEEKLIQDFI	ILEATQAWRS	1320
	DGRNFLCSDN	PYAPTRKRKF	RGCLPGSQDD	QSDEARSLC			1359

Seq ID NO: C319 Protein Sequence  
Protein Accession #: XP\_002914.4

80	1	11	21	31	41	51	
	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
	LDASMHSLR	ILDEEHKPKG	YHGLSALKP	IRTSKHQHP	VDNAGLFSCM	TFSWLSLAR	120
	VHKKKGELSM	EDVWSLSKHE	SSDVNCRRLE	RLWQEELNEV	GPDAASLRV	VWIFCRTL	180

5  
10  
15  
20

LSIVCLMITQ LAGFSGPAFM VKHLLLEYTQA TESNLQYSLL LVIGLLLTETI VRSWSLALTW 240  
ALNYRTGVR L RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300  
PVVAIILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKRCVAA TDERVQKME 360  
VLTYIKFIKM YAWWKAQSQS VQKIREEERR ILEKAGYFQS ITVGAVPIVV VIASVVTFSV 420  
HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK 480  
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKDK RASRGKKEKV RQLQRTTEHQ 540  
VLAQKQHLL LDSDERPSPE EEEGKHILG HLRQLRTLHS IDLEIQEGKL VGICGSVSGG 600  
KTSLSAISLG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660  
CCLRPDLAIL PSSDLTEIGE RGNLSSGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720  
NHIFNSAIRK HLKSKTVLVF THQLQYLVD DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780  
FNNLLIGETP PVEINSKKEP SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840  
VPWSVYGVYI QAAGGFLAFL VIMALFMLNV GSTAFSTWWL SYNIKQSGSN TTVTRGNETS 900  
VSDSMKDNPH MQYYASIAL SMAVMLILKA IRGVVFKGT LRASSRLHDE LFRILRSPM 960  
KFFDTTPTGR ILNRFSKMD EVDVRLPFQA EMFIQNVILV PFCVGMIAGV FFWFLVAVGP 1020  
LVILFSVLHV KKVSTIKPK EKIGIVGRGT SGKSSLMAL FRLVELSGGC IKIDGVRISD 1080  
LDNQAPFFL FTCAMRLAV RDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140  
GLPQFTVRLA SETEARTSV ERINHYIKTL SLEAPARIKN KAPSPDWQE GEVTFENAEM 1200  
RYRENLPVLV KKVSTIKPK EKIGIVGRGT SGKSSLMAL FRLVELSGGC IKIDGVRISD 1260  
IGLADLRSLK SIIPQEVLF SGTVRSNLD FNQYTEDQIW DALERTHME CIAQLPLKLE 1320  
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380  
MLTIAHRLHT VLGSRLMVL AQGVVEFDT PSVLLSNDSS RPYAMFAAE NKVAVKG 1437

Seq ID NO: C320 Protein Sequence  
Protein Accession #: NP\_005679.1

25  
30  
35  
40  
45  
50

1 11 21 31 41 51  
MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFR TRPLECQDAL ETAARAEGLS 60  
LDASMSQLR ILDEEHPKKG YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120  
VAHKKGELSM EDVWLSKHE SSVNCRRL RLVQEELENEV GPDAASLRV VWIFCRRLI 180  
LSIVCLMITQ LAGFSGPAFM VKHLLLEYTQA TESNLQYSLL LVIGLLLTETI VRSWSLALTW 240  
ALNYRTGVR L RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300  
PVVAIILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKRCVAA TDERVQKME 360  
VLTYIKFIKM YAWWKAQSQS VQKIREEERR ILEKAGYFQS ITVGAVPIVV VIASVVTFSV 420  
HMTLGFDLTA AQAFVTVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK 480  
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKDK RASRGKKEKV RQLQRTTEHQ 540  
VLAQKQHLL LDSDERPSPE EEEGKHILG HLRQLRTLHS IDLEIQEGKL VGICGSVSGG 600  
KTSLSAISLG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660  
CCLRPDLAIL PSSDLTEIGE RGNLSSGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720  
NHIFNSAIRK HLKSKTVLVF THQLQYLVD DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780  
FNNLLIGETP PVEINSKKEP SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840  
VPWSVYGVYI QAAGGFLAFL VIMALFMLNV GSTAFSTWWL SYNIKQSGSN TTVTRGNETS 900  
VSDSMKDNPH MQYYASIAL SMAVMLILKA IRGVVFKGT LRASSRLHDE LFRILRSPM 960  
KFFDTTPTGR ILNRFSKMD EVDVRLPFQA EMFIQNVILV PFCVGMIAGV FFWFLVAVGP 1020  
LVILFSVLHV KKVSTIKPK EKIGIVGRGT SGKSSLMAL FRLVELSGGC IKIDGVRISD 1080  
LDNQAPFFL FTCAMRLAV RDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140  
GLPQFTVRLA SETEARTSV ERINHYIKTL SLEAPARIKN KAPSPDWQE GEVTFENAEM 1200  
RYRENLPVLV KKVSTIKPK EKIGIVGRGT SGKSSLMAL FRLVELSGGC IKIDGVRISD 1260  
IGLADLRSLK SIIPQEVLF SGTVRSNLD FNQYTEDQIW DALERTHME CIAQLPLKLE 1320  
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380  
MLTIAHRLHT VLGSRLMVL AQGVVEFDT PSVLLSNDSS RPYAMFAAE NKVAVKG 1437

Seq ID NO: C321 Protein Sequence  
Protein Accession #: NP\_005553.1

55  
60  
65  
70  
75

1 11 21 31 41 51  
MPALWLGCC L CFSLLPAAR ATSRREVCDC NGKSRQCIFD RELHRQTGNG FRCILNCNDNT 60  
DGIHCECKN GFYRHRERDR CLPCNCSKG SLSARCDNSG RCSCKPGVTG ARCDRLCPGF 120  
HMLTDAGCTQ DQRLLDSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYNNLDGDN 180  
PEGCTQCFY GHSASCRSSA EYSVHKITST FHQVDVGNKA VQNGSPAKL QWSQRHQDV 240  
SSAQRLLDPV FVAPAKFLGN QVSYGQSL SFDYRVDGRGR HPSAHVILE GAGLRITAPL 300  
MPLGKTLPCG LTKYTYTFLN EHPNNWSPQ LSYFEYRRL RNLTLALRIRA TYGEYSTGYI 360  
DNVTLISAR VSGAPAPWVE QCICPVGYKG QPCQDCASGY KRDSARLGPF GTCIPCNCG 420  
GGACDPDTGD CYSNENPDI ECADCFIGFY NDFHDPSCCK PCPCNNGPSC SVMPEEEV 480  
CNCPPGVGTG ARCELADG YGDFPGEHGP VRPCQPCQCN NVNDPSASGN CDRLTGRCLK 540  
CIHNTAGIYQ DQCKAGYFGD FLAPNPAKDC RACNCPMGS EPVGCSDGT CVCKPGFGGP 600  
NCEHGAFCSP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQAQEQAL 660  
QOILRDAQIS EGASRLGLQ LAKVRSQENS YQSRLLDLKM TVERVRALGS QYQNRVRDTH 720  
RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRIAESHVE SASNMEQLTR 780  
ETEDYSKQAL SLVRKALREG VSGSGSPDG AVVQGLVEKL ETKTSLAQQL TREATQAEIE 840  
ADRSYQHSRL LLDVSRLQ VSDQSPQVEE AKRIKQKADS LSTLVTRHMD EFKRTQNLG 900  
NWKEAQQLL QNGKSGREKS DQLLSRANLA KSRQAQALSM GNATPYEVES ILKNLREFDL 960  
QVDNRKAABE EAMKRLSYIS QKVSADSKT QQAERALGSA AADAQRAKNG AGEALEISSE 1020  
IEQIGISNLN EAVVTADGAL AMEKGSLASL SEMREVEGEL ERKLEBFDIN MDAVQMVITE 1080  
AQKVDTAKN AGVTIQDTLN TLDGLLHMD QPLSVDEEGL VLEQLKSLRA KTQINSQLRP 1140  
MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQ 1193

80  
Seq ID NO: C322 Protein Sequence  
Protein Accession #: NP\_066924.1

1 11 21 31 41 51  
MANAGLQLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEG LWMSCVSQSTG 60

QIQCKVFDLS LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120  
 IGGAIFFLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGA 180  
 LLCCSCPRKT TSYPTPRPYP KPAPSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence  
 Protein Accession #: AAM77876

1 11 21 31 41 51  
 10 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLTIIVD SGLKFAVAKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPASN LAAPNLVTEE GKISITLSCSV AGDPVPNNMYW DVGNLVSKHM 240  
 15 NETSHTQGS L RITNISSDDS GKQISCAVEN LVGEDQDSVN LTVHFAPIT FLESPTSDDH 300  
 WCIPFTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHPMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKGTREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence  
 Protein Accession #: NP\_006171.1

1 11 21 31 41 51  
 25 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLTIIVD SGLKFAVAKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPASN LAAPNLVTEE GKISITLSCSV AGDPVPNNMYW DVGNLVSKHM 240  
 NETSHTQGS L RITNISSDDS GKQISCAVEN LVGEDQDSVN LTVHFAPIT FLESPTSDDH 300  
 30 WCIPFTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHPMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKGTREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGPASV ISNDDDSASP 480  
 LHHISNGSNT PSSSEGGGDA VIIGMTKIPV IENPQYFGIT NSQLKEDTFV QHKKRHNIVL 540  
 KRELGEAGFG KVFLEACYNL CPEQDKILVA VKTLKADSDN ARKDFHREAE LLTNLQHEHI 600  
 35 VKFYGVCEG DPLIMVFEYM KHGDLNKLFLR AHGPDPAVLMA EGNPPTTELQ SQMLHIAQQI 660  
 AAGMVYLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG GHTMLPIRM 720  
 PPESIMYRK F TTESDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ 780  
 EYVELMLGCG QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG 822

40 Seq ID NO: C325 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 45 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLTIIVD SGLKFAVAKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPASN LAAPNLVTEE GKISITLSCSV AGDPVPNNMYW DVGNLVSKHM 240  
 NETSHTQGS L RITNISSDDS GKQISCAVEN LVGEDQDSVN LTVHFAPIT FLESPTSDDH 300  
 50 WCIPFTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHPMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKGTREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence  
 Protein Accession #: NP\_570843.1

1 11 21 31 41 51  
 60 MPLKHLYLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60  
 LNTHITELNE SPFFINISALI ALRIEKNELS RITPGAFNRL GSLRYLSLAN NKQLVLPGL 120  
 FQGLDSLES L LSSNQQLLQI QPAHFSQCSN LKELQLHGNN LEYIPDGAFD HLVLGTRKLN 180  
 GKNSLTHISP RVFOHLNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240  
 PHNNHNLQRL VLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRLEWL 300  
 YDNHISLDP NVFNSNLRLQ VLILSRNQIS FISPGAPNGL TELRELSLHT NALQDLGDNV 360  
 65 FRMLANLQNI SLQNNRLRLQ PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCERL 420  
 YDNPWRCDS ILPLRNWLL NQPRLGTDIV PFCFSPANVR GQSLIIINVN VAVPSVHVP 480  
 VPSYPETPWY PDTPSYDDT SVSSTIELTS PVEDYDILT IQVTDDRSVW GMTQAQSGLA 540  
 IAAIVIGIVA LACSLAACVG CCCCCKRSQA VLMQMKAFNE C 581

70 Seq ID NO: C327 Protein Sequence  
 Protein Accession #: NP\_002649.1

1 11 21 31 41 51  
 75 MRALLARLLL CVLVVSDSKG SNEHQVPSN CDCINGGTCV SNKYFSNIHW CNCPKPKGGQ 60  
 HCEIDKSKTC YBGNHGFYRG KASTDTMGRP CLPWN SATVL QQTYHAHRSD ALQLGLGKH 120  
 YCRNPDRNR PWCYVQGLK PLVQECMVHD CADGKKPSPS PEELKFCQCG KTLRPRFKII 180  
 GGEFTIENQ PWFAIYRRH RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDIYVYL 240  
 RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNDAIALK IRSKEGRCAQ PSRTIQTICL 300  
 80 PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVVKLI SHRECCQPHY YGSEVITKOL 360  
 CAADPQWKTD SCQGDGGGPL VCSLQGRMTL TGVVSNRGRC ALKDKPGVYT RVSHFLPWIR 420  
 SHTKEENGLA L 431

Seq ID NO: C328 Protein Sequence  
 Protein Accession #: XP\_087254.1

1 11 21 31 41 51  
5 MQFRECSING MKYQEINGRL VPEGPTPDSS EGNLSYLSL SHLNNLSHLT TSSSFRTSPE 60  
NETELIKEHD LFFKAIVSLCH TVQISNVQTD CTGDGPWQSN LAPSQLEYA SSPDEKALVE 120  
AAARIGIVFI GNSEETMEVK TLGKLERYKL LHILEFDSR RRMSVIVQAP SGEKLLFAKG 180  
AESSILPKCI GGEIEKTRIH VDEPALKGLR TLCIAYRKFT SKEYEEIDKR IFEARTALQQ 240  
REEKLAAVFQ FIEKDLILLG ATAVEDRLQD KVRETIEALR MAGIKVWVLT GDKHETAVSV 300  
10 SLSCGFHFHQ MNILELINQK SDSECAEQLR QLARRITEDH VIQHGLVVDG TSLSLALREH 360  
EKLMEVCERN CSAVLCCRMA PLQAKVIRL IKISPEKPIT LAVGDGANDV SMIQEAHVGI 420  
GIMGKEGRQA ARNSDYAIAR FKFLSKLLFV HGHFYIIRIA TLVQYFFYKN VCFITPQFLY 480  
QFYCLFSQQT LYDSVYLTLY NICFTSLPIL IYSLLEQHVH PHVLQNKPTL YRDISKNRLL 540  
SIKTFLYWTI LGFSHAFIFF FGSYLLIGKD TSLLGNGQMF GNWTFGLTVF TVMVITVTVK 600  
15 MALETHFWTW INHLVTWGS IYFVFSLFY GGILWPFLLS QNMYFVFIQL LSSGSAWFAI 660  
ILMVVTLCLF DIKKVFDORH LHPTSTAKAQ LTETNAGIKC LDSMCCFPFG EAACASVGRM 720  
LERVIGRCSP THISRSWSAS DPFFYNDRSI LTLSTMDST C 761

Seq ID NO: C329 Protein Sequence  
Protein Accession #: XP\_087461.1

20 1 11 21 31 41 51  
MLPLAALLA AACPLPPVRG GAADAPGLLG VPSNASVNAS SAASPSPRGC WPRRPPGPPS 60  
25 ARARRRRRRR RRLCNISVQR QMLSSLLVRW GRPRGFCQDL LLFSTNAHGR AFFAAAFHRV 120  
GPPLLIHHLG LAAGGAQDDL RLCVCGGWR GRRTGRLRPA AAPSAATAA GAPALPAPY 180  
AAEPGPPLWL QGEPHPLFCL DFSLEELQGE PGNRLNRKPI ESTLVACFMT LVIVVWSVAA 240  
LWVPVPIAG FLPMGMEQRR TTAATTAATP AAVPAGTTAA AAAAAAAAA AVTSGVATK 299

Seq ID NO: C330 Protein Sequence  
Protein Accession #: XP\_051522.2

30 1 11 21 31 41 51  
35 MDLHLFDYSE PGNFSDISWP CNSSDCIIVD TVMCPNMPNK SVLLYTLSEI YIFIFVIGMI 60  
ANSVVVVWNI QAKTTGYDTH CYILNLAIAD LWVVLITPVV VVSLVQHNQW PMGELTCKVT 120  
HLIFSINLFG SIFFLTCSMV DRYLSITYFT NTPSSRKMMV RRVVCILVWL LAFCVSLPDT 180  
YYLKTVTSAS NNETYCRSFY PEHSIKEWLI GMELVSVVLG FAVPFSSIAV FYFLARAI 240  
40 ASSDQKHSS RKIIFSYVVV FLVCWLPYHV AVLLDIFSL HYIPFTCRLE HALFTALHVT 300  
QCLSLVHCCV NPVLYSFINR NYRYELMKAF IPKYSAKTGL TKLIDASRV ETEYSALEQS 360  
TK 362

Seq ID NO: C331 Protein Sequence  
Protein Accession #: NP\_000341.1

45 1 11 21 31 41 51  
MGFVRQIQLL LMKNWTLRKR QKIRFVVVEL WPLSLPLVLI WLRNANPLYS HHECHFPNKA 60  
MPSAGMLPWL QGIFCNVNNP CFQSPPTGES PGIVSNYNS ILARVYRDFQ ELLMNAPESQ 120  
50 HLGRINTEHL ILSQFMDTLR THPERIAGR IRIRDILKDE ETLTLPLIKN IGLSDSVVYL 180  
LINSQVRPEQ FAHGVDPDL KDIACSEALL ERFIIPSQRR GAKTVRYALC SLSQGTQLWI 240  
EDTLYANVDF FKLPRVLPPL LDSRSQGINL RSWGILSDM SPRIQEFIR PSMQDQLWVT 300  
RPLMQNGGPE TFTKLMGILS DLLCGYPEGG GSRVLSFNWY EDNRYKAPLG IDSTRKDIY 360  
SYDRRTTSFC NALIQSLESN PLTKIAWRAA KPLLMGRILY TPDSPAARRI LKNANSTFEE 420  
55 LEHYRKLKVA WEEVGPIQWY FFDNSTQNMN IRDTLGNPTV KDFLNRQLGE EGITAEAILN 480  
FLYKGPRESQ ADDMANFDWR DIFNITDRTL RLNVQYLECL VLDKFESYND ETQLTORALS 540  
LLEENMFVAG VVFPDMYFPT SSLPPIVYK IRMDIDVVEK TNKIKDRYWD SGRADPVED 600  
FRYIWGGPAY LQDMVEQGIT RSQVQAEAPV GIYLOQMPYP CFVDDSPHII LNRCFPIFMV 660  
LAWIYSVMT VKSIVLEKEL RLKETLKNQG VSNVAVICTW FLDSFSIMSM SIFLLTIFIM 720  
60 HGRILHYSDP FILLPLFLLAF STATIMLCPL LSTFFSKASL AAACSGVIYF TLYLPHILCF 780  
AQDRMTAEL KKAVSLLSPF AFGFGTEYLV RFEEQGLGLQ WSNIGNSPTE GDEFSELLSM 840  
QMMLLDAACY GLLAWYLDQV FPGDVGTPLP WYELLQESYM LSGEGCSTRE ERALEKTEPL 900  
TEETEDPEHP EGINDSFFER EHPGVVPGVC VKNLVKIFEP CGRPAVDRLN ITFYENQITA 960  
FLGHNGAGKT TTLSILTGLL PPTSGTVLVG GRDIETSLDA VRQSLGMCQP HNILFHLTV 1020  
65 AEHMLFYAQL KGKSEEAQAL EMEAMLEDTG LHKRNEEAQ DLSSGMQRKL SVAIAFVGDA 1080  
KVVILDEPTS GUDPYSSRSI WDLLKYSRSG RTIIMPTHM DEADHQGDRI AIIAQGRLYC 1140  
SGTFLPLKNC FGTGLYTLV RKMKNIQSOR KGSEGTCSKS SKGFSTTCFA HVDDLTPQV 1200  
LDGDVNELMD VVLHVVPEAK LVEICQELI FLLPNQNFH RAYASLFREL EETLADLGLS 1260  
SPGISDTPLE EIFLKVTEDS DSGPLFAGGA QOKRENVNPR HPCLGPREKA GQTPQDSNVC 1320  
70 SPGAPAAHPE GQPPPEPECP GPQLNTGTQL VLQHVQALLV KRFQHTIRSH KDFLAQIVLP 1380  
ATFVFLALML SIVILPFGEY PALTLHPMIY GQYTFFSMD EPGSEQFTVL ADVLLNKPGF 1440  
GNRCLKEGWL PEYPCGNSTP WKTSPSVSPNI TQLFQKQKWT QVNESPSCRC STREKLTMLP 1500  
ECPEGAGGLP PPQRTQRSTE ILQDLTDRI SDFLVKTYPA LIRSSLKSKF WVNQRYGGI 1560  
SIGGKLPVVF ITGEALVGLF SDLGRIMNVS GGPIREASK EIPDFLKHLE TEDNIKWVFN 1620  
75 NKGHALVIF LNAVNAAILR ASLPKDRSPE EYGITVISQP LNLTKQLSE ITVLTTSVDA 1680  
VVAICVFISM SVFPAFVLY LIQERVNKS KHLQFISGVSP TTYVNTFLW DIMNYSVSAG 1740  
LVVGIPIGFQ KKAYTSPENL PALVALLLLY GWAVIEMMYP ASFLFDPST AYVALSCANL 1800  
FIGINSSAIT FILELFDNRR TLLRFNAVLR KLLIVFPHFC LGRGLIDLAL SOAVTDVYAR 1860  
FGEEHSANPF HWDLIGKPLF AMVVEGVVYF LLTLLVQRHF FLSQWIAEPT KEPIVDEDDD 1920  
80 VABERQRIIT GGMKTDILRL HELTKIYLG SSPAVDRICV GVRPGECFGL LGVNGAGKTT 1980  
TFQMLGDTT VTSGDATVAG KSILTNISEV QNMGYCQPF DAIDELLTGR EHLVLYARLR 2040  
GVPAEBIEKV ANNSIKSLGL TVYADCLAGT YSGGNKRKLS TAILALGICPP LVLLDEPTTG 2100  
MDPQARRMLN NVIVSIIRKG RAVVLTSHSM EECEALCTRL AIMVKGAFCR MGTIQLHLSK 2160  
FGDGIYVTKM IKSPKDDLLP DLNPFVEQFFQ GNFFGSVQRE RHYNMLQFQV SSSSLARIFQ 2220  
LLLSHKDSLL IEESVYQTIT LDQVFNFAK QQTESHDLPL HPRAAGASRQ AQD 2273

Seq ID NO: C332 Protein Sequence  
Protein Accession #: NP\_006662.2

5 1 11 21 31 41 51  
| | | | | |  
MVPHAILARG RDVCRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQEISYF QPFGELLMRM 60  
LKMMILPLVV SSLMSGSLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIIHPGSAA 120  
QKETTEQSGK PIMSSADALL DLIRNMFPAN LVEATFKQYR TKTTTPVVKSP KVAPEEAPPR 180  
10 RILYGVQEE NGSHVQNFAL DLTPEPEVVY KSEPGTSDGM NVLGIVFFSA TMGIMLGRMG 240  
DSGAPLVSPC QCLNESVMKI VAVAVWYFPF GIVFLIAGKI LEMDDPRAVG KKLGPYSVTV 300  
VCGLVHGLF ILPLLYFFIT KKNPIVPFIRG ILQALLIALA TSSSSATLPI TFKCLLENMH 360  
IDRIARFVL PVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA 420  
15 GIPQAGLVMT VIVLTSVGLP TDDITLIIAV DWALDRFRMT INVGLDALAA GIMAHICRKD 480  
PARDTGTGK LFCETKPVSL QEIVAAQONG CVKSVAEASE LTLGPTCPHH VPVQVERDEE 540  
LPAASLAHCT IQISELETNV 560

Seq ID NO: C333 Protein Sequence  
Protein Accession #: NP\_005680.1

20 1 11 21 31 41 51  
| | | | | |  
MVTVGNCEYA EGPVGPAMWQ DGLSPCFFFT LVPSTRMALG TLALVLALPC RRRERPAGAD 60  
25 SLSWGAGPRI SPYVLQLLLA TLQAALPLAG LAGRVGTARG APLPSYLLLA SVLESAGAC 120  
GLWLLVVERS QARQLAMGI WIKPRHSPGL LLLWTVAFAA ENLALVSWNS PQWWARADL 180  
GQQVQFSLWV LRYVVSGLLF VLGLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQQTNR 240  
DFGRKLRLLS GYLWPRGSPA LQLVVLICLG LMGLERALNV LVPIFYRNIV NLLTEKAPWN 300  
SLAWTVTSYV FLKPLQGGGT GSTGPFVSNLR TFLWIRVQQF TSRRVELLIF SHLHELRLW 360  
30 HLGRRTGEVL RIADRGTSV TGLLSYLVEN VIPTLADIII GIIFYSMFFN AWFGLIVFLC 420  
MSLYTLTIV VTEWRTKFR AMNTQENATR ARAVDSLNF ETVKYNAES YEVEYREAI 480  
IKYQGLEWKS SASLVLLNQT QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYYIQL 540  
YMLNWFGTY YRMIQTNFID MENMFDLLKE ETEVKDLPGA GPLRFQKRI EFENVHFSYA 600  
DGRETLDQVS FTVMPQQTIA LVGPSGAGKS TILRLFRFY DISSGCIRID QDISQVTA 660  
35 SLRSHIGVVP QDVLFNFTI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM APPEGYRTQV 720  
GERGLKLSGG EKORVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTV 780  
VAHRLSTVNV ADQILVIKDG CIVERGRHEA LLSRGGVYAD MWQLQQQEE TSEDTKPQTM 840  
ER 842

Seq ID NO: C334 Protein Sequence  
Protein Accession #: NP\_000667.1

40 1 11 21 31 41 51  
| | | | | |  
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVGLFA 60  
45 IFAITISLG FCTDFYGCLE LACFVLVLTQ SSIFSLLAVA VDRYLAICVP LRYKSLVTGT 120  
RARGVIAVLW VLAFGIGLTP FLGNSKDSA TNNCTEPWDG TTNESCLVK CLFENVVPM 180  
YMYVFNFFGC VLPLLLIMLV IYIKIFLVAC RQLQTELM D HSRTTLQREI HAAKSLAMIV 240  
GIFALCWLFP HAVNCVTLFQ PAQGNKPKK AMNMAILLSE ANSVNPIVY AYRNRDFRYT 300  
50 FHKIISRYLL CQADVSKNG QAGVQPALGV GL 332

Seq ID NO: C335 Protein Sequence  
Protein Accession #: NP\_443164

55 1 11 21 31 41 51  
| | | | | |  
MGLGARGAWA ALLLGTQLVL ALLGAHESA AMAETLQHPV SDHTNETSNS TVKPPTSVAS 60  
DSSNTVTITM KPTAASNTT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMTVTHNS 120  
SVTSAASSVT ITTTHSEAK KGSKFDTSF VGGIVLTIGV LSILYIGCM YYRRRGIRYR 180  
60 TIDEHDAII 189

Seq ID NO: C336 Protein Sequence  
Protein Accession #: NP\_004186.1

65 1 11 21 31 41 51  
| | | | | |  
MAQHGMAGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60  
YPGECCSEW DCMCVQPEFH CGDPCCTTCR HHPCPGQGV QSQKPSFGF QCIDCASGTF 120  
SGGHEGCKP WTDCTQFGFL TVFPGNKTHN AVCVPGSPPA EPLGWLTIVL LAVAACVLLL 180  
70 TSAQLGLHIW QLRSCMMPR ETQLLLEVPP STEDARSCQF PEEERGERSA EEKRLGDLW 240  
V 241

Seq ID NO: C337 Protein Sequence  
Protein Accession #: BAC03767.1

75 1 11 21 31 41 51  
| | | | | |  
MGCDGRVSG LARNLQPTLT YWSVFFSFLG CIAFLGPTLL DLRCQTHSSL PQISWVFSQ 60  
QLCLLGSAL GGVFKRTLAQ SLNALFTSSL AISLVFAVIP PCRDKVLAS VMALAGLAMG 120  
CIDIYANMQL VRMYQDSAV FLQVLHFFVG FGALLSPLIA DPFLSEANCL PANSTANTTS 180  
80 RGLFHVSRV LGQHVDAPK WSNQTFEGLT PKDGAGTRVS YAFWIMALID LFPVMAVIML 240  
LSKERILLTC PQRRLLLSA DELALETQPP EKEDASSLPP KFQSHLGHEE LFSCCQRKNL 300  
RGAPYSFFAI HITGALVLEF TDGLTGRAYSA FVYSYAVEKP LSVGHKVAGY LPSLFWGFIT 360  
LGRLLSIPIS SRMKPATMVF INVVGVVVTF LVLLIFSYNV VFLFVGTSAL GLFLSSTPFS 420  
MLAYTEDSLQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QSSYSFLVCG VIFGCLAPTF 480

YILLFFHRM HGPLSPVPTQ DRSIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence  
Protein Accession #: NP\_002194.1

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

1	11	21	31	41	51	
MGPERTGAAP	LPLLLVLALS	QGILNCCLAY	NVGLPEAKIF	SGFSSEQFGY	AVQQFINPKG	60
NWLLVGSFWS	GFENRMGDV	YKCPVDLSTA	TCEKLNQTS	TSIPNVTEMK	TNMSLGLILT	120
RNMGTGGFLT	CGPLWAQCG	NQYTTGVCS	DISPDFQLSA	SFSPATQPCP	SLIDVVVVCD	180
ESNSIYPWDA	VKNFLEKFKVQ	GLDIGPTKTQ	VGLIQYANNP	RVVFNLTNYK	TKEEMIVATS	240
QTSQYCGDLT	NTFGAIQYAR	KYAYSASGG	RRSATKVMVV	VTDGESHDGS	MLKAVIDQCN	300
HDNILRFGIA	VLGYLNRNAL	DTKNLIKEIK	AIASIPTERY	FFNVSDAAL	LEKAGTLGEO	360
IPSEIGTVQG	GDNFQMEMSQ	VGFSADYSQ	NDILMLGAVG	AFGWSGTIVQ	KTSHGHLIFP	420
KQAFDQILQD	RNHSSYLGYS	VAAISTGEST	HFVAGAPRAN	YTGQIVLYSV	NENGNIIVIQ	480
AHRGDQIGSY	FGSVLCSDV	DKDTITDVL	VGAPMYMSDL	KKEEGRVYLF	TIKKGILGQH	540
QPLEGPEGIE	NTRFSGAIAA	LSDINMDGFN	DVIVGSPLEN	QNSGAVVIYN	GHQGTIRTKY	600
SQKILGSDGA	FRSHLYQFGR	SLDGYGDLNG	DSITDVSIGA	FGQVVQLWSQ	SIADVAIEAS	660
FTPEKITLVN	KNAQIILKLC	FSAKFRPTKQ	NNQVAIVYNI	TLDADGFSSR	VTSRGLFKEN	720
NERCLQKNMV	VNQASCPHE	IYIQEPSDV	VNSLDLRVDI	SIENPGTSPA	LEAYSETAKV	780
ESIPIFKHCG	EDGLCISDLV	LDVRQIPAAQ	EQPFIVSNQN	KRLTFSVTLK	NKRESAYNTG	840
IUVDFSENLF	FASFSLPVDG	TEVTCQVAAS	QKSVACDVGY	PALKREQVQT	PTINFDFNLQ	900
NLQNASLSF	QALSESQEEEN	KADNLVNLKI	PLLYDAEHL	TRSTNINFYE	ISSDGNVPSI	960
VHSEFVGVK	FIFSLKVTTC	SVPVSMATVI	IHIPQYTKK	NPLMYLTGVQ	TDKAGDISCN	1020
ADINPLKIGQ	TSSSVFSKSE	NFRHTKELNC	RTASCNVTC	WLKDVHMKGE	YFVNVTIRIW	1080
NGTFASSTFQ	TVQLTAAAEI	NTYNPEIYVI	EDNTVTIPLM	IMKPDEKAEV	PTGVIIGSII	1140
AGILLALLLV	AILNKLGF	RYKRYMTKNP	DEIDETTELS	S		1181

Seq ID NO: C339 Protein Sequence  
Protein Accession #: NP\_113648.1

30  
35  
40  
45  
50

1	11	21	31	41	51	
MYRPRARAAP	EGRVRCGAVP	STVLLLLLAYL	AYLALGTGVF	WTEGRAAQD	SSRSFQDKW	60
ELLQNFTCLD	RPALDSLIRD	VQAYKNGAS	LLSNTTSMGR	WELVGSFFFS	VSTITTIGYG	120
NLSPTNMAAR	LFCIEFFALVG	IPLNLVVLNR	LGHLMQGGVN	HWASRLGGTW	QDPDKARWLA	180
GSGALLSGLL	LELLLPILLF	SHMEGWSYTE	GFYFAFITLS	TVGFGDYVIG	MNPSQRYPLW	240
YQNMVSLWLE	FGMAWLALII	KLILSQLETP	GRVCSCHHS	SKEDFKSQSW	RQGEDREPES	300
HSPQGGCYE	GPMGIQHLE	PSAHAAGCGK	DS			332

Seq ID NO: C340 Protein Sequence  
Protein Accession #: NP\_004145.1

40  
45  
50

1	11	21	31	41	51	
MEWDNGTGQA	LGLPPTTCVY	RENFKQLLLP	PVYSAVLAAG	LPLNICVITQ	ICTSRRALTR	60
TAVYTLNLAL	ADLLYACSLP	LLIYNYAQGD	HWPFQDFACR	LVRFLFYANL	HGSILFLTIC	120
SFQRYLGICH	PLAPWHKRG	RAAMLVCAV	VWLAVTTQCL	PTAIFAATGI	QRNRTVCYDL	180
SPPALATHYM	PYGMALTVIG	FLLPFAALLA	CYCLLACRLC	RQDGPAPVPA	QERRGKAARM	240
AVVVAAPFAI	SPLPFIHTKT	AYLAVERSTPG	VPCTVLEAFA	AAYKGTTPFA	SANSVLDPIL	300
FYFTQKKFRR	RPHELLQLKT	AKWQRQGR				328

Seq ID NO: C341 Protein Sequence  
Protein Accession #: NP\_009128.1

55  
60  
65  
70

1	11	21	31	41	51	
MQRPGFRLWL	VLQVMGSCAA	ISSMDMERPG	DGKCQPIEIP	MCKDIGVNTM	RMPNLMGHEN	60
QREAAIQLEE	FAPLVEYGCH	GHLRFFLCSL	YAPMCTEQVS	TPIPACRVMC	EQARLKCSPI	120
MEQNFNFKWD	SLDCRKLPNK	NDPNYLCMEA	FNNGSDEPTR	SGSLFPPLFR	PQRPHSAQEH	180
PLKDGPGGRG	GCDNPGKPHH	VEKSASCAPL	CTPGVDVYWS	REDKRFVAVW	LAIWAVLCFF	240
SSAFTVLTFL	IDPARFRYPE	RPIIFLSMCY	CVYSVGYLIR	LFAGAESIAAC	DRDSGQLYVI	300
QEGLESTGCT	LVLVLVLYPG	MASSLWVVVL	TLTWFLAAGK	KWGHEAIEAN	SSYFHLAANA	360
IPAVKTILIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGFVLI	PLACYLVIGT	SFILSGFVAL	420
PHIRRVMTKG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLNMD	YWKILAAQHK	480
CKMNQTKTL	DCLMAASIPA	VEIFPMVKIFM	LLVVGITSGM	WIWTSKTLQS	WQVCSRRLLK	540
KKSRRKPASV	ITSGGIYKKA	QBPQKTHHGK	YEIPAQSFTC	V		581

Seq ID NO: C342 Protein Sequence  
Protein Accession #: NP\_005752.1

70  
75  
80

1	11	21	31	41	51	
MEVSRRKAPP	RPPRPAAPLP	LLAYLLALAA	PGRGADEFVW	RSEQAIGAIA	ASQEDGVFVA	60
SGSCLDQLDY	SLEHSLSRLY	RDQAGNCTEP	VSLAPPARPR	PGSSFSKLLL	PYREGAAGLG	120
GLLLTGFTDY	RGACEVRPLG	NLSRNSLRNG	TEVVSCHPQG	STAGVVYRAG	RNNRWYLAVA	180
ATYVLPPEPET	ASRCNPAASD	HDATAALKOT	EGRSLATQEL	GRLLKCEGAG	SLHFVDAPFW	240
NGSIYFPYYP	YNYTSGAATG	WPSMARIAQS	TEVLFOGQAS	LDCGHGHPDG	RRLLSSSLV	300
EALDVWAGVF	SAAAGEGQER	RSPTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
ERVQFIASST	LHSDLTSVY	GTVMNRTVL	PLGTGDGQLL	KVILGENLTS	NCPEVIYEIK	420
BETPVFYKLV	PDVKNYIYI	LTAGKEVRR	RVANCNKHKS	CSECLTATDP	HCGWCHSLQR	480
CTFQGDVCHS	ENLEWLDIS	SGAKKCPKIQ	IIRSSKEKTT	VTMVGSFSPR	HSKCMVKNVD	540
SSRELQCNKS	QPNRTCTCSI	PTRATYKDV	VNVVMFSPGS	WNLSDRFNFT	NCSLKECPA	600
CVETGCAWCK	SARRCIHPFT	ACDPSDYERN	QEQCPVAVEK	TSGGGRPEKEN	KGNRTNQALQ	660
VFYIKSIEPQ	KVSTLGKSNV	IVTGANFTRA	SNITMILKGT	STCDKDVIVQ	SHVLNDTHMK	720



5 FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMMGRNFD 780  
 VIDNLIISHE LKGNINVSSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLOQ 840  
 REDPRPTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LPHGNGQLN CSFENITRNO 900  
 DLTTLCKIK GIKTASTIAN SSKVVRVKG NLELYVEQES VPSTWYFLIV LPVLLVIVIF 960  
 AAVGVTRHKS KELSRKQSQQ LELLESELRK EIRDGFALQ MDKLDVVDSE GTVPFLDYKH 1020  
 FALRTFFPES GGFTHIPTED MNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS 1080  
 VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLLRTE SVVEKLLTNW 1140  
 MSVCLSGFLR ETVGEPFYLL VTLNQKINK GPVDVITCKA LYTLNEDWLL WQVPEFSTVA 1200  
 10 LNVVPEKIPE NESADVCRNI SVNVLCDDTI GQAKEKIFQA FLSKNGSPYG LQLNEIGLEL 1260  
 QMGTROKELL DIDSSSVILE DGITKLNTIG HYEISNGSTI KVPFKIANFT SDVEYSDDHC 1320  
 HLILPDSEAF QDVQGRHRG KHKEFKVEMY LTKLLSTKVA IHSVLEKLF SIWSLPNSRA 1380  
 PFAIKYFFDF LDAQAENKKI TDPDVVHIWK TNSLPLRFVW NILKNPQFVF DIKTPHIDG 1440  
 CLSVIAQAFM DAFSLTEQQL GKEAPTNNLL YAKDIPTYKE EVKSYKPAIR DLPLSLSEM 1500  
 15 EEPLTQESKK HENEFNEEVA LTEIYKIVK YFDEILNKLE RERGLEEAQK QLLHVVKVLF 1560  
 EKKCKKWM 1568

Seq ID NO: C343 Protein Sequence  
 Protein Accession #: NP\_002176.1

20 1 11 21 31 41 51  
 | | | | | |  
 MTILGTTFGM VFSLLQVVSQ ESGYAQNGDL EDALDDYSF SCYSQLEVNG SOHSLTCAFE 60  
 DDDVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK 120  
 25 IDLTIVKPE APFDLSVIYR EGANDFVVF NTSLQKKYV KVLMDVAYR QEKDENKWTN 180  
 VNLSSTKLTL LQRKLQPAAM YEIKVRSIPD HYFKGFSEW SPSYFFRTE INNSSGEMDP 240  
 ILLTISILSF FSVALLVILA CVLKKRIKP IVWPSLPDHK KTLHLCKGP RKNLNVSFNP 300  
 ESFLDQIHR VDDIARDEV EGFLQDTFPQ QLEESEKQRL GGDVQSPNCP SEDVVVPES 360  
 FRDRSSLTCL AGNVACDAP ILSSSRSLDC RESGRNGPHV YQDLLSLGT TNSTLPPFFS 420  
 30 LQSGILTLPN VAQQPILTS LGSNQEEAYV TMSSFYQNG 459

Seq ID NO: C344 Protein Sequence  
 Protein Accession #: NP\_002713.1

35 1 11 21 31 41 51  
 | | | | | |  
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60  
 TRPRYGRKHK EDTLAFSEWG SPAAVPREL SPLDL 95

Seq ID NO: C345 Protein Sequence  
 Protein Accession #: NP\_115934.1

40 1 11 21 31 41 51  
 | | | | | |  
 MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNNTSSHFE 60  
 45 VTGSAEGWGP EEPLPYSRAF GEGASARPRC CRNGGTCVLG SPCVCPAFT GRYPEHDQRR 120  
 SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHANGP SAGGAPSLLL 180  
 LLPCALLHRL LRPDAPAHPR SLVPSVLORE RRPCGRPGLG HRL 223

Seq ID NO: C346 Protein Sequence  
 Protein Accession #: NP\_006524.1

50 1 11 21 31 41 51  
 | | | | | |  
 MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LDYMAPDCR 60  
 55 FLTIHRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPKQVD 120  
 VKTDKNDFYC Q 131

Seq ID NO: C347 Protein Sequence  
 Protein Accession #: Eos sequence

60 1 11 21 31 41 51  
 | | | | | |  
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GKNTFPVEKP TENLGNITLT 60  
 65 TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSPTLI 120  
 TSRTKLSSIT SEATGNESHV YLNKDGSKG IHAGQMEND SPPAWAIVIV VLVAVILLV 180  
 FLGLIFLVSY MMRTRRLTQ NTQYNDAEDE GGFNSYPVYL MEQQLGMGQ IPSR 235

Seq ID NO: C348 Protein Sequence  
 Protein Accession #: NP\_543146.1

70 1 11 21 31 41 51  
 | | | | | |  
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GKNTFPVEKP TENLGNITLT 60  
 75 TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTS SHLNKTEVTH QVPTGSPTLI 120  
 TSRTKLSSIT SEATGNESHV YLNKDGSKG IHAGQMEND SPPAWAIVIV VLVAVILLV 180  
 FLGLIFLVSY MMRTRRLTQ NTQYNDAEDE GGFNSYPVYL MEQQLGMGQ IPSR 235

Seq ID NO: C349 Protein Sequence  
 Protein Accession #: FGENSEH predicted

1 11 21 31 41 51  
 | | | | | |

5	MMPLAFCCW GLALVSGWAT FQOMSPSRNF SFRLFPETAP GAPGSIPAPP APGDEAAGSR 60
	VERLGOAFRR RVRLRLRESE RLELVFLVDD SSSVGEVNFRL SELMFVRKLL SDFPVVPTAT 120
	RVAIVTFSSK NYVVRVDYI STRRARQHKC ALLLQEIPIA SYRGGGYTK GAFQQAQIL 180
	LHARENSTKV VFLITDGYSN GGDPRPIAAS LRDSGVEIFT FGIWQGNIRE LNDMASTPKE 240
	EHCYLLHSFE EFELALARRAL HEDLPSGSFI QDDMVHCSYL CDEGKDCDR MGSCCKGTH 300
	GHFECICEKG YYGKGLQYEC TACPSGTYPK EGSPGGISSC IPCFDENHTS PPGSTSPEDC 360
	VCRESYRASG QTCELVHCPA LKPPENGYFI QNTCNNHFNA ACQVRCHPGF DLVGSIIILC 420
	LPNGLWSGSE SYCRVRTCPH LRQPKHGHIS CSTREMLYKT TCLVACDEGY RLEGSCLKTC 480
10	QGNSSQWDGPE PRCVERHCST FQMPKDVIIIS FHNCGKQPAK FGTICTVSCR QGFILSGVKE 540
	MLRCTTSGKP NVGVAQAVCK DVEAPQINCP KDIEAKTLEQ QDSANVTWQI PTAKDNSGEK 600
	VSVHVPAPT PPYLFPIDGV AIVYTATDLS GNQASCFIHI KVDAEPPVI DWCRSPPPVQ 660
	VSEKHAAASG DEPOFSDNSG AELVITRSHT QGDLFPOGET IVQYATDPS GNNRTCDIHI 720
	VIKGSPCEIP FTPVNGDFIC TPDNTGVNCT LTCLEGYDFT EGSTDYKYCA YEDGVWKFTY 780
15	TTWPDCAK RFANHGKSF EMFYKAARCD DTDLMKKFSE AFETTLGKMV PSFCSAEDI 840
	DCRLEENLTK NGVQAVVYD ENGAIGPGG WGAANRLDYS YDDFLDTVQE TATSIGNAKS 900
	SRKRSAPLS DYKIKLIFNI TASVPLPDER NDTLEWENQ RLLQTLTIT NKLKRTLNKD 960
	PMYSQLASG ILLADINSLE TKKASPFRCR GSULRGRMCV NCPGLTYNLL EHTCESCRI 1020
	GSYQDEEQGL ECKLCPSGMY TEYIHSRNIIS DCKAQCKQGT YSYSGLETCE SCPLGTYPQK 1080
20	FGSRSCLECP ENTSTVKRGA VNISACGVPC PEGKFSRSLG MPCHPCRDY YQPNAGKAF 1140
	LACPYGTTP FAGSRITFC STSVLNTITF GGFHLELLN CPSEVHECF FNPCHNSGTC 1200
	QQLGRGYVCL CPLGYTGLKC ETDIDECSPL PCLNNGVCKD LVGEFICECP SGYTQRCCE 1260
	NINECSSPC LKNGICVDG AGYRCTCVKG FVGLHCETE NECQSNPCLN NAVCEDQVGG 1320
	FLCKCPGRL GTRCGKNVDE CLSQPCNGA TCKDQANSFR CLCAAGTGS HCELNINECQ 1380
25	SNPCRNQATC VDELANYSCK QPFGSGKRC ETEQSTGPNL DFEVSGIYGY VMLDGMPLPSL 1440
	HALTCTFMK SSDDMNYGTF ISYAVDNGSD NTLTLDYNG WVLVYNGREK ITNCPVNDG 1500
	RWHIAITWT SANGIKWYI DGKLSGGAG LSVGLPIPGG GALVLGQEQD KKGEGSPAE 1560
	SFVSGISQNL LWDYVLSPOG VKSLATSCPE ELKGNVLAH PDLFSLGVK VKIDSKSIFC 1620
	SDCPRLGGSV PHLTASEDL KPGSKVNLFC DPGFQLVGNP VQYCLNQGW TOPLPHCERI 1680
30	SCGVPPPLEN GFHSADDFYA GSTVTYQCNN GYLLGDSRM FCTDNGSWG VSPSCLDVDE 1740
	CAVGSDSEH ASCLNVDSGY ICSCVPPYTQ DGKNCAPPIK CKAPGNPENG HSSGEIYTVG 1800
	AGVTFSQCEG YQMGVTKIT CLESGEWNHL IPYKAVSCG KPAIPENGCI EELAFTEGSK 1860
	VTRYCNKGYT LKDGKSSCL ANSSWSHSP VCEPVKCSSP ENINNGKYIL SGLTYLSTAS 1920
	YSCDTGYSLO GPSIIIECTAS GIWDRAPPAC HLVFCGEPPA IKDAVITGN FTRNTVTYT 1980
35	CKEGYTLAFL DTIECLADGK WSRSDQCLA VSCDEPIVD HASPETAHL FGDIIFYCS 2040
	DGYSLADNSQ LLCNAQGNV PPEGQDMPRC IAHFCEKPPS VSYSILESVS KAKFAAGSVV 2100
	SFKCMGGFNL NTSKIECMR GGQWNPSPMS IQCIPVRCEG PPSIMNGYAS GSNYSFGAMV 2160
	AYSCNKGFFI KGEKKTCEA TGQWSSPIPT CEFVSCGEPV KVENGFEHT TGRIFESEVR 2220
	YQCNPGYKSV GSPVFCQAN RHWHSSEPLM CVPLDCGKPP PIQNGFMKE NFEVGSKVQF 2280
40	FCNEGVELVG DSSWTCQKSG KWNKSNPKC MPAKCEPEPL LENQLVLKEL TTEVGVTFS 2340
	CKEGBVLQSG VCLNCLFSQ WDSFPVCKI VLCTPPPLIS FGVPISSAL HFGSTVKYSC 2400
	VGGFFLRGNS TTLQPDGTW SSPLPECVPV ECPQPEEIPN GIIDVQGLAY LSTALYTCKP 2460
	GFELVGNITT LCGENGHWLG GKPTCKAIEC LKPKELNGK PSYTDLHYGQ TVTYSNCRGP 2520
	RLEGPSALTC LETGDWDVDA PSCNAIHCD SPOPIENGFE GADYSYGAI IYSCFPFGV 2580
45	AGHAMQCEE SGWSSSIPTC MPIDCGLPPH IDFGDCTKLK DDQGYFEQED DMMEVPTVP 2640
	HPPYHLGAVA KTWENTKESP ATHSSNLYG TMVSYTCNPG YELGNPVL I CQEDGTWNGS 2700
	APSCISIEDC LPTAPENGL RFTETSMGSA VQYSCPKGHI LAGSDLRCL ENRKWSGASP 2760
	RCEAISCKP NPVNGSIKIG SNYTYLSTLY YECDPGYVLN GTERRTCQDD KNWDEDEPIC 2820
	IPVDCSSPPV SANGQVRGDE YTFQKELEYT CNEGFLLEGA RSRVCLANGS WSGATPDCVP 2880
50	VRCATPPQLA NGVTEGLDYG FMKEVTFHCH EGYILHGAPK LTCQSDGNWD AEIPLCKPVN 2940
	CGPPEDLAHG PFNGFSPFHG GHIQYQCFPG YKLHGNSSRR CLSNGSWSGS SPSCLPCRS 3000
	TPVIEYGTN GTDDCGKAA RIQCFKGFKL LGLSEITCEA DGQWSSGFFH CEHTSCGSLP 3060
	MIPNAFSET SSWKENVITY SCRSYGVIOG SSDLICTEKG VWSQPYVCE PLSCGSPPSV 3120
	ANAVATGEAH TYESEVKLRC LEGYTMDDT DTFTQCKDGR WFFERISCSK KKCPLPENIT 3180
55	HILVHGDDFS VNRQVSVSCA EGYTFEGVNI SVCQLDGTWE PPFSDSCSP VSCGKPESPE 3240
	HGFVVGSKYT FESTIYQCE PGYELEGNRE RVCQENRQMS GGVAICKETR CETPLEFLNG 3300
	KADIENRTTG PNVVYSCNRG YSLEGPSEAH CTENGTSWHP VPLCKENPCP VPFVIPENAL 3360
	LSEKEFVVDQ NVSIKREGF LLQHGHIITC NPDETWTQTS AKCEKISCOP PAHVENALAR 3420
	GVHYQYQDMI TYSCSYGYML EGFLRSVCLC NGTWTSPPIC RAVCRPPCQN GGICQRFNAC 3480
60	SCPEGWMLR CEEPICILPC LINGRCVAPY QCDCPPGWIG SRCHTAVCQS PCLNGGKCVR 3540
	PNRCHCLSSW TGHNCSE 3557

Seq ID NO: C350 Protein Sequence  
Protein Accession #: FGENESH predicted

65	1 11 21 31 41 51
	MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLQCPAPR CGDKIYNPLE 60
	QCCYNDIAVS LSETRQCGPP CTFWPCFELC CLDSPLGLTND FVVLKLVQGV NSQCHSSPIS 120
70	SKCERGRIC 129

Seq ID NO: C351 Protein Sequence  
Protein Accession #: AAH35671.1

75	1 11 21 31 41 51
	MVPGARGGGA LARAAGRGLL ALLLAVSAPL RLQASELGDG CGHLVTYQDS GMTSKNYPG 60
	TYPNHTVCEK TITVPKGRLL ILRLGDLDE SQTCAADYLL FTSSSDQYGP YCGSMTVPKE 120
	LLNTSEVTV RFESGSHISG RGPLLTAYASS DHPDLITCLE RASHYLKTEY SKFCPAGCRD 180
80	VAGDISGMNV DGYRDTSLC KAAIHAGIIA DELGQISVL QRKGISRYEG ILANGVLSD 240
	GSLSDRFLP TSNGCSRSL SFEPDGQIRAS SSWQSVNESG DQVHWSGQA RLQDQGPSWA 300
	SGDSSNNHNP REWLEIDLGE KKKITGIRTT GSTQSNFNFY VKSFVMNFKN NNSKWKTYKG 360
	IVNNEEKVFQ GNSNFDPVQ NNFIPPIVAR YVRVVPQTH QRIALKVELI GCQITQGNDS 420
	LWVRKTSQST SVSTKKEDET ITRPIPSEET STGINITTVA IPLVLLVVLV FAGMGIFAAP 480
	RKXKKKGSFY GSABEQKTDK WKQIKYPPAR HQSAEFTISY DNEKEMTKL DLITSDMAG 539

Seq ID NO: C352 Protein Sequence  
Protein Accession #: Eos sequence

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1	11	21	31	41	51	
MGFGAGQRLR	FVPAPRSSAE	EAARPGQLRL	GIRRGAEALA	KLAPSGVMVP	GARGGGALAR	60
AAGRGLLALL	LAVSAPLRLO	AEELGDGCGH	LVTYQDSGTM	TSKNYPGTYP	NHTVCEKTI	120
VPGKRLILR	LGDLDESQT	CASDYLLFTS	SSDQYGPYCG	SMTVPKELL	NTSEVTVRPE	180
SSSHISGRGF	LLTYASSDHP	DLITCLERAS	HYLKTEYSKF	CPAGCRDVAG	DISGNMVDGY	240
RDTSLLCKAA	IHAGIIADEL	GGQISVLQRK	GISRVEGILA	NGVLSRDGSL	SDKRFLFTSN	300
GCSRSLSFEP	DGQIRASSSW	QSNVNESGDQV	HWSPGQARLQ	DQGPASWASGD	SSNNHKPREW	360
LEIDLGEKKK	ITGIRTTGST	QSNFNFYVKS	FVMNFKNNNS	KWKTYKGIVN	NEEKVPQGNS	420
NFRDPVQNNF	IPPIVARYVR	VVPQTWHQRI	ALKVELIGCQ	ITQGNDSLWV	RKTSQSTSVS	480
TKKDEETITR	PIPSEETSTG	INITTVAIPL	VLLVVLVFAG	MGIFAAPRKK	KKKGSPYGSA	540
EAQKTDCKWQ	IKYPFARHQS	AEFTISYDNE	KEMTQKLDLI	TSDMAG		586

Seq ID NO: C353 Protein Sequence  
Protein Accession #: FGENESH predicted

25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80  
85  
90  
95  
100  
105  
110  
115  
120  
125  
130  
135  
140  
145  
150  
155  
160  
165  
170  
175  
180  
185  
190  
195  
200  
205  
210  
215  
220  
225  
230  
235  
240  
245  
250  
255  
260  
265  
270  
275  
280  
285  
290  
295  
300  
305  
310  
315  
320  
325  
330  
335  
340  
345  
350  
355  
360  
365  
370  
375  
380  
385  
390  
395  
400  
405  
410  
415  
420  
425  
430  
435  
440  
445  
450  
455  
460  
465  
470  
475  
480  
485  
490  
495  
500  
505  
510  
515  
520  
525  
530  
535  
540  
545  
550  
555  
560  
565  
570  
575  
580  
585  
590  
595  
600  
605  
610  
615  
620  
625  
630  
635  
640  
645  
650  
655  
660  
665  
670  
675  
680  
685  
690  
695  
700  
705  
710  
715  
720  
725  
730  
735  
740  
745  
750  
755  
760  
765  
770  
775  
780  
785  
790  
795  
800  
805  
810  
815  
820  
825  
830  
835  
840  
845  
850  
855  
860  
865  
870  
875  
880  
885  
890  
895  
900  
905  
910  
915  
920  
925  
930  
935  
940  
945  
950  
955  
960  
965  
970  
975  
980  
985  
990  
995  
1000

1	11	21	31	41	51	
MFQRQERFLD	LSSAEVAAM	ILHQHPDIIN	KGDGCGHLVT	YQDSGTMSTK	NYPGTYPNHT	60
VCEKTIITVPK	GKRLILRLGD	LDIESQTCAS	DYLLFTSSSD	QYGMQKEEET	EVLCLSVAGA	120
QRVDIPVQLL	PSFLEGWKSH	ADARGPYCGS	MTVPKELLN	TSEVTVRFES	GSHISGRGFL	180
LTASSDHPD	LITCLERASH	YKTEYSKFC	PAGCRDVAGD	ISGNMVDGYR	DTSLCKAAI	240
HAGIIADELG	GQISVLQRKQ	ISRYEGILAN	GVLSRDGSL	DKRFLFTSNG	CSRSLSFEPD	300
GQIRASSSWQ	SVNESGDQVH	WSPGQARLQD	QGPASWASGDS	SSNNHKPREWL	EIDLGEKKKI	360
TGIRTTGSTQ	SNFNFYVKSF	VNMFKNNNSK	WKTYKGIVNN	EEKVPQGNNS	FRDPVQNNFI	420
PPIVARYVRV	VVPQTWHQRIA	LKVELIGCQI	TQGNDSLWVR	KTSQSTSVST	KKDEETITRP	480
IPSEETSTDA	MPVQIVGDHT	QMISQRENLG	PDEGKIPFKG	TAESMVRVVF	AVVVNDLGML	540
PLAHTPEEDI	DHYCNKQIKY	PFARHQSAPF	TIISYDNEKEM	TQKLDLITSD	MADYQQPLMI	600
GGTVTRKRS	TERPMDTDAE	EAGVSTDAAG	HYDCPQQRGR	HEYALPLAPP	EPEYATPIVE	660
RHVLRHTFS	AQSGYRVVPG	QPGHKHSLSS	GGFSPVAVGV	AQDGDYQRP	SAQPADRGYD	720
RPKAVSALAT	ESGHPSQKPF	PTHPTSDSY	SAPRDLCTPL	NQTAMTALL		769

Seq ID NO: C354 Protein Sequence  
Protein Accession #: NP\_004607.1

40  
45  
50  
55  
60  
65  
70  
75  
80  
85  
90  
95  
100  
105  
110  
115  
120  
125  
130  
135  
140  
145  
150  
155  
160  
165  
170  
175  
180  
185  
190  
195  
200  
205  
210  
215  
220  
225  
230  
235  
240  
245  
250  
255  
260  
265  
270  
275  
280  
285  
290  
295  
300  
305  
310  
315  
320  
325  
330  
335  
340  
345  
350  
355  
360  
365  
370  
375  
380  
385  
390  
395  
400  
405  
410  
415  
420  
425  
430  
435  
440  
445  
450  
455  
460  
465  
470  
475  
480  
485  
490  
495  
500  
505  
510  
515  
520  
525  
530  
535  
540  
545  
550  
555  
560  
565  
570  
575  
580  
585  
590  
595  
600  
605  
610  
615  
620  
625  
630  
635  
640  
645  
650  
655  
660  
665  
670  
675  
680  
685  
690  
695  
700  
705  
710  
715  
720  
725  
730  
735  
740  
745  
750  
755  
760  
765  
770  
775  
780  
785  
790  
795  
800  
805  
810  
815  
820  
825  
830  
835  
840  
845  
850  
855  
860  
865  
870  
875  
880  
885  
890  
895  
900  
905  
910  
915  
920  
925  
930  
935  
940  
945  
950  
955  
960  
965  
970  
975  
980  
985  
990  
995  
1000

1	11	21	31	41	51	
MAGVSACIKY	SMFTFNFLFW	LCGILILALA	IWVRVNSDSQ	AIFGSEDVGS	SSYVAVDILI	60
AVGAILMILG	FLGCCGAIKE	SRMILLFFI	GLLLILLLQV	ATGILGAVFK	SKSDRIVNET	120
LYENTKLKSA	TGESEKQFKE	AIIVFQEEFK	CCGLVNGAAD	WGNFQHYTPE	LCACLDKQRP	180
CQSYNGKQVY	KETCISFIKD	FLAKNLIIVI	GISPLGLAVIE	ILGLVFSMVL	YCQIGNK	237

Seq ID NO: C355 Protein Sequence  
Protein Accession #: NP\_004608.1

50  
55  
60  
65  
70  
75  
80  
85  
90  
95  
100  
105  
110  
115  
120  
125  
130  
135  
140  
145  
150  
155  
160  
165  
170  
175  
180  
185  
190  
195  
200  
205  
210  
215  
220  
225  
230  
235  
240  
245  
250  
255  
260  
265  
270  
275  
280  
285  
290  
295  
300  
305  
310  
315  
320  
325  
330  
335  
340  
345  
350  
355  
360  
365  
370  
375  
380  
385  
390  
395  
400  
405  
410  
415  
420  
425  
430  
435  
440  
445  
450  
455  
460  
465  
470  
475  
480  
485  
490  
495  
500  
505  
510  
515  
520  
525  
530  
535  
540  
545  
550  
555  
560  
565  
570  
575  
580  
585  
590  
595  
600  
605  
610  
615  
620  
625  
630  
635  
640  
645  
650  
655  
660  
665  
670  
675  
680  
685  
690  
695  
700  
705  
710  
715  
720  
725  
730  
735  
740  
745  
750  
755  
760  
765  
770  
775  
780  
785  
790  
795  
800  
805  
810  
815  
820  
825  
830  
835  
840  
845  
850  
855  
860  
865  
870  
875  
880  
885  
890  
895  
900  
905  
910  
915  
920  
925  
930  
935  
940  
945  
950  
955  
960  
965  
970  
975  
980  
985  
990  
995  
1000

1	11	21	31	41	51	
MCTGGCARCL	GGTLIPLAFF	GFLANILLFF	PGGKVIDDND	HLSEQIWFEG	GILGSGVIMI	60
FPALVFLGLK	NNDCCGCCGN	EGCGKRFAMP	TSTIFAVVGF	LGAGYSFIIS	AISINKGPKC	120
LMANSTWGYF	FHDGDLNDE	ALWNKCREPL	NVVPWNLTIF	SILLVVGIGI	MVLCAIQVVN	180
GLLGLTLCGDC	QCCGCCGSDG	PV				202

Seq ID NO: C356 Protein Sequence  
Protein Accession #: NP\_002372.1

60  
65  
70  
75  
80  
85  
90  
95  
100  
105  
110  
115  
120  
125  
130  
135  
140  
145  
150  
155  
160  
165  
170  
175  
180  
185  
190  
195  
200  
205  
210  
215  
220  
225  
230  
235  
240  
245  
250  
255  
260  
265  
270  
275  
280  
285  
290  
295  
300  
305  
310  
315  
320  
325  
330  
335  
340  
345  
350  
355  
360  
365  
370  
375  
380  
385  
390  
395  
400  
405  
410  
415  
420  
425  
430  
435  
440  
445  
450  
455  
460  
465  
470  
475  
480  
485  
490  
495  
500  
505  
510  
515  
520  
525  
530  
535  
540  
545  
550  
555  
560  
565  
570  
575  
580  
585  
590  
595  
600  
605  
610  
615  
620  
625  
630  
635  
640  
645  
650  
655  
660  
665  
670  
675  
680  
685  
690  
695  
700  
705  
710  
715  
720  
725  
730  
735  
740  
745  
750  
755  
760  
765  
770  
775  
780  
785  
790  
795  
800  
805  
810  
815  
820  
825  
830  
835  
840  
845  
850  
855  
860  
865  
870  
875  
880  
885  
890  
895  
900  
905  
910  
915  
920  
925  
930  
935  
940  
945  
950  
955  
960  
965  
970  
975  
980  
985  
990  
995  
1000

1	11	21	31	41	51	
MPRPAPARRL	PGLLLLLLWPL	LLPSAAPDP	VARPGFRRL	TRGPGGSPGR	RPSAAPDGA	60
PASGTSEPGR	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRII	DTLDIGPADT	120
RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVEAGA	180
REPSNIPKV	AIIVTDGRQP	DQVNEVAARA	QASGIELYAV	GVDRA DMASL	KMMASEPLEE	240
HVFYVETYG	IEKLSSRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHCE	CSQGYTLNAD	300
KKTCALDRD	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCSAQD	KCALGTHGCO	360
HICVNDRTGS	HNCECYEGYT	LNADKKTCVS	RDKCALGSHG	CQHICVSDGA	ASYHCDCYPG	420
YTLNEDKKT	SATEARRLV	STEDACGCEA	TLAQDKVSS	YLQRLNLTLD	DILEKLKINE	480
YQQIHR						486

Seq ID NO: C357 Protein Sequence  
Protein Accession #: NP\_057723.1

75  
80  
85  
90  
95  
100  
105  
110  
115  
120  
125  
130  
135  
140  
145  
150  
155  
160  
165  
170  
175  
180  
185  
190  
195  
200  
205  
210  
215  
220  
225  
230  
235  
240  
245  
250  
255  
260  
265  
270  
275  
280  
285  
290  
295  
300  
305  
310  
315  
320  
325  
330  
335  
340  
345  
350  
355  
360  
365  
370  
375  
380  
385  
390  
395  
400  
405  
410  
415  
420  
425  
430  
435  
440  
445  
450  
455  
460  
465  
470  
475  
480  
485  
490  
495  
500  
505  
510  
515  
520  
525  
530  
535  
540  
545  
550  
555  
560  
565  
570  
575  
580  
585  
590  
595  
600  
605  
610  
615  
620  
625  
630  
635  
640  
645  
650  
655  
660  
665  
670  
675  
680  
685  
690  
695  
700  
705  
710  
715  
720  
725  
730  
735  
740  
745  
750  
755  
760  
765  
770  
775  
780  
785  
790  
795  
800  
805  
810  
815  
820  
825  
830  
835  
840  
845  
850  
855  
860  
865  
870  
875  
880  
885  
890  
895  
900  
905  
910  
915  
920  
925  
930  
935  
940  
945  
950  
955  
960  
965  
970  
975  
980  
985  
990  
995  
1000

1	11	21	31	41	51	
MARGSLRRL	RLVLGLWLA	LLRSVAGEQA	PGTAPCSRGS	SWSADLDKCM	DCASCRRAPH	60
SDFCGCAAA	PPAPFRLLWP	ILGGALSLTF	VLGLLSGLFL	WRRCRRRREK	TTPIETTGGE	120
GCPAVALIQ						129

Seq ID NO: C358 Protein Sequence  
Protein Accession #: NP\_001810.1

1 11 21 31 41 51  
MQPTLLLSLL GAVGLAAVNS MPVDNRNHNH GMVTRCIIEV LSNALSKSSA PPITPECRQV 60  
5 LKTSRKDVVD KETTENTNKT FEVRLLDPA DASEAHESST RGEAGAPGEE DIQGPTKADT 120  
EKWAEQGGHS RERAEPQWS LYPSSDSQVSE EVKTRHSEKS QREDEEEEGG ENYQKGERGE 180  
DSSEKHLLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG 240  
EEAGSQENHP QESKQQPRSQ EESEEGEEDA TSEVDKRRTR PRHHHGRSRP DRSSQGGSLP 300  
SEEKGHPQEE SEESNVSMAS LGEKRDHST HYRASEEPE YGEEIKGYPG VQAPEDLEWE 360  
10 RYRGRGSEY RAPRPOSEES WDEEDKRNYP SLELDKMAHG YGEESEERG LEPGKGRHHR 420  
GRGGEPRAYF MSDTREKRF LGEGHHRVQE NQMDKARRHP QGAWKELDRN YLNYGEEGAP 480  
GKMQQQDLQ DTKENREAR FQDKQYSSHH TAEKRRLGE LFNPHYDPLQ WKSSHFERRD 540  
NMNDNLEGE EENELTLNEK NFFPEYNYDW WEKKPPSEDV NWGYEKNLA RVPKLDLKRQ 600  
YDRVAQLDLQ LHYRKSAEF PDFYDSKEPV STHQEAENEK DRADQTVLTE DEKKELENLA 660  
15 AMDLELQKIA EKFSQRG 677

Seq ID NO: C359 Protein Sequence  
Protein Accession #: XP\_093082.1

1 11 21 31 41 51  
MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QMLTELEFSE TKLEASALKL 60  
20 LYGGKDPNC KLQKLNQPS LSVTAALKPV GMVGNCSGFS GSLVQSHFGY CQDSSPKCDL 120  
CKLLWPSTRV AAADKCGSPK SFLSEGLNWA GRLEAVEEVL GLGVLVQPGD PASQGGHCE 180  
25 NYGSRDLVD LEVKAEPKSLR KGGMDLQRP LQVLLCKIF SLKFLFIAL PNSPGQSVV 240  
QVTIPDGFVN VTVGSNVTLI CIYTTVASR EQLSIQWSFF HKKEMEPISS PWEEGKWDV 300  
EAVKGTLDGQ QAEQIYFQ GQOAVAIQF KDRITGSNDP GNASITISHM QPADSGIYIC 360  
DVNNPPDFLG QNQGILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLSAIG TPSFVYVWHK 420  
LEGRDIVPVK ENFNPTTGL VIGNLTNFEQ GYYQCTAINR LGNSSCEIDL TSSHEVGGII 480  
30 VGALIGSLVG AAIISVVCV ARNKAKAKAK ERNSKTIAEL EPMTKINPRG ESEAMPREDA 540  
TQLEVTLPSS IHETGPDITQ EPDYEPKPTQ EPAPEPAPGS EPMVAVDLDI ELELEPETQS 600  
ELEPEPEPEP ESEPGVVVER LSEDEKGVVK A 631

Seq ID NO: C360 Protein Sequence  
Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
MVPAFWKVFL ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICITYTTTVA SREQLSIQWS 60  
35 FPHKKEMEPI SSFWEKGKWP DVEAVKGTLD GQQAELQIYF SQGQQAIVAG QFKDRITGSN 120  
40 DPGNASITIS HMOPADSGIY ICDVNNPPDF LGQNOGILNV SVLVKPSKPL CSVQGRPETG 180  
HTISLSCLSA LGTPSPVYVY HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYQCTAI 240  
NRLGNSSCEI DLTSSHEVVG IIVGALIGSL VGAAIISVSV CFARNKAKAK AKERNKTYA 300  
ELEPMKINP RGESEAMPRE DATQLEVTLF SSIHETGPDITQ EPDYEPKPTQ EPAPEPAP 360  
45 GSEPMVAVDL DIELELEPET QSELEPEPEP EPESEPGVVV EPLSEDEKGV VKA 413

Seq ID NO: C361 Protein Sequence  
Protein Accession #: NP\_003011.1

1 11 21 31 41 51  
MVSRMVSTML SGLLFWLASG WTPAPAYSPP TFDRVSEADI QRLLEGVMEQ LGIARPRVEY 60  
50 PAHQAMNLVG PQSIEGGAHE GLQHLGPFPG IPNIVAELETG DNIPKDPSED QGYDPDPNCP 120  
PVGKTDGCL ENTFTDAEFS REFQLHQHLE DPEHDYPLGL KWNKKLLYEK MKGGERRRR 180  
55 SVNPLYQGR LDNVVAKKSV PHFSDEKDP E 211

Seq ID NO: C362 Protein Sequence  
Protein Accession #: NP\_076926.2

1 11 21 31 41 51  
MTIMQMEQA MPGAGPGVPO LCNMAVIHSH LWKGLQEKFL KGEKVLGVV QILTALMSLS 60  
60 MGITMMCMAS NTYGSNPISV YIGYTINGSV MFIISGSLSI AAGIRTTKGL VRGSLGNIT 120  
SSVLAASGIL INTFSLAFYS FHPYCNYYG NSNNCHGTMS ILMGLDGMVL LLSVLEPCIA 180  
65 VLSAFAQCKV LCCTPGGVVL ILPSHSHMAE TASPTPLNEV 220

Seq ID NO: C363 Protein Sequence  
Protein Accession #: NP\_002082.1

1 11 21 31 41 51  
MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKSTGESSS 60  
70 VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPO PKALGNQQPS WDSSESSNFK 120  
DVSGKGVGR LSAPGSQREG RNPQLNQ 148

Seq ID NO: C364 Protein Sequence  
Protein Accession #: NP\_036393.1

1 11 21 31 41 51  
80 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60  
EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRG HSQSELQVFW VDRAYALKML 120  
FVKESHNSK GPEATWRLSK VQPVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180  
EQQAQTTISL ASSDPQKTVT MILSAVHIQ FDIISDFVPS EEHKCPVDER EQLEETLPLI 240  
LGLILGLVIM VTLAIYHVHH KMTANQVQIP RDRSQYKHM 280

Seq ID NO: C365 Protein Sequence  
Protein Accession #: NP\_003217.1

5 1 11 21 31 41 51  
MLGLVLALLS SSSAEEYVGL SANQCAVPAK DRVDCGYPHV TPKECNNRGC CFDSRIPGVP 60  
WCFKPLTRKT ECTF 74

10 Seq ID NO: C366 Protein Sequence  
Protein Accession #: NP\_002984.1

15 1 11 21 31 41 51  
MSLPSSRAAR VPGPSGSLCA LIALLLLLTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60  
KTIGKLQVFP AGPQCSKVEV VASLKNKGKV CLDPEAPFLK KVIQKILDSG NKGK 114

20 Seq ID NO: C367 Protein Sequence  
Protein Accession #: NP\_005233.2

25 1 11 21 31 41 51  
MRSPSAAWLL GAAILLAASL SCSGTIQGTN RSSKGRSLIG KVDGTSHTVG KGVTVETVFS 60  
VDEFSASVLT GKLTITVFLPI VYITIVFVVL PSNGMALWVF LFRTKKKHPA VIYMANLALA 120  
DLLSVIWFPL KIAYHIHANN WIYGEALCNV LIGFFYGNMY CSILFMTCLS VQRYWVIVNP 180  
MGHSRKKANI AIGISLAIDL LILLVTIPLY VVKQTFIPA LMITTCHDVL PEQLLVGDMF 240  
NYFLSLAIGV FLFPALFAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLCIF 300  
TPSNLLLVVH YFLIKSQQS HVYALYIVAL CLSTLNSCID PFVYFVSHD FRDHAKNALL 360  
CRSVRTVKQM QVSLTSKSHS RKSSSYSSSS TTVKTSY 397

30 Seq ID NO: C368 Protein Sequence  
Protein Accession #: NP\_003460.1

35 1 11 21 31 41 51  
MAEAKTHWLG AALSLIPLIF LISGAEEASF QRNQLLQKEP DLRLNVQKF PSPEMIRALE 60  
YIENLRQAAH KEESPDPYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRILLEALRQ 120  
AENEPQSAPK ENKPYALNSE KNFFPMDSDD YETQONPERK LKHMQFFPMY EENSNDNPFK 180  
RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDBE DDIYKANNIA 240  
YEDVVGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQQLGI QEEDLRKESK 300  
DQLSDVSKV IAYLKRLLVA AGSGLRQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLIQ 360  
PPEDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYKPTPG 420  
RAGTEALPDG LSVEDIILNLL GMESAANQKT SYFENPYNQE KVLPRLPYGA GRSRSNQLPK 480  
AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIN SNQVKRPVPG GSSEDDLQEE 540  
EQIEQAIKEH LNQSSQETD KLAPEVSKRFP VGPPKNDTDP NRQYWEDELL MKVLEYLNQE 600  
KAEGREHIA KRAMENM 617

50 Seq ID NO: C369 Protein Sequence  
Protein Accession #: NP\_112217.1

55 1 11 21 31 41 51  
MPCAQRSWLA NLSVVAQLLN FGALCYGRQP QPGPVRFPDR ROEHFIKGLP EYHVVGPEVRV 60  
DASGHFLSYG LHYPTITSSRR KRDLDGSEDW VYIRISHEEK DLFFNLITVQ GPLSNSYIME 120  
KRYGNLSHYK MMASAPLCH LSGTVLQQGT RVGTAALSAC HGLTGFFQLP HGDFPIEPVK 180  
KHLPLVGGYH PHIVYRRQKV PETKEPTCGL KDSVNISQKQ ELWREKWERH NLPSSRLSRR 240  
SISKERWVET LVVADTKMIE YHGSENVESY ILTIMNMVTG LFHNPSIGNA IHIVVRLIL 300  
LEEEEQGLKI VHHAETLSS FCKWQKSINP KSDIAPVHHD VAVLLTRKDI CAGFNRPCEB 360  
LGLSHLSGMC QPHRSCNINE DSGPLAFTI AHELGHSGFI QHDGKENDCE FVGRHPYIMS 420  
RQLQYDPTPL TWSKCSSEYI TRFLDRGWGF CLDDIPKKKG LKSKVIAPGV IYDVHHQCQL 480  
QYGENATFCQ EVENVCQTLW CSVKGFCSRK LDAAADGTQC GEKKWCMAGK CTVGKPKPES 540  
IPGGWGRWSP WSHCSRTCGA GVQSAERLCN NPEPKFGGKY CTGERKRYRL CNVHPCRSEA 600  
PTFRQMOCSE FDTVPYKNEI YHWPIFNPA HPCELYCRPI DQGFSEKMLD AVIDGTPCFE 660  
GGNSRNVGIN GICKMVGCDY EIDSNATEDR CGVCLGDGSS CQTVRKMFQK KEGSGYVDIG 720  
LIPKGARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGPIIQ WNGNYKLAGT VFQYDRKGDL 780  
EKLMAITGPTN ESWIQLLFQ VTNPGIKYEV TIQKDGDLND VEQMYFWQYG HWTECSVTG 840  
TGIRRTAHAC IKKGRGMVKA TFCDPETQFN GRQKKCHEKA CPFRWAGWEG EACSATCGPH 900  
GEKKRTVLICI QTMVSDQAL PPTDCQHLLK PKTLLSCNRD ILCPSDWTVG NWSECSVSCG 960  
GQVRIRSVTC AKNHDEPCDV TRKPNRSLC GLQCCPSSRR VLKPNKGTIS NGKNPPTLKP 1020  
VFPPTSRRPM LTTPTGPESM STSTPAISSP SPTTASKEGD LGGKQWQDSS TQPELSSRYL 1080  
ISTGTSQPI LTSQSLSIQ SEENVSSSDT GPTSEGGGLVA TTTSGSGLSS SRNPITWVPT 1140  
PFYNTLTKGP EMBIHSGSGE EREQPEDKDE SNFVIWTKIR VPGNDAPVES TEMPLAPPLT 1200  
PDLRESHWPP PFSTVMEGLL PSQRPTTSET GTPRVEGMVT EKPANTLLPL GGDHQPPEPSG 1260  
KTANRNHLKL PNNMNQTKSS EPVLTEEDAT SLITEGFLN ASNYKQLTNG HGSAHWIVGN 1320  
WSECTTCLG GAYWKRVCT TQMSDCAAI QRPDPKRCCH LRPCAGWKVG NWSKCSRNC 1380  
GGFKIREIQC VDSRDRHLNR PFHCQFLAGI PPFLSMSCNP EPCAWQVEP WSQCSRSCGG 1440  
GQERGRVFCP GGLCDWTKRP TSTMSCNEHL CCHWATGNWD LCSTSCGGGF QKRIVQCVPS 1500  
EGNKTEDQDQ CLCDHKPRPP EPKKCNQOAC KKSADLLCTK DKLSASFCQT LKAMKQCSVP 1560  
TVRABCCFSC PQTHITHQQR QRRQRLQKS KEL 1593

80 Seq ID NO: C370 Protein Sequence  
Protein Accession #: NP\_001053.1

1 11 21 31 41 51

5	1	MRQSHQLPLV	GLLLFSFIPS	QLCEICEVSE	ENYIRLKLPL	NTMIQSNYNR	GTSAVNVVLS	60
	2	LKLVGIIQIQT	LMQKMIQKIK	YNVKSRLSDV	SSGELALIL	ALGVCRNAEE	NLIYDYHLTD	120
	3	KLENKFQAEI	ENMEAHNGTP	LTNYYQLSLD	VLALCLFNGN	YSTAEVVMHF	TPENKNYYFG	180
	4	SQFSVDTGAM	AVLALTCVKK	SLINGQIKAD	EGSLKNISII	TKSLVEKILS	EKKENGLIGN	240
	5	TFSTGEAMQA	LFVSSDYNE	NDWNCQQTIN	TVLTEISQGA	FSNPNAAAQV	LPALMGKTPL	300
10	6	DINKDSSCVS	ASGNFNISAD	EPITVTPPDS	QSYISVNVSV	RINETYFTNV	TVLNGSVPLS	360
	7	VMEKAQXMD	TIFGFTMEER	SWGPIYITCIQ	GLCANNNDRT	YWELLSGGEP	LSQGAGSYVV	420
	8	RNGENLEVRW	SKY					433
	9	Seq ID NO: C371 Protein Sequence						
	10	Protein Accession #: NP_004582.1						
15	11	1	11	21	31	41	51	
	12	MCCTKSLLLA	ALMSVLLHL	CGESEAAANF	DCCLGYTDRI	LHPKFIVGFT	QLANEGCDDI	60
	13	NAIIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KKVKNM			96
	14	Seq ID NO: C372 Protein Sequence						
	15	Protein Accession #: NP_037403.1						
20	16	1	11	21	31	41	51	
	17	MAGSPLLWGP	RAGGVGLLVL	LLGLFRPPP	ALCARPVKEP	RGLSAASPPL	AETGAPRRFR	60
	18	RSVPRGEAAG	AVQELARALA	HLLEAERQER	ARAEAQEAED	QQAARVLAQLL	KVWGAPRNSD	120
	19	PALGLDDDDP	APAAQLARAL	LRARLDPAAL	AAQLVPAPVP	AAALRPFPV	YDDGAPGPA	180
	20	EEAGDETPDV	DRELLRYLLG	RILAGSADSE	GVAAPRRLRR	AADHDVGSSEL	PPEGVLGALL	240
25	21	RVKRLTAP	QVPARRLLPP					260
	22	Seq ID NO: C373 Protein Sequence						
	23	Protein Accession #: NP_002236.1						
	24	1	11	21	31	41	51	
	25	MLQSLAGSSC	VRLVERHRS	WCFGFLVLGY	LLYLVFQAVV	FSSVELPYED	LLRQELRKLK	60
30	26	RRFLEEHECL	SEQLEQFLG	RVLEASNYGV	SVLSNASGNW	NWFTSALFF	ASTVLSTTGY	120
	27	GHTVPLSDGG	KACFIYSVI	GIPFTLLFLT	AVVQRITVHV	TRRPVLYPHI	RWFGSKQVVA	180
	28	IVHAVLLGFV	TVSCFFFIAP	AVFSVLEDDW	NFLESPIYCF	ISLSTIGLGD	YVPEGGYNQK	240
	29	FRELYKIGIT	CYLLGLLIAM	LVLVLETFCEL	HEKKPKKMF	YVKDKDQEDQ	VHIIEDQLS	300
	30	FSSITDQAG	MKEDQKQNEP	FVATQSSACV	DGPANH			336
35	31	Seq ID NO: C374 Protein Sequence						
	32	Protein Accession #: NP_005463.1						
	33	1	11	21	31	41	51	
	34	METTINGETW	YESLHVLKA	LNATLHSNLL	CRPGFGLGPD	NQTEERRASL	PGRDDNSYMY	60
	35	ILFVMEFLFAV	TVGSLILGYT	RSRKVDKRS	PYHVYIKNRV	SMI		103
40	36	Seq ID NO: C375 Protein Sequence						
	37	Protein Accession #: NP_005236.1						
	38	1	11	21	31	41	51	
	39	MGRHLALLLL	LLLLFQHFQD	SDGSQRLEQT	PLQFTHLEYN	VTQENSAAK	TYVGHFVKMG	60
	40	VYITHPAWEV	RYKIVSGDSE	NLFKAEYIL	GDFCFIRIRT	KGNTAILNR	EVKDHYYTLIV	120
45	41	KALEKNTVE	ARTKVRVQVL	DTNDRPLFS	PTSYSVSLPE	NTAIRTSIAR	VSATDADIGT	180
	42	NGEFYYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGISSM	240
	43	AKLTVHIEQA	NECAPVITAV	TLSPESELD	PAYAIIVTDD	CDQGANGDIA	SLSIVAGDLL	300
	44	QQPRTVRSFP	GSKEYVKAI	GDIDWDSHPF	GYNLTQAKD	KGTTPQFSSV	KVIHVTSPQF	360
	45	KAGPVKEKED	VYRAEISEFA	PPNTPVVMVK	AIPAYSHLRY	VFKRTPGKAK	FSLNNTGLI	420
50	46	SILEFVKRQK	AAHFELEVTT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AFDENVPITG	480
	47	TIMSLSAVDP	DEGENGYVTY	SIANLNHVFP	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	540
	48	SDWGLPYRRE	VEVLATITLN	NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	600
	49	LVQYQIEAGN	ELDLFSLNPN	SGVLSLKRSL	MDGLGAKVSF	HSLRITATDG	ENPATPLYIN	660
	50	ITVAASHKLIV	NLQCEETGVA	KMLAEKLLQA	NKLNHQGEVE	DIFFDSHSVN	AHIPQFRSTL	720
55	51	PTGIQVKENQ	PVGSSVIFMN	STDLDTGFGN	KLVYAVSGGN	EDSCFMIDME	TGMLKILSPL	780
	52	DRETTDKYTL	NITVYDLGIP	QKAARLLLEV	VVDANDNPP	EFLQESYFVE	VSEDKEVHSE	840
	53	IIQVEATDKD	LGPNGHVYS	ILTDITDTFSI	DSVTGVVNIA	RPLDRELQHE	HSLKIEARDQ	900
	54	AREEPQLFSD	VVVVKSLEDV	NDNPPTFIPP	NYRVKVREDL	PEGTVIMWLE	AHDPDLQSGG	960
	55	QVRYSLLDHG	EGNFVDVKLS	GAVRIVQQLD	FEKKQVYNLT	VRAKDKGKPV	SLSSTCYVEV	1020
60	56	EVVDNENLH	PPVFSSEFVK	GTVKEDAPVG	SLVMTVSAHD	EDAGRDEGEIR	YSIRDGSGVG	1080
	57	VFKIGETGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS	SFIEIYIEVE	DVNDNAPQTS	1140
	58	EPVYYPEIME	NSPKDVSVQ	IEAFDPDSSS	NDKLMYKITS	GNPQGFPSIH	PKTGLITTS	1200
	59	RKLDREQQDE	TGSLYTVTDN	GSPPKSTIAR	VIVKILDEND	NKPQFLQKPY	KIRLPEREKP	1260
	60	DRERNARREP	LYRVIAATDK	EGPNAREISYS	IEDGNEHGKF	FIEPKTGVS	SKRPSAAGEY	1320
65	61	DILSIKAVDN	GRPQSSSTR	LHIEWISKPK	QSLEPISFEE	SFFTFTVMES	DPVAHMIGVI	1380
	62	SVEPPGIPLW	FDITGGNYDS	HFDVDKGTGT	IIVAKPLDAE	QKSNYNTLVE	ATDGTITILT	1440
	63	QKFKIVDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VDQDEKNKLI	YTIQSSRDPL	1500
	64	SLKFKRLDPA	TGSLYTVTDN	DHEAVSPAHL	TVMVRDQDVP	VKNRFARIVV	NVSDTNDHAP	1560
	65	WFTASSYKGR	SVSAEAVGSV	VLQVATLADK	KGKNAEVLVS	IESGNIGNIG	NSFMIDPVLG	1620
70	66	SIKTAKELDR	SNQAEYDLMV	KATDKGSPPM	SEITSVRIFV	TIADNASPKF	TSKEYSVLS	1680
	67	ETVSGISFVG	MVTAHSQSSV	VYEIKDQNTG	DAFDINPHSG	TIITQKALDF	ETLPIYTLII	1740
	68	QGTINMAGLST	NTTVLVHLQD	ENDNAPVFMQ	AEYTGILISES	ASINSVVLTD	RNVPLVIRAA	1800

	DADKDSNALL	VYHIVEPSVH	TYFAIDSSTG	AIHTVLSLDY	EETSIFHFTV	QVHDMGTPRL	1860
	FAEYANVTV	HVIDINDCP	VFAKPLYEAS	LLLPTYKGVK	VITVNATDAD	SSAFSOLYIS	1920
	ITEGNIGKEF	SMOYKTGALT	VQNTTQLRSR	YELTVRASDG	RFAGLTSVKI	NVKESKESHL	1980
5	KFTQDVYSAV	VKENSTEAE	LAVITAIGSP	INEPLFYHIL	NPDRRFKISR	TSGVLSTTGT	2040
	FFDREQQAEF	DVVVEVIEEH	KPSAVAHVVV	KVIVEDQNDN	APVFVNLPHY	AVVKVDTEVG	2100
	HVIRYVTAVD	RDSGRNGEVH	YYLKEHHEHF	QIGPLGEISL	KKQFELDTLN	KEYLVTVVAK	2160
	DGGNPAFSAE	VIVPITVMKN	AMPVFEKPFY	SABIAESSIQ	HSPVVHVQAN	SPEGLKVYFS	2220
	ITDGDPPSQF	TINFNTGVIN	VIAPLDFAEH	PAYKLSIRAT	DSLTAHAHEV	FVDIIVDDIN	2280
10	DNPPVFAAQS	YAVTLSEASV	IGTSVVQVRA	TDSDSEPNRG	ISYQMFNGHS	KSHDHFHVDS	2340
	STGLISLLRT	LDYEQSRQHT	IFVRAVDGGM	PTLSSDVIVT	VDVTDLNGNP	PLFEQQIYEA	2400
	RISEHAPHGH	FVTCVKAYDA	DSSDIDKLQY	SILSGNDHGH	FVIDSATGII	TLNHLRHHAL	2460
	KPFYSLNLVS	SDGVFRSSTQ	VHVTVIGGNL	HSPAFLQNEY	EVELAENAPL	HTLVMEVKTT	2520
15	DGDSGIYGHV	TYHIVNDFAK	DRFYINERGQ	IFTLEKLDRE	TPAEKVISVR	LMAXDAGGKV	2580
	AFCTVNVILT	DDNDNAPQFR	ATKYEVNIGS	SAAKGTSVVK	SASDADEGSN	ADITYAIED	2640
	SESVKENLEI	LDYEQSRQHT	ESLIGLENEF	FTFVRAVDN	GSPSKESVVL	VYVKILPEPM	2700
	QLPKFSEPFY	TTTYSSEVVP	GTEIDLIRAE	HSGTVLYSLV	KGMTPESNRD	ESFVIDRQSG	2760
	RLKLEKSLDH	ETTKWYQFSI	LARCTQDDHE	MVASVDVSIQ	VKDANDNSPV	FESSPYEAFI	2820
20	VENLPFGSSRV	IQRASDADS	GTNGQVMYSL	DQSQSVEVIE	SFAINMETGW	ITTLKELDHE	2880
	KRDNYQIKVV	ASDHGKIQI	SSTAIVDVTV	TDVNDSPPRF	TAEYIKGTVS	EDDPQGGVIA	2940
	ILSTTDADSE	ENNRQYTYFI	TGGDPLGQFA	VETIQNEKWK	YVKKPLDREK	RDNYLLTITA	3000
	TGDTFSSKAI	VEVKVLDAND	NSPVCCKTLY	SDTIPEDVLP	GKLIQMSAT	DADIRSNAEI	3060
	TYTLGSGAE	KFKLNPDGCE	LKTSTPLDRE	EQAVVHLVLR	ATDGGGRFCQ	ASIVVTLEDV	3120
25	NDNAPEFSAD	PYAITVFENT	EPGTLTLRVQ	ATDADAGLNR	KILYSLIDSA	DQQFSINELS	3180
	GIQLEKFLD	RELQAVYTLS	LKAVDQGLPR	RLTATGTIVV	SVLDINDNPP	VFEYREYGAT	3240
	VSEDILVGTE	VLQVYAASRD	IEANAEITYS	IISGNEHGKF	SIDSKTGAVF	IENLDYESS	3300
	HEYILTVEAT	DGGTSPSLDV	ATVNVNVTDI	NDNTPVFSQD	TYTTVISED	VLEQSVITVM	3360
	ADDADGSPNS	HIRYSIIDGN	QSSSFTIDPV	RGEVKVTKLL	DRETISGYTL	TVOASDNGSP	3420
	PRVNTTNNI	DVSDVNDNAP	VFSRGNYSVI	IQENKPVGFS	VLQLVVTDED	SSHNGPPFPF	3480
30	TIVTGNDEKA	FEVNPQGVLL	TSSAIKRKEK	DHYLLQVKA	DNGKPKQLSSL	TYIDIRVIEE	3540
	SIYPPAILEL	EIPIYSSGEE	YSGGVIGKIH	ATDQDVYDIL	TYSLDPQMDN	LFSVSSTGGK	3600
	LIAHKKLDIG	QYLLNVSVTD	GKFTTVADIT	VHIRQVTQEM	LNHTIAIRFA	NLTPEEFVGD	3660
	YWRNFQRLAL	NILGVRRNDI	QIVSLQSSSE	HPHLDVLLFV	EKPGSAQIST	KQLLHKINSS	3720
	VTDIEEIIIG	RILNVFQKLC	AGLDCPWKFC	DEKSVSDSEV	MSTHSTARLS	FVTPRHRAA	3780
35	VCLCKEGRCP	PVHHCEDDDP	CPGSECVSD	PWEEKHTCVC	PSGRFGQCPG	SSSMTLTGNS	3840
	YVKYRLTENE	NKLEMLTMR	LRTYSTHAVV	MYARGTDYSI	LEIHHGRLQY	KFDGSGPGPI	3900
	VSVQSIQVND	QOMHVALEV	NGNYARLVLD	QVHTASGTAP	GTLLKTLNLDN	VYFFGGHIRQ	3960
	QGTRHGRSPQ	VGNGFRGCMQ	SIYLNQQLP	LNSKPRSYAH	IEESVDVSPG	CFLTATEDCA	4020
	SNPCQNGGVC	NPSAPAGGYC	KCSALYIGTH	CEISVNPCCS	NPCLYGGTCV	VNDGGFVQCQ	4080
40	RGLYTQQRQ	LSPYCKDEPC	KNGGTCFDSL	DGAVCQCDG	FRGERQCSDI	DECSGNPLCH	4140
	GALCENLTHS	YHCNCSHEFR	GRCEDAAPN	QYVSTPNWIG	LAEGIGIVVF	VAGIFLLVVV	4200
	FVLCKRMISR	KKKHQAEPKD	KHLGPATAFL	QRPFYDSKLN	KNIYSDIPPQ	VPVRPISTYP	4260
	SIPSDSRNNL	DRNSFECSAI	PEHPEPSTFN	PESVHGHRKA	VAVCSVAPNL	PPPPPSNPS	4320
	SDSIQKPSW	DFDYDTKVVD	LDPLCSKKPL	EKPSQPYSA	RESLSEVQSL	SSFQSESCDD	4380
45	NGYHWDTSW	MPSVPLFDIQ	EPFNYEVIDE	QTPLYSADPN	AIDTDYYPGG	YDIESDFPPP	4440
	PEDEPADEL	PPLPEFSNQ	FESIHPPRDM	PAAGSLGSSS	RNRQRFNLQ	YLFNPFYPLDM	4500
	SEPQTKGTGE	NSTCREPHAP	YPPGYQRHFE	APAVESMMS	VYASTASCSD	VSACCEVESE	4560
	VMSDYESGD	DGHFEVVTIP	PLDSQQHTEV				4590

Seq ID NO: C376 Protein Sequence  
Protein Accession #: NP\_055035.1

	1	11	21	31	41	51	
55	MCYKGCARCI	GHSVLGLALL	CIAANILLYF	PNGETKYASE	NHLSRFVWFF	SGIVGGGLLM	60
	LLPAFVFIGL	EQDDCCCGCG	HENCGKRCAM	LSSVLAALIG	IAGSGYCVIV	AALGLAEGPL	120
	CIDSLGQWNY	TPASTEGQYL	LDTSWSECT	EPKHIVEWNV	SLFSILLALG	GIEFILCLIQ	180
	VINGVLGGIC	GFCCSHQQQY	DC				202

Seq ID NO: C377 Protein Sequence  
Protein Accession #: NP\_003750.1

	1	11	21	31	41	51	
65	MSTENVEGKP	SNLGERGRAR	SSTFLRVVQP	MFNHSIFTS	VSPAARIRF	ILGEEDDSPA	60
	PPQLFTELDE	LLAVDQEME	WKETARWIKF	EERKEVGGER	WSKPHVATLS	LHSLFELRTC	120
	MEKGSIMLDR	EASSLPOLVE	MIVDHIQSTG	LLKPELKDKV	TYTLRLKRHH	QTKKSNLRLS	180
	ADIGKTVSSA	SRMFTNPONG	SPAMTHRNLT	SSSLNDISDK	PEKDQLKNKF	MKKLPRDAEA	240
	SNVLGVEVDF	LDTPPIAFVR	LQQAVALGAL	TEVPVPTREF	FILLGPKGKA	KSYHEIGRAI	300
70	ATLMSDEVFH	DIAYKAKDRH	DLIAGIDEFL	DEVIVLPGE	WDPAIRIEPP	KSLPSSDKRK	360
	NMYSQGENVQ	MNGDTFHDGG	HGGGGHGDCE	ELQRTGRFCG	GLIKDIKRKA	PPFASDFYDA	420
	LNQALSAIL	FIYLATVINA	ITFGGLGDA	TDMQGVLES	FLGTAVSGAI	FCLFAGQFLT	480
	ILSSTGPVLV	FERLLNPNFSK	DNNFDYLEFR	LWIGLWSAPL	CLILVATDAS	FLVQYPTFT	540
	EEGFSSLSIF	IFIYDAFKKM	IKLADYYPIN	SNFKVGYNTL	FSCTCVPPDP	ANISISNDTT	600
75	LAFEYLPTMS	SDTMVHTTF	DWAFLSKKEC	SKYGGNLVGN	NCNFVPDITL	MSFILFLGT	660
	TSSMALKKFK	TSYPFPTTAR	KLISDFAILL	SILIFCVIDA	LGVVDTPKLI	VPSEFKPTSP	720
	NRGWFVPPFG	ENPWVWCLAA	AIPALLVITL	IFMDQQITAV	IVNRKEHKLK	KGAGYHLDLF	780
	WVAILMVICS	LMALPFWYAA	TVISIAHIDS	LKMETETSAP	GEQPKFLGVR	EQRVTGTLVF	840
	ILTGLSVFMA	PILKFIKMPV	LYGVFLYMGV	ASLNGVQFMD	RLKLLMLPLK	HQPDRIYLRH	900
80	VPLRRVHLFT	FLQVCLALL	WILKSTVAI	IFPVMILALV	AVRKGMDYLF	SOHDLSPFLD	960
	VIPEKDKKKK	EDEKDKKKKK	GSLDSNDNDS	DCPYSEKVP	IKIPMDIMEQ	QPFLSDSKPS	1020
	DRERSPTFLE	RHTSC					1035

Seq ID NO: C378 Protein Sequence  
Protein Accession #: NP\_000949.1

1 11 21 31 41 51  
 5 MSTPGVNSSA SLSPDRLNSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFFYTLVCG 60  
 LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERILA 120  
 INHAYFYSHY VDKRLAGLTL FAVYASNVLF CALPNMGLGS SRLQYPTDWC FIDWITNVTA 180  
 HAAYSYMYAG FSSFLILATV LCNVLVCGAL LRMHRQFMRR TSLGTEQHHH AAAASVASRG 240  
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICSIPLVV RVFVNQLYQP 300  
 10 SLEREVSQNP DLQAIRIASV NPILDPMIYI LLRKTVLSKA IEKIKCLFCR IGSSRRERSG 360  
 QHCSDSQRTS SAMSGHSRSF ISRELKEISS TSQTLPLDLS LPDLSENGLG GRNLLPGVPG 420  
 MGLAQEDTTS LRTLRISETS DSSQGDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480  
 LNLSEKCI 488

Seq ID NO: C379 Protein Sequence  
 Protein Accession #: NP\_002650.1

1 11 21 31 41 51  
 20 MGHPPLLPPL LLLHTCVPAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWEEGEL 60  
 ELVEKSTHS EKTNTLSYR TGLKITSLTE VVCGLDLCNQ GNSGRAVYTS RSRYLECISC 120  
 GSSDMSCERG RHQSLOCRSP EEQCLDVVTH WIQEGEGRF KDRHLRGCG YLPGCPGSG 180  
 FHNNDTFHFL KCCNTTKCNE GPILELENLP QNGRQCYSCK GNSHGCSSE ETEFLIDCRGP 240  
 MNQCLVATGT HEPKQSYMV RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNHPDLV 300  
 25 QYRSGAAPQP GPAHLSTLIT LMTARLWGG TLLWT 335

Seq ID NO: C380 Protein Sequence  
 Protein Accession #: BAB55406.1

1 11 21 31 41 51  
 30 MDEFSGQVDP LASVILPPNL LENLSPEDSV LVRRRAQFTFP NKTGLFQDVG PQRKTLVSTV 60  
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDLN KNSFGGWNT SGCVAHRDSD 120  
 ASETVCLCNH FTHFGVLMDL PRSASQLDAR NTKVLTPIFY IGCGISAIFS AATILTYVAF 180  
 35 EKLRDYPSPK ILNNLSTALL FLNLLFLLDG WITSFNVDEL CIAVAVLLHF PLLATFTWVG 240  
 LEAIIHMYIAL VKVFNTYIRR YILKFCIIGW GLPALVVSUV LASRNNNEVY GKESYGKEKG 300  
 DEFCWQDPV IFYVTCAGYF GVMFFLNIAF FIVVMVQICG RNSGRSNRTL REEVLRNLRS 360  
 VVSLTFLLGM TWGFAPFANG PLANIPFMYLF SIFNSLQGLF IFIFHCAMKE NVQKQWRRHL 420  
 40 CCGRFRLLADN SDWSKTATNI IKKSSDNLGK SLSSSSISGN STYLTSKSKS SSTTYFKRNS 480  
 HTDNVSYEHS FNRSGSLRQC FHGQVLVKTG PC 512

Seq ID NO: C381 Protein Sequence  
 Protein Accession #: NP\_000565.1

1 11 21 31 41 51  
 45 MTVARPSVPA ALPLLGLPRL LLLVLLCLP AVWGDGCLPP DVPNAQPALE GRTSFPEDTV 60  
 ITYKCEESFV KIPGEKDSVI CLKGSQWSDI EPCNRSCEV PTRLNSASLK QPYITQNYFP 120  
 VGTVVEYECR PGYRREPSSL PKLTCLQNLK WSTAVEPCKK KSCPNPGEIR NGQIDVPGGI 180  
 50 LFGATISFSC NTGYKLFPGT SSFCLISGSS VQWSDPLEPC REIYCPAPPQ IDNGIIQGER 240  
 DHYGYRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PEGRGKSLTS KVPPTVQKPT 300  
 TVNVPTTEVS PISQKTTTKT TTPNAQATRS TPVSRTTKHF HETTPNKGSG TTSGTTRLLS 360  
 GHTCFTLTGL LGTLVTMGLL T 381

Seq ID NO: C382 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 60 MDTSLRGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120  
 LQNNQLRHVP TEALQNLRLS QSLRLDANH I SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVHLHLNN RIHSLGKKCF DGLHSLTLD 240  
 65 LNYNNLDEFP TAIRTLNLSK ELHFYDNPIQ FVGRSAFOHL PELRTLTLNG ASQITEFPDL 300  
 TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSPFSVCQ KLQKIDLRN 360  
 EIYEIKVDTF QQLLSRLSLN LAWNKIAIHH PNAFSTLPFL IKLDLSSNLL SSFFTGLHG 420  
 LTHLKLTLGNH ALQSLISSEN FPFLKVIEMP YAYOCCAFGV CENAYKISNQ WNKGDNSMD 480  
 DLHKKDAGMF QAQDERDLED FLDDFEEDLK ALHSVQCSPS PGPFKPCFEL LDGWLIRIGV 540  
 70 WTI AVLALTC NALVTSTVPR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAPTFGSF 600  
 ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSKPFET KAPFSSLKVI 660  
 ILLCALLALT MAAPVLLGGS KYGASPLCLP LPFGEPSTMG YMVALLILNS LCFLMMTIAY 720  
 TKLYCNLDKG DLENINWDCSM VKHIALLLFT NCILNCPVAF LSPSSILNLT FISPEVIKFI 780  
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840  
 75 TQALVTFSS SITYDLPPSS VPSPAYPVTE SCHLSSVAFV PCL 883

Seq ID NO: C383 Protein Sequence  
 Protein Accession #: NP\_003658.1

1 11 21 31 41 51  
 80 MDTSLRGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120  
 LQNNQLRHVP TEALQNLRLS QSLRLDANH I SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVHLHLNN RIHSLGKKCF DGLHSLTLD 240  
 LNYNNLDEFP TAIRTLNLSK ELGFHSNNIR SIPEKAFVGN PSLITIHFYD NPIQFVGRSA 300



5 FOHLPELRLT LINGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360  
 YNLLEDLPSP SVCQKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIIHPNAPST 420  
 LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELKV IEMFYAYQCC 480  
 AFGVCENAYK ISNQWNGKDN SSMDDLHKGD AGMFQAQDER DLEDPLLDPE EDLKAHLSVQ 540  
 CSPSPGPFKP CEHLDDGGLI RIGVWTIAVL ALTGNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 AVNMLTVGSS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL 660  
 ERGFSVKYSA KPETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEP 720  
 STMGYMVALI LLNSLCFLMM TIATYKLYCN LDKGDLENIW DCSMVGHIAL LLFTNCILNC 780  
 PVAFLSPSSL INLTIFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTVV 840  
 10 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900  
 VAFVPC 907

Seq ID NO: C384 Protein Sequence  
 Protein Accession #: NP\_003497.1

15 1 11 21 31 41 51  
 MEMFTLLTLC IFPLPLRGHS LFTCEPITVP RCMKAMAYNMT FFPNLMGHYD QSIAAVEMEH 60  
 20 FLEPLANLSCS PNIEITFLCKA FVPTCIEQIH VVPPCRKLCE KVISDCCKLI DTFGIRWPEE 120  
 LECDRLOYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPHRLKTSKG QGYKFLGIDQ 180  
 CAPPENMYF KSELEFAKS FIGTVSIFCL CATLFTPLTF LIDVRRFRYP ERPIIYYSVC 240  
 YSIVSLMYFI GFLLDSTAC NKADEKLELG DTVVIGSQNK ACTVLFMLLY FFTMAGTVWW 300  
 VILTTTWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCVFG 360  
 25 LYDLDAARYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKI KKFMRIGVF 420  
 SGLYLVLVLT LLGCYVEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALPMIKY 480  
 LMTLIVGISA VFVVGSKKTC TEWAGFPKRN RKRDPISER RVLQESCEFF LKHSKVKHK 540  
 KKHYPSSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQBTLEIQ TSPETSMREV 600  
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660  
 30 TGLAQSNLQ VPSSESPSSL KGSTSLLVHF VSGVRKEQGG GCHSDT 706

Seq ID NO: C385 Protein Sequence  
 Protein Accession #: NP\_000573

35 1 11 21 31 41 51  
 MRIAVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQMLLAPQTL 60  
 PSKSNESHDH MDDMDEDDDD DHVDSQDSID SNDSDDVDDT DSHQSDSH HSDESEDLVT 120  
 DFPDLPATE VFTFVVTVD TYDGRGDSV YGLRSKSKFP RRPDIQYPA TDEDITSHME 180  
 40 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240  
 NEHSDDVIDSQ ELSKVSREFH SHEPHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN 300

Seq ID NO: C386 Protein Sequence  
 Protein Accession #: NP\_002812

45 1 11 21 31 41 51  
 MGAARGSPAR PRRLPLLSVL LPLLLGGTQT AIVFIKQPSS QDALQRRAL LRCEVEAGP 60  
 VHVYWLDDGA FVQDTERFPA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN 120  
 50 IKWIEAGFVV LKHPASEAEI QPQTQVTLRC HIDGHPRTY QWFRDGTPLS DGQSNHTVSS 180  
 KERNLTLRPA GEHSGLYSC CAHSAGGQAC SSQNFLLSIA DESFARVULA PQDVVVARYE 240  
 EAMFHQFSA QPPSLQWLF EDETPTNRS RPFHLRRATV FANGSLLLTQ VRPRNAGIYR 300  
 CIGQGQGRGP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG 360  
 VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD 420  
 55 SLEEGKFGY LDOCLQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEYDGTWYR 480  
 CMSSTPAGSI EAQARVQVLE KLKFTPPFPQ QQCEFDKEA TVPCSATGRE KPTIKNERAD 540  
 GSSLEPWVTD NAGTLHFARV TRDDAGNYTC IASNGPQGI RAHVQLTVAV FITFKVEPER 600  
 TTVYQGHATL LQCEAQGDPK PLIQWKGKDR ILDPTKLGR MHIFQNGSLV IHDVAPEDSG 660  
 RYTCTAGNSC NIKHTBAPLY VVDKPVPEES EGPSPPPPYK MIQTIGLSVG AAVAYIIAVL 720  
 60 GLMFYCKKRC KAKRIQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780  
 KRHSTDCKMH FPRSSLQPIIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840  
 LDFRRELEMP GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSK 900  
 PLSTKQKVAL CTQVALGMEH LSNNREVVHK LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960  
 YHFRQAWVPL RWMSPEAILE GDFSTKSDWV AFGVLMWEVF THGEMPHGQ ADDEVVLADLQ 1020  
 65 AGKARLPQPE GCPSKLYRLM QRCWALSPKO RPSFSEIASA LGDSTVDSKP 1070

Seq ID NO: C387 Protein Sequence  
 Protein Accession #: NP\_002300.1

70 1 11 21 31 41 51  
 MKVLAAGVVP LLLVLHWKHG AGSPLPITPV NATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60  
 ALPILYTTAQ GEPPFNLDK LCGENVTDPP PFHANGTEKA KLVELYRIVV YLGTSLGNIT 120  
 RDQKILNPSA LSLHSLKNAT ADILRGLLSN VLCRLCSKYH VGHVDVITYG DTSGKDVFPQK 180  
 75 KKLGCQLGK YKQIIAVLAQ AF 202

Seq ID NO: C388 Protein Sequence  
 Protein Accession #: XP\_097508

80 1 11 21 31 41 51  
 MGRPRLTIVC HVSIIISARD LSMNNLTQL PGLFHHRLFL EELRLSGNHL SHIPGQAFSG 60  
 LYSLKILMLQ NNQIGGIPAE ALWELPSLQS LRLDANLISL VPERSFEGLS SLRHLWLDN 120  
 ALTEIPVRAL NNLPAQAMT LALNRISHIP DYAFQNLTSV VVHLHLNNRI QHLGTHSFEG 180  
 LHNLETLDLN YNKIQEPPVA IRTLGRLEL GFHNNNIKAI PEKAFMGNPL LQTHFYDNP 240

5 IQFVGRSAFQ YLPKHLTSL NGAMDIQEPF DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300  
 RLRVLELSHN QIEELPSLHR CQKLEELGLQ HNRWEIGAD TFSQLSSLOA LDLSWNAIRS 360  
 IHPEAFSTLH SLVKLDLTDN QLITLPLAGL GGLMHLKLG NLALSQAFSK DSFFKLRILE 420  
 VPHYACCCPY GMCASFFKAS GQWEAEDLHL DDEESSKRPL GLLARQAENH YDQDLDELQL 480  
 EMEDSKPHPS VQCSPTPGPF KPCEYLPESW GIRLAVWAIV LLSVLCNGLV LLTVFAGGPV 540  
 PLPPVKFVVG AIAGANTLTG ISCGLLASVD ALTFGQFSEY GARWETGLGC RATGFLAVLG 600  
 SEASVLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660  
 ASPLCLPYAP PEGQPAALGF TVALVMMSNF CFLVAGAYI KLYCDLPRGD FEAVWDCAMV 720  
 10 RHVAWLIFAD GLLYCPVAFI SFASMLGLEP VTPEAVKSVL LVVLPPLACL NPLLYLLFNP 780  
 HFRDRLRLR PRAGDSGLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840  
 TYGFPSVTLI SCQPGAPRL ESHHCVEPEG NHFQNPQPSM DGELLRAEG STPAGGGLSG 900  
 GGGFQPSGLA FASHV 915

15 Seq ID NO: C389 Protein Sequence  
 Protein Accession #: NP\_570901

20 1 11 21 31 41 51  
 MASLVSLEIG LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLLNT LADRVHCTNG 60  
 PCGKCLSVED ALGLGEPEG GLPPGPVLEA RYVARLSAAA VLYLSNPEG CEDTRAGLWA 120  
 SHADHLALL ESPKALTPGL SWLLQRMQAR AAGQTPKTAC VDIQQLLEE VAGAGPSAG 180  
 GVLAALLDHV RSGSCFHAL SPQYFVDFVF QQHSSEVPMT LAELSALMR LGVGREAHSD 240  
 HSHRHGASS RDPVPLISS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP EAWAQLSPAL 300  
 25 LQQQLSGACT SQSRPPVQDQ LSQSERLYG SLATLLICLC AVFGLLLTTC TGRGVVAHYI 360  
 LQTFSLAVG ALTDGAVLHL TPKVLGLHTH SEEGLSPQPT WRLLAMLAGL YAPFLFENLF 420  
 NLLLPDPED LEDGFCGHSS HSHGHSHGV SLQAPSELRL QPKPHEGSR ADLVAEESPE 480  
 LLNPEPRRLS PELRLPYMI TLGDVHNFA DGLAVGAFA SSWKTGLATS LAVFCHELPH 540  
 ELGDFAAALH AGLSVRQALL LNLASALTAF AGLYVALAVG VSESEAWIL AVATGLFLYV 600  
 30 ALCDMLPAML KVRDPRPWL FLHNVLGLG GWTVLLLSL YEDDITF 648

Seq ID NO: C390 Protein Sequence  
 Protein Accession #: NP\_061844

35 1 11 21 31 41 51  
 MANASEPGGS GGGEEAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPIYLLLDL 60  
 CLADGLRALA CLPAVMLAAR RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLGVGVT 120  
 YLAIAHRRFY AERLAGWPCA AMLVCAAWAL ALAAAPPPVL DGGGDEEDAP CALEQRPDGA 180  
 40 PGALGFLLL AVVVGATHLV YLRLLFFIHD RRMMPARLV PAVSHDWTFF GPGATGQAAA 240  
 NWTAGFGRGP TFPALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LFLLLMGFPY 300  
 VVASYLRLV REGAVPQAYL TASVWLTFQA AGINPVVCFI FNRELDCFR AQFPCCQSPR 360  
 TTQATHPCDL KGIGL 375

45 Seq ID NO: C391 Protein Sequence  
 Protein Accession #: NP\_005622

50 1 11 21 31 41 51  
 MAAARPARGP ELPLGLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP 60  
 LSHCGRAAPC EPLRYNCLG SVLPYGATST LLAGDSDSQE EAHGKLVLS GLRNAPRCWA 120  
 VIQPLLCVAV MPKCEMDRVE LPSRTLQAT RGPCAIVERE RGWPDFLRCT PDRFPPEGCTN 180  
 EVQNIKFNSS GQCEPVLVRT DNPKSWEDEV EGCGIQQNP LFTAEHQDM HSYIAAFGAV 240  
 TGLCTLFILA TVADVWRNSN RYPAVILFYV NACFFVGSIG WLAQFMDGAR REIVCRADGT 300  
 55 MRLGEPTNE TLSCVIIIFI VYVALMAGV WVVVLYAWH TSPKALGTYY QPLSGKTSYF 360  
 HLLTNSLFFV LTVALLAVA VDGDVSGIC FVGKYNRYR AGFVLAPIGL VLIIVGGYFLI 420  
 RGVMTLFSIK SNIAPGLSEK AASKINETML RLIGFGLFAP GFVLITFSCH FYDFPNQAEW 480  
 ERSFDRYVLC QANVTGLPT KQIPDCEIK NRPSLLVEKI NLFAMGTGI AMSTWVWTKA 540  
 TLLIWRRTWC RLTGQSDDEP KRIKSKMIA KAFSKRHELL QNPQELSPS MHTVSHDGFV 600  
 60 AGLAPDLNEP SADVSSAWAQ HVTMVARRG AILPQDISVT PVATPVPEE QANLWLVAE 660  
 ISPELQKRLG RKKKRRKRK EVCPLAPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG 720  
 AGDSCROGAW TLVSNFFCPE PSPQDPFLP SAPAFVAWAH GRRQGLSPIH SRTNLMDEL 780  
 MDADSDF 788

65 Seq ID NO: C392 Protein Sequence  
 Protein Accession #: BAC04382

70 1 11 21 31 41 51  
 MGARSARGA LLLALLCWD PRLSQAGRKR SGEVLPDSFP SAPAEPLPYF LQEPQDAYIV 60  
 KNKPVELRCR APPATQIYFK CNGENVSOND HVTQEGLEDEA TLGARGGLRV REVQIEVSRQ 120  
 QVEELFGLD YWQCQVAMSS AGTTKSRAY VRIAYLRKNF DQEPGLKEVP LDHEVLLQCR 180  
 PEGVPVAVY EWLKNEEDVID PTQDTNFLT IDHNLIRQA RLSDTANYTC VAKNIVAKRR 240  
 STTATVIVYV NGGWSSWAEW SPCSNRCGRG WQKRTTRCTN PAPLNGGAFC EQAPQKTAC 300  
 75 TTICPVDAW TEWSKWSACS TECAHWSRE CMAPPQNGG RDCSGTLDS KNCTDGLQW 360  
 NKKTLSDPNS HLLASGDAA LYAGLVVAIF VVVAIIMAVG VVVYRRNCRD FDTDITDSSA 420  
 ALTGPHFVN FKTARPENPQ LHPSPVPPDL TASAGIYRGP VYALQDSTDK IPMTNSPLLD 480  
 PLPSLKVEYV SSSITGSGPG LADGADLLGV LPPGTYPSEF ARDTHFLHLR SASLGSQQLL 540  
 GLPRDPGSSV SGTGCLGGR LSIPGTGVSL LVPNGAIPQG KPYEMYLLIN KAESTLPLSE 600  
 80 GTQTVLSPV TCGPTGLLLC RPVILTMFHC AEVSARDWIF QLKTAHQGH WEVVTLDEE 660  
 TIATPCYQQL EPRACHILLD QLGTIVFTCE SYSRSVAVKRL QLAVFAPALC TSLEYSRLVY 720  
 CLEDTVPALK EVLELERTLG GYLVEEPKPL MFKDSYHNL LSLHDLPHAH WRSKLLAKYQ 780  
 EIPPYHIWSG SQKALHCTFT LERHSLASTE LTCKICVRQV EGEGQIFQLH TTLAETPAGS 840  
 LDTLCSAPGS TVTTQLGPYA FKIPLSIRQK ICNSLDAPNS RGNDRWMLAQ KLSMDRYLNY 900  
 FATKASPTGV ILDLWEALQQ DDGDLNLSAS ALEEMGKSEM LVAVATDGDC 950

Seq ID NO: C393 Protein Sequence  
Protein Accession #: NP\_004616

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MNRKARRCLG HLFSLGIMVY LRIGGFSSVV ALGASTICNK IPGLAPRQRA ICQSRFDAIL 60
VIGESQMGL DECQFQFRNG RWNCSALGER TVFGKELKVG SREAAFTYAI IAAGVAHAIT 120
10    AACTQGNLSD CGCDKEKQGG YHRDEGWKMG GCSADIRYGI GFACVFVDAR EIKQNARTLM 180
NLHNNAGARK ILEENMKLEC KCHGVSGSCT TKTCTTLFPQ FRELGVVLKD KYNEAVHVEP 240
VRASNRKRPK FLKIKKPLSY RKPMOTDLVY IEKSPNYCEE DPTVGSVGTQ GRACNKTAPO 300
ASGCDLMCCG RGYNTHQYAR VWCNCKPFW CCYVKONTCS ERTEMYTCK 349

```

Seq ID NO: C394 Protein Sequence  
Protein Accession #: NP\_003777

```

15      1      11      21      31      41      51
|      |      |      |      |      |
MDALCGSGEL GSKFWSNLS VHTENPDLT CPQNSLLAWV PCIYLNVALP CYLLYLRRHC 60
20    RGYIILSHLS KLMVLGVLL WCVSWADLFY SFHGLVHGRA PAFVFFVTPL VVGVTMLLAT 120
LLIQYERLQG VQSSGVLIIIF WFLCVVCAIV PFRSKILLAK ABGEISDPFR FTFYIHFAL 180
VLSALILACP REKPPFFSAK NVDPNYPET SAGFLSRLFF WWTKMAIYG YRHPLLEKDL 240
WSLKEEDRSQ MVVQQLLEAW RKQEKQTAAR KASAAPGKNA SGEDEVLLGA RPRPRKPSFL 300
25    KALLATFGSS FLISACFKLI QDLSFINPQ LLSLIRFIS NPMAPSWWGF LVAGLMFLCS 360
MMQSLILQHY YHIFVTVGVK FRTGIMGVY RKALVITNSV KRASTVGEIV NLMVSDAQR 420
MDLAPLNLIL WSAPLQIILA IYFLWQNLGP SVLAGVAPMV LLIPNGAVA VKMRAFQVKQ 480
MKLKDRIKML MSEILNGIKV LKLYANEPSP LKQVEGIRQG ELQLLRTAAY LHTTTTFTWM 540
CSFFLVTLIT LMVYVVDPN NVLDAEKAFV SVSLFNILRL PLNMLPQLIS NLTQASVSLK 600
30    RIQQFLSQEE LDPQSVERTK ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV 660
GPVGCCKSSL VSALLGEMEK LEGKVMKGS VAYVPOQAWI QNCTLQENVL FGKALNPKRY 720
QQTLEACALL ADLEMLPGGD QTEIGKGIN LSGGQRQVRS LARAVYSDAD IPLLDDPLSA 780
VDSHVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTDI IIVLADGQVS EMGPYPALLQ 840
RNGSFANFLC NYAPDEDQGH LEDSWTALEG AEDKEALLIE DTLNHTDLT DNDPVTYVVO 900
35    KQPMRQLSAL SSDGEGQGRP VPRRHLPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW 960
DYAKAVGLCT TLAICLLYVG QSAAAIGANV WLSAWTNDAM ADSRQNTSL RLGVYAALGI 1020
LQGFVLMALM MAMAAGGQIA ARVLHQALLH NKIRSPQSF DTTPSGRILN CFSKDIYVVD 1080
EVLAPVILML LNSFFNAIST LVVIMASTPL FTVVILPLAV LYLTVQRYFA ATSRQLKRL 1140
SVSRSPYISH FSETVTGASV IRAYNRSRDF EIISDTKVDA NQRSCYPYII SNRWLSIGVE 1200
40    FVGNQVVLFA ALFAVIGRSS LNPGLVGLSV SYSLQVTFAL NNMIRMSDL ESNIVAVERV 1260
KEYSKTETEA PWVVEGSRPP EGWPPRGEVE FRNYSVRYRP GLDLVLRDLS LHVHGGEKVG 1320
IVGRTGAGKS SMTLCFLRIL EAKGEIRID GLNVADIGLH DLRSQLTIIIP QDPILFSGTL 1380
RMNLDPFGSY SEEDINWALE LSHLHTFVSS QPAGLDFOCS EGGENLSVGQ RQLVCLARAL 1440
45    LRKSRILVLD EATAAIDLET DNLIQATIRT QFDTCTVLT I AHRLNTIMDY TRVLVLDKGV 1500
VAEFDSPANL IAARGIFYGM ARDAGLA 1527

```

Seq ID NO: C395 Protein Sequence  
Protein Accession #: NP\_004617

```

50      1      11      21      31      41      51
|      |      |      |      |      |
MRARPQVCEA LLFALALQTG VCYGIKWLAL SKTPSALALN QTOHCKQLEG LVSAQVQLCR 60
SNLELMHTTV HAAREVMKAC RRAFADMWVN CSSIELAPNY LLDLERTRE SAFVYALSAA 120
AISHAIARAC TSGDLPGCSC GPVPGEPGP GNRWGGCADN LSYGLMGAK FSDAPMKVKK 180
55    TGSQANKLMR LMSSEVGRQA LRASLEMKCK CHGVSGSCSI RTCWKLQEL QDVAADLKTR 240
YLSATKVVRH PMNTRKHLVP KDLDIRPVKD SELVYLQSSP DFCMKNEKV SHGTQDRQCN 300
KTSNGSDSCD LMCCGRGYNP YTRVVERCH CKVHWCCYVT CRRCERTVER YVCK 354

```

Seq ID NO: C396 Protein Sequence  
Protein Accession #: NP\_114072

```

60      1      11      21      31      41      51
|      |      |      |      |      |
MEWGYLLEVT SLLAALALLQ RSSGAAAASA KELACQBITV PLCKGIGYNY TYMPNQFNHD 60
TQDEAGLEVH QFWPLVEIQ SPDLKFPLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP 120
65    LMRQYGFAMP DRMRCDRLPE QGNPDTLCMD YNRDILTAA PSPPRRLPPF PFGEQPPSGS 180
GHGRPPGARF PHRGGGRGG GGDAAAPPAR GGGGGGKARP PGGAAPCEP GCQCRAPMVS 240
VSSERHPLYN RVKTCQIANC ALPCHNFFPS QDERAFTVFW IGLNSVLCFV STFATVSTFL 300
IDMERFKYPE RPIIFLSACY LFSVGYLVR LVAGHEKVAC SGGAPGAGGA GGAGGAAAGA 360
70    GAAGAGAGGP GGRGEYEELG AVEQHVRVET TGPALCTVVF LLVYFFGMAS SIWWVILSLT 420
WFLAAGMKNG NEAIAGYSYQ FHAAWLVPS VKSIAVLALS SVDGDPVAGI CYVGNQSLDN 480
LRGEVLAPLV IYLEIGTMFL LAGFVSLFRI RSVIKQDQGP TKTHKLEKLM IRLGLFTVLY 540
TVPAVVVAC LFYEQHNRPR WEATHNCPCL RDLQFDQARR PDYAVFMLKY FMCLVVGITS 600
75    GVWWSGKTL ESMRSLCTRC CWASKGAAVG GGAGATAAGG GGGPGGGGGG GPGGGGGPGG 660
GGGSLYSVDS TGLTWSGTA SSVSYPKQMP LSQV 694

```

Seq ID NO: C397 Protein Sequence  
Protein Accession #: XP\_050625

```

80      1      11      21      31      41      51
|      |      |      |      |      |
MLQGPGLLL LFLASHCCLG SARGLFLFGQ PDFSYKRSNC KPIPANLQLC HGIEYQNMRL 60
PNLLGHETMK EVLEQAGANI PLVMKQCHPD TKKFLCSLFA PVCLDDDET IQPCHSLCVQ 120
VDRCAPVMS AFGFPWDMLE ECDRPPQDND LCIPASSDH LLPATEEAPK VCEACKNKND 180
DDNDIMETLC KNDPALKIKV KEITYINRDT KIILETKSKT IYKLVGVSER DLKKSVLWLK 240

```

DSLQCTCEEM NDINAPYLVM GQKQGGLVI TSVKRWQKQK REFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence  
Protein Accession #: NP\_001297.1

5  
10  
1  
11 21 31 41 51  
MSMGLBITGT ALAVLGNLGT IVCCALPMWR VSAFIGSNII TSONIWEGLW MNCVVQSTGQ 60  
MQCKVYDSSL ALPQDLQAAR ALIVVAILLA AFGLLVALVG AQCTNCVQDD TAKAKITIVA 120  
GVFLPLAALL TLVPVWSAN TIIRDYPNPV VPEAQKREMG AGLYVGWAAA ALQLLGGALL 180  
CCSCPPEKK YTATKVYISA PRSTGPGASL GTGYDRKDYV 220

Seq ID NO: C399 Protein Sequence  
Protein Accession #: NP\_036581.1

15  
20  
1  
11 21 31 41 51  
MESRKDITNQ EELWQMKPRR NLEEDDYLHK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60  
LQHTQELFPQ WHLPKIAAAI IASLTFLYTL LREVIHPLAT SHQYFYKIP ILVINKVLPM 120  
VSITLLALVY LPGVIAAIVQ LHNQTKYKPK PHWLDKMWLT RKQFGLLSFF FAVLHAIYSL 180  
SYPMRRSYRY KLLNWAYQQV QONKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240  
VSDSLTWREF HYIQSKLGIV SLLLGTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV 300  
VLIFKSLIFL PCLRKILKI RHGWEDVTKI NKTEICSQL 339

Seq ID NO: C400 Protein Sequence  
Protein Accession #: NP\_001766.1

25  
30  
35  
1  
11 21 31 41 51  
MANCEFPVPS GDKPCCLRSR RAQLCLGVSI LVLILVVVLA VVPRWRQWV SGPQTTRKFP 60  
ETVLARCVKY TEIHPEMRHV DCQSVWDAFK GAFISKHPCN ITEEDYQPLM KLGTQTVPCN 120  
KILLWSRIKD LAHQPTQVQR DMFTLEDTL L GYLADDLTWC GEFNTSKINY QSCPDRKDC 180  
SNPNVSVFWK TVSRFPABAA CDVVHVMLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLFA 240  
WVIHGGREDS RDLQCDPTIK ELESIIISRN IQFSCNKIYR PDKFLQCVKN PEDSSCTSEI 300

Seq ID NO: C401 Protein Sequence  
Protein Accession #: XP\_120513.2

40  
45  
50  
1  
11 21 31 41 51  
MVSCTFSGPL RETNENVKKF YALRAFMRM SSEAAMLGES RTPKPRKHRA TTRAKIFKRF 60  
FSEGESNSR LVEELAVIHT YSDDPAFTTS PSSVQPREFG VMQAPRARF GSRTPPAAAE 120  
ASSPHLIGIE AACQSGARAA APRAGARRCQ PQRQAAAAA TAQTHLPHA RTRADPAGRR 180  
RRHRSPAPG GEGTCSGPA PRRRMEEMQ PAEEGSPVPK IYKQSPYSV LKTFPSKRPA 240  
LAKRYERPTL VELPHGHLRT PAQPPASPAA ASSSSFAAV VRLGAPPRPP RRGFRARGTI 300  
PLLLPAPGVA GTLLPPPTSS SPPSPRPRPW HAAAPRGGTS HTHMWSQST LPGSDTMVSV 360  
FGLMAQRRWQ HRSLLKQFEG ILGSWGTWPC QDWLEKEGO VAVLLPRSEG NTAPKSRMI 420  
LDAFAQQCSR VLSLLNCGGK LLDNSHSQSM ISCVKQEGSS YNERQEHCHI KGKGVHSQTS 480  
NVDIEMQYM RKQQTSAFLR VFTDSLQNYL LSGSFPTPNP SSASEYGHIA DVDPLSTSPV 540  
HTEINISLDS TASLCKSRHL SREPPVKSDP PNPLQALAG GASRPFGSAQ QSIAYRVNSE 600  
LEDGIRSPVP LSCAELMDL TSLGSKQLLN NYPVYITSQ WDEAVNSKK DGRRLRLYLI 660  
RFVPTDELK YSCGLGKRKR SVQSGETGPE RRPLDPVKVT CLRGTASFRS VSPSVISFHR 720  
IGCGSPRTSV QPSVF 735

Seq ID NO: C402 Protein Sequence  
Protein Accession #: BAA92562.1

55  
60  
65  
70  
1  
11 21 31 41 51  
METTVLSGIN FEYKGMTGWE VAGDHIYTA GASDNDFMIL TLVVPGRFP QSVMDTENK 60  
EVARITVFVE TLCVNCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTITSFTWA 120  
FORTTFHEAS RKYTNDAVAKI YSINVTVNMN GVASYCRPCA LEASDVGSSC TSCPAGYID 180  
RDSGTCHSCP PNTILKAHQF YGVQACVPCG PGTRNKIHS LCYNDCTFSR NTPTRTFNYN 240  
FSALANTVTL AGGSPFTSKG LKYFHHFTLS LGNQGRKMS VCTDNVTDLR IPEGESGFSK 300  
SITAYVCQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESGLI 360  
PDVIFFRSN DVTQSCSSGR STTIRVRCSF QKTVEGSLLL PGTCSDGTCD GCNFHPLWES 420  
AAACPLCSVA DYHAISSCV AGIQKTTYVW REPKLCSGGI SLPEQRTVIC KTIDFWLKV 480  
ISAGTCTAIL LTVLTCYFWK KNQKLEYKYS KLVNMATLKD COLPADSCA IMEGEDVEDD 540  
LIFTSKSLF GKIKSFTSKQ PAPVTISLSE DS 572

Seq ID NO: C403 Protein Sequence  
Protein Accession #: NP\_055139.1

75  
80  
1  
11 21 31 41 51  
MALQGISVVE LSGLAPGRXC AMVLADFGAR VVRVDRPGSR YDVSRLGRGK RSLVLDLKQP 60  
REPRAAASVQ AVGCAAGALP PRCHGETPAG PRDSAAGKSK AYLQCAEWI PVQESFCRLA 120  
GHDINYLALS GVLSKIGRSG ENPYAPLNLV ADFAGGGLMC ALGIIMALFD RTRTDKQVQI 180  
DANNVETAY LSSFLWKTQK SSLWEAPRGQ NMLDGGAPFY TTYRTADGEF MAVGAIEPQF 240  
YELLIKGLGL KSDLPNQMS TDDWPEMKKK FADVFARKTK AEWCQIFDGT DACVTPVLTF 300  
EEVVHHDHMK ERGSFITSEE QDVSPRLAPL LLNTPAIPSS KGDPFIGEHT EEILEEFGFS 360  
REEIYQLNSD KIIESNKVKA SL 382

Seq ID NO: C404 Protein Sequence

Protein Accession #: XP\_091332.1

```

1      11      21      31      41      51
5      |      |      |      |      |
MQRMTLWAAA FLTLHSAQAF PQTDISISPA LPFLPLPSLC PLFWMEFKGH CYRFFPLANK 60
WAEADLYCSE FSVGRKSAKL ASIHSEWENV FVYDLVNSCV PGIPADVWTG LHDHRQEGQF 120
ENTDGSYDY SYWDGSPDD GVHADPEED CVQIWYRPTS EQLQAPPEQL PLSISEATDV 180
YLPEDFPAEP KLMDQSWVSR KSLKPSKSHL MEPPTPVAKH QKAKTRHRSR RGVWVPSGKA 240
GSWKERMNAD YGRRKRSAPR QEGRRLRCRER RLRAASGQGR PEGQRKQRQQ ERQERGWEEEL 300
GGVSPMRGAQ ANQHGGLGAGS QRGAAPECGE NHQAPELGST WRGQRLOPQT AALCHFALRK 360
LPGNAHGLAA AFVQPALQVQ EEKNNRTRFS GAYFTMSDPT CDQDSKEQSL RRRGREAEKD 420
GPYRLVKKKR GPVACPSFFE LQSGGEVCLD FPVELRAGTW IAREPP 466

```

Seq ID NO: C405 Protein Sequence  
Protein Accession #: XP\_054869.2

```

1      11      21      31      41      51
20     |      |      |      |      |
MHTCCPPVTI EQDLHRKMHS WMLQTLFAV TSLVLSCAET IDYYGEICDN ACPCEEKDIGI 60
LTVSCENRGI ISLSISIPPR FPIYHLLLSG NLLNRLYPNE FVNYTGASIL HLGSNVIQDI 120
ETGAFHGLRG LRRLHLNNNK LELLRDDTFL GLENLEYLQV DYNYSVIEP NAFGKLHLHQ 180
VLILADNLLS SLFNNLFRFV PLTHLDLRGN RLKLLPYVGL LQHMDKVVEL QLEENPWNCSS 240
CELISLKDWL DSISYSALVG DVVCETPPRL HGRDLDEVSK QELCPRLIS DYEMRPQTPL 300
STTGYLHTTP ASVNSVATSS SAVYKPLKP PKGTRQPNKP RVRPTSRQPS KDLGYSNYGP 360
25     SIAYQTKSPV PLECPACSC NLQISDLGLN VNCQERKIES IAELOPKPYN PKMYLTENY 420
IAVVRTDFL EATGDLHLH GNNRISMIQD RAFGDLTNLR RLNYLGNRIE RLSPELFYGL 480
QSLQYLFQY NLRIRISQST FDPVFNQLL FLNNLLQAM PSQVFSGLTL LRLNLRNHF 540
TSLPVSGLD QLSLIQIDL HDNPWDCTCD IVGMKLWVEQ LKVGVLVDEV ICKAPKKPAE 600
TDMRSIKSEL LCPDYSVVV STPTSSSIQV PARTSAVTPA VRLNSTGAPA SLGAGGGGSS 660
30     VPLSVLILSL LVVFMVSFV AAGLFVLVMK RRKNQSDHT STNNSDVSSF NMQSVYVGG 720
GGTGHPHAAH VHRGPALEPK VKTPAGHYVE YIPHLGHMC KNPIYRSREG NSVEDYKDLH 780
ELKVYYSNNH HQQQQQPPP PQQPQQQPP POLQLQPGEE ERRESHLRS PAYSVSTIEP 840
REDLLSPVQD ADRFYRGILE PDKHCSTTPA GNSLPEYKPK PCSPAAYTFS PNYDLRRPHQ 900
35     YLHPGAGDSR LRPVLYSPP SAVFVEPNRN EYLELKAKLN VEPDYLEVLE KQTTFSQF 958

```

Seq ID NO: C406 Protein Sequence  
Protein Accession #: NP\_000784.2

```

1      11      21      31      41      51
40     |      |      |      |      |
MGILSVLLI TLQILPVFFS NCLFLALYDS VILLKHVVLL LSRSKSTRGE WRRMLTSEGL 60
RCVWKSFLLD AYQKVLGED APNSSVVHVS STEGGDNNGN GTQEKIAGA TCHLLDFASP 120
ERPLVVNFGS ATUPPFTSQL PAFKRLVEEF SSVADFLLVY IDEAHPSDGN AIPGDSLSLP 180
45     EVKHKQNGED RCAAQQLLE RFLSPQCRV VADRMNNAN IAYGVAFERV CIVQRQKIAY 240
LGKGGFSPYN LQEVHRWLEK NFSKRUKKTR LAG 273

```

Seq ID NO: C407 Protein Sequence  
Protein Accession #: NP\_006540.2

```

1      11      21      31      41      51
50     |      |      |      |      |
MSSCVSSQPS SMRAAPQDEL GGRGSSSSSES QKPCEALRGL SLSIHLGME SPIVVTECEP 60
GCAVDLGLAR DRPLEADGQE VPLDSSGSQA RPHLSGRKLS LQERSQGLA AGGSLDMNGR 120
CICPSLPYSP VSSPQSSPRL PRRPTVESHV VSITGMQDCV QLNQYTLKDE IGKGSYGUVK 180
55     LAYNENDNTY YAMKVLSEKK LIRQAGFPFR PPRGTRPAP GGCIQPRGPI EQVYQEIALL 240
KKLDHPNVVK LVEVLDDPNE DHLVMVPELV NQGVMEVPT LKPLESDQAR FYFDLIKGI 300
EYLEYQKIIH RDIKPSNLLV GEDGHKILAD FGVSNEFKGS DALLSNTVGT PAFMAPELSL 360
ETRKIFSGKA LDVWAMGVTL YCFVFGQCPF MDERIMCLHS KIKSQALEPP DQPDIAEDLK 420
60     DLITRMLDKN PESRIVVPBI KLHPVWTRHG AEPLPSEDEN CTLVEVTEEE VENSVKHIPS 480
LATVILVKTM IRKRSFGNPF EGSRREERSL SAPGNLLTKK PTRECBLSLE LKEARQRQP 540
PGRHAPRGG GGSALVRGSP CVESCWAPAP GSPARMHPLR PEEAMEPE 588

```

Seq ID NO: C408 Protein Sequence  
Protein Accession #: NP\_061116.2

```

1      11      21      31      41      51
65     |      |      |      |      |
MGLSLPKEKG LILCLWSKFC RWFQRRESWA QSRDEQNLLQ QKRIWESPLL LAAKDNDVQA 60
LNKLLKYEDC KPHQRGAMGE TALHIAALYD NLEAAMVME AAPLVFEPM TSELYEGQTA 120
70     LHIAVNVQNM NLVRALLARR ASVSARATGT AFRRSPCNLI YFGEHPLSFA ACVNSEIIVR 180
LLIEHGADNI AQDSLGNLTVL HILILQPNKT FACQMYNLLI SYDRHGDHLQ PLDLVPHNQG 240
LTPFKLAGVE GATVMPOHLM QKRKHTQWTY GPLTSTLYDL TEIDSSGDEQ SLELLIITTK 300
KREARQILDQ TPVKELVSLK WKRYGRPYFC MLGAIYLLYI ICFTMCCYR PLKPRTNNT 360
SPRNTLLQQ KLLQEAAYTP KDDIRLVGEL VTIGAILIL LVEVPDIFRM GVTRFFGQTI 420
75     LGGPFHVLI IYAFMVLVTM VMRLISASGE VVPMSPALVL GWCNVMYFAR GFQMLGPFTI 480
MIQKMIFGDL MRFCLMAVAV ILGFASAFYI IFQTEDPEEL GHFYDYPMAL FSTFELFTI 540
IDGPANYVD LFFMYSITYA AFATITALLM LNLIIAMGCD THWRVAHERD ELNRAQIVAT 600
TVMLERKLPR CLWPRSGICG REYGLGDRWF LRVEDRQDLN RQRIQRYAQA FHTRGSEDLD 660
80     KDSVEKLELG CFPSPHLSLP MPFSVSRSTSR SSANWERLRQ GTLRDLRGI INRGLEDGES 720
WEYQI

```

Seq ID NO: C409 Protein Sequence  
Protein Accession #: NP\_068710.1

1 11 21 31 41 51  
 | | | | |  
 MQKVTGLGLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60  
 RSSSEQAGRG WGSPPPLTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence  
 Protein Accession #: NP\_005962.1

10 1 11 21 31 41 51  
 | | | | |  
 MQKVTGLGLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60  
 CKCKFGQKSG HHPGETPPLI TPGSAQS 87

Seq ID NO: C411 Protein Sequence  
 Protein Accession #: NP\_004952.1

15 1 11 21 31 41 51  
 | | | | |  
 20 MLKVLVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60  
 TGSRVGKLE ASRILMTLS NYDHKLRPGI GEKPTVVTV E IAVNSLGPLS ILDMETIDI 120  
 IPSQTWYDER LCNNDTFESL VLNQNVSQL WIPDTFFRNS KRTHHEITM PNQMVRIYKD 180  
 GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIIKWENF KLEINEKNW 240  
 KLFQDFDTGV SNKTEIITTP VGDPMVTIF FNVSRRFYGV AFQNYVPSV TMLSWVSEW 300  
 25 IKTESAPART SLGITSVLMT TLGTFSRKN FPRVSYITAL DFYIACFPV CFCALLEFAV 360  
 LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TTEGSDGEER 420  
 PSCSAQQPPS PGSPGPRSL CSKLACCEWC KRFFKYFCMV PDCGEGSTWQ GRLCIHVYRL 480  
 DNYSRVVPV TFFFNVLVY LVCLNL 506

Seq ID NO: C412 Protein Sequence  
 Protein Accession #: NP\_068819.1

30 1 11 21 31 41 51  
 | | | | |  
 35 MEYTIIDIFS QTWYDERLCY NDTFESLVN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTIIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNWKL F QDFTGVSNK TEIITTPVGD FMVTIFFNV SRRFGYVAFQ NYVPSSVTM 180  
 LSWVSPWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240  
 ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARHQE AFVCQIVTTE 300  
 40 GSDGEERPSC SAQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPC EGSTWQQARL 360  
 CHVYRLDNY SRVVPVTF FNVLYWLV LNL 393

Seq ID NO: C413 Protein Sequence  
 Protein Accession #: NP\_068822.1

45 1 11 21 31 41 51  
 | | | | |  
 MEYTIIDIFS QTWNSKRTH HEITMPNQMV RIYKDGKVLV YIRMTIDAGC SLHMLRFPMD 60  
 SHSCPLSPSS FSYPENEMII KWENFKLEIN EKNSWKLQF DFTGVSNKTE IITTPVGDPM 120  
 50 VMTIFFNVSR RFGYVAFQNY VPSSVTMLT WSVFWIKTES APARTSLGIT SVLTMTTLGT 180  
 FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTKAHASP KLRHPRINSR 240  
 AHARTRARSR ACARQHQEAF VCQIVTTEGS DGEERPSCSA QPPSPGSPF GPRSLCSKLA 300  
 CCEWCKRFKK YFCMVPCDG STWQQGRLCI HVYRLDNYSR VVPVTFGFFF NVLYWLVCLN 360  
 L 361

Seq ID NO: C414 Protein Sequence  
 Protein Accession #: NP\_068830.1

55 1 11 21 31 41 51  
 | | | | |  
 60 MEYTIIDIFS QTWYDERLCY NDTFESLVN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTIIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNWKL F QDFTGVSNK TEIITTPVGD FMVTIFFNV SRRFGYVAFQ NYVPSSVTM 180  
 LSWVSPWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240  
 65 ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARHQE AFVCQIVTTE 300  
 GSDGEERPSC SAQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPC EGSTWQQGR 360  
 CHVYRLDNY SRVVPVTF FNVLYWLV LNL 393

Seq ID NO: C415 Protein Sequence  
 Protein Accession #: NP\_068591.1

70 1 11 21 31 41 51  
 | | | | |  
 MPAVSGPGPL FCLLLLLLD HSPETGCPPL RRFYKLSFK GPRALPGAG IPFWSHHGDA 60  
 ILGLEEVRLT PSMNRNSGAV WSRASVPFSA WEVEVQMRVT GLGRRGAGM AVVYTRGRGH 120  
 75 VGSVLGGLAS WDGIGIFFDS PAEDTQDSPA IRVLASDGH I PSEQPGDGAS QGLGSCWDF 180  
 RNRHPPFRAR ITYWGQRLRM SLNSGLTFS D PGEFCVDVGP LLLVPGGFFG VSAATGTLD 240  
 DHDVSLFLTF SLSEPSPEVP PQPFLEMQLL RLARQLEGLW ARLGLGTRED VTPKSDSEAQ 300  
 GEGERLFDLE ETLGRHRRIL QALRGLSKQL AQAERQWKQ LGPPQARPD GGWALDASCQ 360  
 80 IPSTPGRGGH LMSMLNKDSA KVGALLHGQW TLLQALQEMR DAAVRMAEA QVSYLEVFGIE 420  
 HHFLDLHL GLLQELRGP AKAAKAPRP PQQPRASSC LQPGIFLFLY LIQTGVGFFGY 480  
 VHFRELNKS LQECSTGSL PLGPAPHTPR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence  
 Protein Accession #: XP\_117036.1

1 11 21 31 41 51  
 5 MERRTRGALG SRRPPPPPLPA LRHLCTGLQA AGMAWPGTLW RHTCQGRAXA AEGPWGLFRP 60  
 HRCPRERAGQA PVGSPETQG VAHVCSRARV SVDEREPGGG AYAMRVTPRW KGCHRHSGRT 120  
 VRGSVSWKRP EQAAPETGRG PAVARGSGDG NECGWG 156

Seq ID NO: C417 Protein Sequence  
 Protein Accession #: XP\_167803.2

1 11 21 31 41 51  
 10 MPKGQQRKTA TNKPGGLPGA PGVGIGGHCL YVLECKCFIK NKTKTHHHKK KNFAAKRNEE 60  
 15 KLKKKKKQEK KNHTKFFHHT YPLSQQDFLF AKSYFCGNGP CFLWQGLF 108

Seq ID NO: C418 Protein Sequence  
 Protein Accession #: NP\_079056.1

1 11 21 31 41 51  
 20 MFRIVERYEM PRHEVYVLLI RNIFLKISII GILCYWLT VALSGEECWE TLIGQDIYRL 60  
 LLMDVFVSLV NSFGEFLRR IIGMQLITSL GLQEPDIARN VLELIYAQTL VWIGIFFCPL 120  
 LPFIQIMIMLF IMFYSKNISL MNFQPPSKA WRASQMMTFP IFLFFPSFT GVLCTLAITI 180  
 25 WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNIGSVH FFFILTILVL 240  
 IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP SSLVLERREV 300  
 EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 330

Seq ID NO: C419 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 30 MLDSDHVNEI IIQVENVSSG VQSHPSNQI FQEKVLLDSS INMVLISIDI DVIDSQTISK 60  
 RNDQKGNQVL RFSTSLNESM SQTLSLECM GIDTPGSSHE TVQGQKLIAS LIPMTSRDRI 120  
 35 KAIRNQPRTM EEKRNLRKIV DKEKSKQTHR ILQINCCIQC LNSISRAYRR SKNSLSEILN 180  
 SISLWQKTLK IIGGKFGTSV LSYFNFLRWL LKFNIFSFIL NFSFIIIPQF TVAKKNTLQF 240  
 TGLEFFFGVG YFRDTVMYIG FYTNSTIQHG NSGASYNMQL AYIFTIGACL TTCFFSLIFS 300  
 MAKYFRNNFI NPHIYSGGIT KLIFCWDFTV THEKAVKLKQ KNLSTEIREN LSELRQENSK 360  
 40 LTFNQLLTRF SAYMVAVVVS TGVAIACCAA VYLAENYLE FLKTHSNPGA VLLPFVVS 420  
 INLAVPCIYS MFRIVERYEM PRHEVYVLLI RNIFLKISII GILCYWLT VALSGEECWE 480  
 TLIGQDIYRL LLMDVFVSLV NSFGEFLRR IIGMQLITSL GLQEPDIARN VLELIYAQTL 540  
 VWIGIFPCPL PFIQIMIMLF IMFYSKNISL MNFQPPSKA WRASQMMTFP IFLFFPSFT 600  
 GVLCTLAITI WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNIGSVH 660  
 45 FFFILTILVL IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP 720  
 SSLVLERREV EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 760

Seq ID NO: C420 Protein Sequence  
 Protein Accession #: NP\_002241.1

1 11 21 31 41 51  
 50 MGGDLVLGLG ALRRRRKRLLE QEKSLAGWAL VLAGTGIGLM VLHAEMLWFG GCSWALYLFL 60  
 VKCTISISTF LLLCLIVAFH AKEVQLFMTD NGLRDWRVAL TGRQAAQIVL ELVVCGLHPA 120  
 PVRGPPCQVD LGAPLTSPOF WPGFLGQGEA LLSLAMLRL YLVPRAVLLR SGVLLNASYR 180  
 55 SIGALNQVRF RHWFAKLYM NTHPGRLLG LTLGLMLTTA WVLSVAERQA VNATGHLSDT 240  
 LWLIPITFLT IGYGDVVPQT MWGKIVCLCT GVMGVCCTAL LVAVVARKLE FNKAEKHVHN 300  
 FMMDIQYTKM MKESAARVLF EAMMFYKTR RKESHAARRH QRKLLAANA FRQVRLEGRK 360  
 LREQVNSMVD ISKMHMILVD LQQNLSSSHR ALEKQIDTLA GKLDALTELL STALGPRQLP 420  
 60 BPSQQSK 427

Seq ID NO: C421 Protein Sequence  
 Protein Accession #: NP\_079533.1

1 11 21 31 41 51  
 65 MGGKQRDEDD EAYGKPVKYD PSFRGPIKNR SCTDVICCVL FLLFILGYIV VGIWAWLYGD 60  
 PRQVLYPRNS TGAYCGMGEN KDKPYLLLYFN IPSCILSSNI ISVAENGLQC PTPQVCVSSC 120  
 PEDPWTVGKN EFSQTVEVF YTKNRNFCLE GVPWNMTVIT SLQQLCPSE LPLSAPALGR 180  
 70 CFPWTNITPP ALPGITNDIT IQQGISGLID SLNARDISVK IFEDFAQSWY WILVALGVAL 240  
 VLSLLPILLL RLAVAGPLVLV LILGVLGVLA YGIYCNEEY RVLRDKGASI SQLGFTINLS 300  
 AYQSVQETWL AALIVLAVLE AILLLVLIFL RQRIRIAIAL LKEASKAVGQ MMSTMFYPLV 360  
 TFVLLICIA YWAMTALYPL PTQPATLGYV LWASNISSPG CEKVPINTSC NPTAHLVNSS 420  
 CPGLMCFVQG YSSKGLIORS VFNLIQYGV LGLFWTLNWL ALGQCVLGA FASFYWFHK 480  
 75 PQDIPFPPLI SAFIRTLRYH TGSIAFGALI LTLVQIARVI LEYIDHKLGR VQNPVARCIM 540  
 CCPCCLWCL EKFIKPLNRN AYIMIAIYK NFCVSAKNAP MLMNRNIVRV VVLDKVTDL 600  
 LFFGKLLLVG GVGVLSEFFF SGRIPGLGKD FKSPLNYYW LPIMTSILGA YVIASGPFV 660  
 LFGMCDTLFL CFLEDLERNN GSLDRPYMS KSLKILGKK NEAPPDNKKR KK 712

Seq ID NO: C422 Protein Sequence  
 Protein Accession #: NP\_057264.1

1 11 21 31 41 51  
 80 MGSNSGQAGR HIYKSLADDG PFDSVEPPKR PTERLIMHSM AMFGREFCYA VEAAYVTPVL 60

LSVGLPSSLY SIVWFLSPIL GFLLQPVVGS ASDHCRSRWG RRRPYILTLG VMMLVGMALY 120  
 LMGATVVAAL IANPRRKLWV AISVTMIGVV LFDFAADFID GPIKAYLFDV CSHQDKEKGL 180  
 HYHALFTGGF GALGYLLGAI DWAHLELGRLL LGTEFQVMPF FSALVLTLCF TVHLCSISEA 240  
 PLTEVAKGIP PQQTPQDPPL SSDGMVEYGS IEKVNGYVNV PELAMQGAKN KNHAEQTRRA 300  
 MTLKSLLRAL VNMPPHYRYL CISHLIGWTA FLSNMLFFTD FMGQIVYRGD PYSAHNSTEF 360  
 LIYERGVEVG CWGFCINSVF SSLYSYFQKV LVSYIGLKGL YFTGYLLFGL GTGFIGLFPN 420  
 VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEEKERQQA PGGDPDNSVR KGKMDCATLT 480  
 CMVQLAQILV GGGGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

Seq ID NO: C423 Protein Sequence  
 Protein Accession #: NP\_003264.1

1 11 21 31 41 51  
 | | | | |  
 15 MEGEGGVGGR GTRGFAAKGV WRGRAEERGVP LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60  
 PGKGTGRQRG ANGPRADGV RRRTLGMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSSRR 120  
 RGSATAAARH HVPPAPGGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180  
 AGAQGAGPAR GRSGESEWA RRGKGRPGFY QSLGPAVAE GQELKDKSRL RYPINGFOAL 240  
 VLTALLVGLG MSAGLPLGAL PEMLLPLAFV ATLTAFIPLS FLVYKQAVP VSALAPGNS 300  
 20 GNPIYDFPLG RELNPRICFF DFICYCELPR GLIGWVLINL ALLMKEAELR GSPSLAMWL 360  
 NGFQLLYVGD ALWHEEAVLT TMDITHDGFQ FMLAFGDMAN VPFTYSLQAG FLHHPQPLG 420  
 LPMASVICLI NATGYIFRG ANSQKNTFRK NPSDPRVAGL ETISTATGRK LLVSGWGMV 480  
 RHPNYLGLDI MALAWSLPCG VSHLLPYFYL LYFTALLVHR EARDERSACR STAWPGRSTA 540  
 25 GVCLTASCPT STEAAPPPQV GHVPTPPAH PGPAGSTHLG LKGLHPTQP 589

Seq ID NO: C424 Protein Sequence  
 Protein Accession #: NP\_056535.1

1 11 21 31 41 51  
 | | | | |  
 30 MGRLLRAARL PELLSPLLLL LVGGAFLGAC VAGSDEPGPE GLTSTSLDL LLPTGLEPLD 60  
 SEEPSETMGL GAGLGAPGSG FPSEENEESR ILQPPQYFWE EEEELNDSSL DLGPTADYVF 120  
 PDLTEKAGSI ETSQAQELP NLPSPPLKMN LVEPPNHHMP REEEEEEEEE EEREKEEVEK 180  
 35 QEEEEEEELL PVNGSQBEAK PQVRDFSLTS SSQTGATKS RHEDSGDQAS SGVEVESSMG 240  
 PSLLLPSTVP TTVTPGDQDS TSQEAETATV PAAGLGVEFE APQEAEEAT AGAAGLSGQH 300  
 EEVPALPFFP QTAPSGAEH PDDEDPLGRT SASSPLAPGD MELTPSSATL QGEDLNQQLL 360  
 EQAAEAQSR IPWDSQVIC KDWSNLAKGN YIILNMTENI DCEVFRQHRG PQLLALVEEV 420  
 LPRHSGSHHG AWHISLSKPS EKEQHLMLTL VGEQGVVPTQ DVLSMLGDIR RSLEEIGION 480  
 40 YSTTSSCQAR ASQVRSDYGT LFVVLVVIGA ICIIIALGL LYNCWQRRLK LKHVSHGEE 540  
 LRFVENGCHD NPTLDVASDS QSEMKEHPS LNGGALNGP GSWGALMGK RDPEDSDVFE 600  
 EDTHL 605

Seq ID NO: C425 Protein Sequence  
 Protein Accession #: NP\_001188.1

1 11 21 31 41 51  
 | | | | |  
 45 MSEVRPLSRD ILMETLLYEQ LLEPFTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR 60  
 LACIGDEMVD SLRAPRLAQL SEVAMHSIGL AFIYDQTEDI RDVLRSPMDG FTTLENKIMR 120  
 50 FWRSPNPGSW VSCQVLLAL LLLALLLPL LSGLHLLLK 160

Seq ID NO: C426 Protein Sequence  
 Protein Accession #: AAF76225.1

1 11 21 31 41 51  
 | | | | |  
 55 MATPLPPSP RHLRLRLRL SGLVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPPGA 60  
 HACGFCLOPF QEDQOGLCVP RMRPPGGGR PQPRLEDEID FLAQELARKE SGQSTPPLPK 120  
 60 DRQRLPEPAT LGFSARGQL ELGLPSTPGT PTPPTHTSLG SPVSSDPVHM SPLEPRGGQ 180  
 DGLALVLILA FCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ 240  
 RLQAQSAEMH YQHQROQMLC LERHKEPKK LDTASSDEEN EDGDFTVYEC PGLAPTGEHE 300  
 VRNPLFDHAA LSAPLPAPSS PPALP 325

Seq ID NO: C427 Protein Sequence  
 Protein Accession #: NP\_004436.1

1 11 21 31 41 51  
 | | | | |  
 70 MVSCLWVILL VSSVLALIEV LLDTTGETSE IGWLYTPPGG WDEVSVLDDQ RRLTRTFEAC 60  
 HVAGAPPGTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTCT ETFTLYYRQA 120  
 EEPDSDPSVS SWHLKRWTKV DTIAADESFP SSSSSSSSSS SAANAVGPHG AGQRAGLQLN 180  
 75 VKERSFGPLT QRGFYVAFQD TGACIALVAV RLFSYTCPAV LRSFASFPET QASGAGGASL 240  
 VAAVGTCAVA AEPEEDGVGG QAGGSFPRHL CNBEGKMMVA VGGCRCPQGY QPARGDKACQ 300  
 ACPRLGYKSS AGNAPCSPCP ARSHAFNPAA PFCPCLEGFY RASSDPPEAP CTGPSPAPQE 360  
 LWFEVQGSAL MLHWRLPREL GGRGDLLENV VCKECEGRQE PASGGGGTCH RCRDEVHFD 420  
 80 RQRGLTESRV LVGGRLRAHP YILEVQAVNG VSELSPPDPQ AAANVSTSH EVPSAVPVVH 480  
 QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSETNTA TVTQLSPGHI 540  
 YGFQVRARTA AGHGPYGGKV YFQTLQOGL SSQPLPERLSL VIGSILGALA FLLLAITVL 600  
 AVVFQRKRRG TGYTEQLQY SSPGLGVKYY IDPSTYEDPC QAIRELAREV DPAYIKIEEV 660  
 IGTGSPGEVR QGRLLQPRGR EQTVAILQALW AGGAESLQMT FLGRAAVLQ FQHPNIRLLE 720  
 GVVTKSRFLM VLTEFPELGP LDSFLRQREG QFSSILQIVAM QRGVAAAMQY LSSFAFVHRS 780  
 LSAHSVLVNS HLVCKVARLG HSPQGPSCLL RWAAPVIAH GKHTTSSDVV SFGILMWEVM 840  
 SYGERPYNDM SBOEVLNATE QEFRLPPPG CPGHLHLLML DTWQKDRAR PHFDQLVAAP 900  
 DKMIRKPDTL QAGGDPGERP SQALLTPVAL DFFCLDSQQA WLSAIGLEYC QDNFSKPGLC 960



TFSDVAQLSL EDLPALGITL AGHQKLLHH IQLLQHLRQ QGSVEV

1006

Seq ID NO: C428 Protein Sequence  
Protein Accession #: XP\_043340.2

5

10

```

1      11      21      31      41      51
|      |      |      |      |      |
MPFDFRRFDI YRKVPKDLTQ PTYTGAIIIS CCCLFILFLF LSELTGFITT EVVNELYVDD 60
PKDKSGGKID VSLNISLPNL HCELVLGLDIQ DEMGRHEVGH IDNSMKIPLN NGAGCRFEGQ 120
FSINKVPGNF HVSTHSATAQ PQNPDMTHVI HKLSFGDTLQ VQNIHGAFNA LGGADRLTSN 180
PLASHDYILK IVPITYEDKS GKQRYSYQYT VANKEYVAYS HTGRIIPAIN FRYDLSPITV 240
KYTERRQPLY RPITITCAII GGITVAGIL DSCIFTASEA WKIKQLGKMH 290

```

15

Seq ID NO: C429 Protein Sequence  
Protein Accession #: NP\_002142.1

20

25

```

1      11      21      31      41      51
|      |      |      |      |      |
MAQKEGGRTV PCCSRPKVAA LTAGTLLLLT AIGAASWAIV AVLLRSDDQEP LYPVQVSSAD 60
ARLMVFDKTE GTWRLLCSSR SNARVAGLSC EEMGFRLRAL HSELDVRTAG ANGTSGFFCV 120
DEGRLPHTQR LLEVISVDCD PRGRFLAALC QDCGRRLFPV DRIVGGRTS LGRWFWQVSL 180
RYDGAHLGGG SLLSGDWLIT AAHCFPERNR VLSRWRFVAG AVAQASPHGL QLGVAQVYH 240
GGYLPFRDPN SEENSNDIAL VHLSSPLPLT EYIQPVCLPA AGQALVDGKI CTVTGWGMTQ 300
YYGQAGVLQ EARVPIISND VCGADFYGN QIKPKMFCAG YPEGGIDACQ GDSGGPFVCE 360
DSISRTPKWR LCQIVSWGTV CALAQKPGVY TKVSDFREWI FQAIKTHSEA SGMVTQL 417

```

Seq ID NO: C430 Protein Sequence  
Protein Accession #: BAA92562.1

30

35

40

```

1      11      21      31      41      51
|      |      |      |      |      |
METTVLSGIN FEYKGMTGWE VAGDHIYTAA GASDNDFMIL TLVVPGRFRPP QSVMA DTENK 60
EVARITFVFE TLCSVNCELY PMVGVSRTN TPVETWKGSK GKQSYTYIIE ENTTSFTWA 120
FQRTTFHEAS RKYTNDVAKI YSINVTVNM GVASYCRPCA LEASDVGSSC TSCPAGYIID 180
RDSGTCHSCP PNTILKAHP YGVQACVPCG PGTKNNKIHS LCYNCTFSR NTPTRTFNYN 240
FSALANTVTL AGGSPSTSKG LKYFHHFTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK 300
SITAYVCQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESIGI 360
PDVIFPYRSN DVTQSCSSGR STTIRVRCSP QKTVPGLSLP PGTCSDGTCD GCNHFHLES 420
AAACPLCSVA DYHAISSCV AGIQKTTYVW REPKLCSGGI SLPEQRVTIC KTIDFWLKV 480
ISAGTCTAIL LTVLTCTYFK KQKLEYKYS KLVNMATLKD CDLPAADESCA IMEGEDVEDD 540
LIPTSKSLF GKIKSFTSQ PAPVTISLSE DS 572

```

Seq ID NO: C431 Protein Sequence  
Protein Accession #: NP\_004855.1

45

50

```

1      11      21      31      41      51
|      |      |      |      |      |
MPGQELTVN GSQMLLVLLV LSWLPHGGAL SLAASRASFP GPSELHSED SRFRELKRY 60
EDLLTLRLAN QSWEDSNIDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLEASRL 120
HRAFLRLSPT ASRSVDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPQL 180
ELHLRPAAR GRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVIMC 240
IGACPSQFRA ANMHAQIKTS LHLKPDTEP APCCVPASYN PMVLIQKTTD GVSLQTYDDL 300
LAXDCHCI

```

Seq ID NO: C433 Protein Sequence  
Protein Accession #: NP\_443090.1

55

60

65

```

1      11      21      31      41      51
|      |      |      |      |      |
MEDPSGAREP RARPRERDPG RRPHPDQGR HTDRPRDRPG PRRKRSSDGN RRRDGRDPK 60
RDQERDGNRD RNRDRERERE RERDPDRGFR RDTHRDAGPR AGEHGVWEKP RQSRTRDGR 120
GLTWDAAPP GPAPWEAPEP PQPQKGDGPG RRRPESEPPS ERYLPSTPRP GREEVEYYS 180
EAEGLLECHK CYLCTGRAC CQMLEVLLNL LILACSSVSY SSTGGYTGIT SLGGIYYIQF 240
GGAYSGFDGA DGEKAQQLDV QFYQLKLPV TVAMACSGAL TALCCLFVAM GVLRVPWCEP 300
LLLVTGLLD MLIAGGYIPA LYFYHYLSA AYGSFVCKER QALYQSKGYS GFGCSFHGAD 360
IGAGIFAALG IUVFALGAVL AIKGYRKVRK LKEKPAEMFE F 401

```

Seq ID NO: C435 Protein Sequence  
Protein Accession #: Eos sequence

70

75

80

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPNWPGH DQDHVHIGQ 60
GKTLTLLTSSA TVYSIHISEG GKLVIKDHE PIVLRTRHIL IDNGGELHAG SALCPFGNF 120
TIILYGRADE GIQDPFYGL KYIGVGKGA LELHGQKLS WTLNKLTHP GGMAEGGYFF 180
ERSWGHGRVI VHVDPKSGT VIHSDRFDTY RSKKESERLV QYLNVPDGR ILSVAVNDEG 240
SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVMGNPSS SVEDHIEYHG HRGSAARVF 300
KLQTEHGEY FNVSLSENV QDVWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYVR FLGKFPVRPK LTVTIDTNVN 420
STILNLEDNV QSNKPGDTLV IASTDYSMYQ AEEFQVLPGR SCAPNQVKVA GKPMYLHIGE 480
EIDGVDMRAE VGLLSRNIIV MGEMEDKCYP YRNHCNFFD FDTFGGHIKF ALGFRAAHLE 540
GTGLKMGQQ LVGQYPIHFH LAGDVDERGG YDPPTYIRD LSIHHTFSRCV TVHGSNGLLI 600
KDVVGNSLIG RCFETEDGPE ERNTFDHCLG LLVKSGLTLP SDRDSKMKCM ITEDSYPGYI 660
FKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWPIFH HVPTGPSVGM YSPGYSEHIP 720

```

LGKFYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGSD	VWLDSCFRG	EAQEGFLLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLLK	LVTGSPFAH	VSLAHS				866

5

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein  
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1           1.       A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%  
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,  
4 thereby determining the presence or absence of said pathological cell.
- 1           2.       The method of Claim 1, wherein:  
2           a) said pathology is described in Table 1, including a cancer; and/or  
3           b) said biological sample comprises isolated nucleic acids.
- 1           3.       The method of Claim 1, wherein said biological sample is tissue from an organ  
2 which is affected by said pathology of Table 1, including a cancer.
- 1           4.       The method of Claim 2, wherein said nucleic acids are mRNA
- 1           5.       The method of Claim 2:  
2           a) further comprising a step of amplifying nucleic acids before said step of detecting  
3           said nucleic acid; or  
4           b) where said detecting is of a protein encoded by said nucleic acid.
- 1           6.       The method of Claim 1, wherein said nucleic acid comprises a sequence as  
2 described in Tables 2A-80.
- 1           7.       The method of Claim 2, wherein:  
2           a) said detecting step is carried out by:  
3           i) using a labeled nucleic acid probe;  
4           ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence  
5           as described in Tables 2A-80; or  
6           iii) detecting a polypeptide encoded by said nucleic acid; or  
7           b) said patient is:  
8           i) undergoing a therapeutic regimen to treat said pathology of Table 1; or  
9           ii) is suspected of having said pathology or cancer.
- 1           8.       An isolated nucleic acid molecule comprising a sequence as described in  
2 Tables 2A-80.

- 1           9.     The nucleic acid molecule of Claim 8, which is labeled.
- 1           10.    An expression vector comprising the nucleic acid of Claim 8.
- 1           11.    A host cell comprising the expression vector of Claim 10.
- 1           12.    An isolated polypeptide which is encoded by a nucleic acid molecule  
2 comprising a sequence as described in Tables 2A-80.
- 1           13.    An antibody that specifically binds a polypeptide of Claim 12.
- 1           14.    The antibody of Claim 13:  
2 a) conjugated to an effector component;  
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a  
4 cytotoxic chemical;  
5 c) which is an antibody fragment; or  
6 d) which is a humanized antibody.
- 1           15.    A method for specifically targeting a compound to a pathological cell in a  
2 patient, said method comprising administering to said patient an antibody of Claim 13,  
3 thereby providing said targetting.
- 1           16.    A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1           17.    The method of Claim 16, wherein:  
2 a) said antibody is conjugated to:  
3 i) an effector component; or  
4 ii) a fluorescent label; or  
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1           18.    A method for identifying a compound that modulates a pathology-associated  
2 polypeptide, said method comprising the steps of:

- 3 a) contacting said compound with a pathology-associated polypeptide, said  
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence  
5 at least 80% identical to a sequence as described in Tables 2A-80; and  
6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a  
3 cell isolated therefrom; and  
4 b) comparing the level of gene expression of a polynucleotide that selectively  
5 hybridizes to a sequence at least 80% identical to a sequence as described in  
6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said  
7 polynucleotide in a control cell or mammal, wherein a test compound that  
8 modulates said level of expression of the polynucleotide is a candidate for the  
9 treatment of said pathology.  
10

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
22 May 2003 (22.05.2003)

PCT

(10) International Publication Number  
**WO 2003/042661 A3**

(51) International Patent Classification<sup>7</sup>: **C12Q 1/68**,  
C07H 21/02, 21/04

(21) International Application Number:  
PCT/US2002/036810

(22) International Filing Date:  
13 November 2002 (13.11.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/350,666	13 November 2001 (13.11.2001)	US
60/332,464	21 November 2001 (21.11.2001)	US
60/334,393	29 November 2001 (29.11.2001)	US
60/335,394	3 December 2001 (03.12.2001)	US
60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
60/355,250	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
60/409,450	9 September 2002 (09.09.2002)	US

(71) Applicant (for all designated States except US): **PRO-TEIN DESIGN LABS, INC.** [US/US]; 34801 Campus Drive, Fremont, CA 94555 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **AFAR, Daniel** [CA/US]; 435 Visitation Avenue, Brisbane, CA 94005 (US). **AZIZ, Natasha** [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). **GINSBURG, Wendy, M.** [US/US]; 655 Page Street, San Francisco, CA 94117 (US). **GISH, Kurt, C.** [US/US]; 37 Artuna Avenue, Piedmont, CA 94611 (US). **GLYNNE, Richard** [GB/US]; 2691 Palomino Circle, La Jolla, CA 92037 (US). **HEVEZI, Peter, A.** [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). **MACK, David, H.** [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **MURRAY,**

**Richard** [US/US]; 22643 Woodridge Court, Cupertino, CA 95014 (US). **WATSON, Susan, R.** [GB/US]; 805 Balra Drive, El Cerrito, CA 94530 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

(74) Agent: **KUNG, Viola, T.**; Howrey Simon Arnold White, LLP, Box 34, 301 Ravenswood Avenue, Menlo Park, CA 94025 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv)) for US only

Published:

— with international search report  
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:  
28 October 2004

(15) Information about Correction:

Previous Correction:

see PCT Gazette No. 42/2003 of 16 October 2003, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.

WO 2003/042661 A3

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : C12Q 1/68; C07H 21/02, 21/04

US CL : 435/6; 536/23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
WEST, PubMed**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SATO, H. et al., Cloning and Expression of a Plasma Membrane Cystine/Glutamate Exchange Transporter Composed of Two Distinct Proteins, J. Biol. Chem. 23 April 1999, Vol. 247, No. 17, pp. 11455-11458.	1-7
A	KIM, J. Y. et al., Human cystine/glutamate transporter: cDNA cloning and upregulation by oxidative stress in glioma cells, B.B. Acta. June 2001, Vol. 1512, pp. 335-344.	1-7

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.**\* Special categories of cited documents:****"A"** document defining the general state of the art which is not considered to be of particular relevance**"B"** earlier application or patent published on or after the international filing date**"L"** document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)**"O"** document referring to an oral disclosure, use, exhibition or other means**"P"** document published prior to the international filing date but later than the priority date claimed**"T"**

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

**"X"**

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

**"Y"**

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

**"&"**

document member of the same patent family

Date of the actual completion of the international search

04 August 2004(04.08.2004)

Date of mailing of the international search report

**13 SEP 2004**

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, Virginia 22313-1450

Facsimile No. (703) 872-9306

Authorized officer

Teresa Strzelecka

Telephone No. (571) 272-1600



# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO: 19

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING**

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, drawn to a special technical feature of a method for determining presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

Group II, claim(s) 8-11, drawn to a special technical feature of an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, expression vector comprising the nucleic acid and a host cell comprising the expression vector.

Group III, claim(s) 12, drawn to a special technical feature of an isolated polypeptide which is encoded by an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

Group IV, claim(s) 13, 14, drawn to a special technical feature of an antibody which specifically binds to polypeptide of claim 12.

Group V, claim(s) 15, drawn to a special technical feature of a method for specifically targeting a compound to a pathological cell in a patient, comprising administering to a patient an antibody of claim 13.

Group VI, claim(s) 16, 17, drawn to a special technical feature of a method for determining the presence or absence of a pathological cell in a patient, comprising contacting a biological sample with an antibody of claim 13.

Group VII, claim(s) 18, drawn to a special technical feature of a method for identifying a compound that modulates a pathology-associated polypeptide by contacting the compound with a pathology-associated polypeptide encoded by a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 and determining the functional effect of the compound on the polypeptide.

Group VIII, claim(s) 19, drawn to a special technical feature of a drug screening assay comprising the steps of: administering a test compound to a mammal having pathology of Table 1 or a cell isolated therefrom; comparing the level of gene expression of a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal.

The inventions listed as Groups I-VIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: claim 8 is anticipated by a sequence with accession No. BE440042 (Table 2A, first entry) (July 25, 2000), therefore there is no contribution of claim 8 over prior art.

## CORRECTED VERSION

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
22 May 2003 (22.05.2003)

PCT

(10) International Publication Number  
**WO 03/042661 A2**

(51) International Patent Classification<sup>7</sup>: **G01N**  
(21) International Application Number: PCT/US02/36810  
(22) International Filing Date:  
13 November 2002 (13.11.2002)

Richard [US/US]; 22643 Woodridge Court, Cupertino, CA 95014 (US). WATSON, Susan, R. [GB/US]; 805 Balra Drive, El Cerrito, CA 94530 (US). WILSON, Keith, E. [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). ZLOTNIK, Albert [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

(25) Filing Language: English

(26) Publication Language: English

(74) Agents: BASTIAN, Kevin, L. et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111 (US).

## (30) Priority Data:

60/350,666	13 November 2001 (13.11.2001)	US
60/332,464	21 November 2001 (21.11.2001)	US
60/334,393	29 November 2001 (29.11.2001)	US
60/335,394	3 December 2001 (03.12.2001)	US
60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
60/355,250	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
60/409,450	9 September 2002 (09.09.2002)	US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

## Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv)) for US only

## Published:

— without international search report and to be republished upon receipt of that report

(71) Applicant (*for all designated States except US*): EOS BIOTECHNOLOGY, INC. [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).

## (72) Inventors; and

(75) Inventors/Applicants (*for US only*): AFAR, Daniel [CA/US]; 435 Visitacion Avenue, Brisbane, CA 94005 (US). AZIZ, Natasha [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). GINSBURG, Wendy, M. [US/US]; 655 Page Street, San Francisco, CA 94117 (US). GISH, Kurt, C. [US/US]; 37 Artuna Avenue, Piedmont, CA 94611 (US). GLYNNE, Richard [GB/US]; 2691 Palomino Circle, La Jolla, CA 92037 (US). HEVEZI, Peter, A. [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). MACK, David, H. [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). MURRAY,

## (48) Date of publication of this corrected version:

16 October 2003

## (15) Information about Correction:

see PCT Gazette No. 42/2003 of 16 October 2003, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



WO 03/042661 A2